



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 168695

TO: Patricia Duffy
Location: rem/3B05/3C18
Art Unit: 1645
Wednesday, July 13, 2005
Case Serial Number: 10/063546

From: Toby Port
Location: Biotech-Chem Library
REM-1A59
Phone: 571-272-2523
toby.port@uspto.gov

Search Notes

Examiner Duffy,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Toby Port
X22523

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Duffy, Patricia

From: Duffy, Patricia
Sent: Sunday, July 10, 2005 10:27 AM
To: STIC-Biotech/ChemLib
Subject: SPDI search

10/063,546

SEQ ID NO:38 and oligomers thereof.
standard spdi output.

Patricia A. Duffy, Ph.D.
Art Unit 1645
Remsen 3B05; Mailbox 3C18
571-272-0855

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STIC-Biotech/ChemLib

158696

mg

From: Duffy, Patricia
Sent: Sunday, July 10, 2005 10:27 AM
To: STIC-Biotech/ChemLib
Subject: SPDI search

10/063,546

SEQ ID NO:38 and oligomers thereof.
standard spdi output.

Patricia A. Duffy, Ph.D.
Art Unit 1645
Remsen 3B05; Mailbox 3C18
571-272-0855

RECEIVED
JUL 11 2005
STIC

Needs wrap.spdi

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2-_____
Date Searcher Picked up: _____
Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA#: _____ AA#: _____
Interference: _____ SPDI: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure#: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

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GenCore version 5.1.6
OM protein - protein search, using sw model
Run on: July 12, 2005, 17:08:52 / Search time 168 Seconds
(without alignments)
1657,544 Million cell updates/sec

Title: US-10-063-546-38
Perfect score: 3945
Sequence: 1 MEGACTQTGLTFLQLLLS.....LSTAFKVLPEFKDMERNMK 720
Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
Searched: 2105692 seqs, 386760381 residues
Total number of hits satisfying chosen parameters: 2105692
Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database: A_GeneSeq_16Dec04:*
1: geneseqp19608:*
2: geneseqp19908:*
3: geneseqp20008:*
4: geneseqp20018:*
5: geneseqp20028:*
6: geneseqp20038:*
7: geneseqp20038:*
8: geneseqp20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match	Length	DB	ID	Description
RESULT 1						
ID	AAV6695	standard;	protein;	720	AA.	DE Membrane-bound protein PRO1344.
PN	W09963088-A2.					
PD	09-DEC-1999.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 3945;	DB 3;	Length 720;		
Best Local Similarity	100.0%;	Pred. No. 1.5e-204;				
RESULT 2						
ID	AAU29108	standard;	protein;	720	AA.	DE Human PRO polypeptide sequence #85.
PN	W0200168848-A2.					
PD	20-SEP-2001.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 3945;	DB 4;	Length 720;		
Best Local Similarity	100.0%;	Pred. No. 1.5e-204;				
RESULT 3						
ID	AA87544	standard;	protein;	720	AA.	DE Human PRO1344.
PN	W0200116318-A2.					
PD	08-MAR-2001.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 3945;	DB 4;	Length 720;		
Best Local Similarity	100.0%;	Pred. No. 1.5e-204;				
RESULT 4						
ID	AA65218	standard;	protein;	720	AA.	DE Human PRO1344 (UNQ659) protein sequence SEQ ID NO:231.
PN	W0200073454-A1.					
PD	07-DEC-2000.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 3945;	DB 4;	Length 720;		
Best Local Similarity	100.0%;	Pred. No. 1.5e-204;				
RESULT 5						
ID	AA695869	standard;	protein;	720	AA.	DE Human secreted/transmembrane protein PRO1344.
PN	US2002119130-A1.					
PD	29-AUG-2002.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 3945;	DB 5;	Length 720;		
Best Local Similarity	100.0%;	Pred. No. 1.5e-204;				
RESULT 6						
ID	ABU58484	standard;	protein;	720	AA.	DE Novel human secreted and transmembrane protein PRO1344.
PN	US2003036147-A1.					
PD	13-FEB-2003.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 3945;	DB 6;	Length 720;		
Best Local Similarity	100.0%;	Pred. No. 1.5e-204;				
RESULT 7						
ID	ABU8032	standard;	protein;	720	AA.	DE Novel human secreted and transmembrane protein PRO1344.
PN	US2003032127-A1.					
PD	13-FEB-2003.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 3945;	DB 6;	Length 720;		
Best Local Similarity	100.0%;	Pred. No. 1.5e-204;				
RESULT 8						
ID	ABU84347	standard;	protein;	720	AA.	DE Human secreted/transmembrane protein (PRO) #85.
PN	US2003032112-A1.					
PD	13-FEB-2003.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 3945;	DB 6;	Length 720;		
Best Local Similarity	100.0%;	Pred. No. 1.5e-204;				
RESULT 9						
ID	ABR6221	standard;	protein;	720	AA.	DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN	US2003027278-A1.					
PD	06-FEB-2003.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 3945;	DB 6;	Length 720;		
Best Local Similarity	100.0%;	Pred. No. 1.5e-204;				
RESULT 10						
ID	ABR65611	standard;	protein;	720	AA.	DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN	US2003036159-A1.					
PD	20-FEB-2003.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 3945;	DB 6;	Length 720;		
Best Local Similarity	100.0%;	Pred. No. 1.5e-204;				
RESULT 11						
ID	ABU9551	standard;	protein;	720	AA.	DE Human secreted/transmembrane protein (PRO) #85.
PN	US2003040070-A1.					
PD	27-FEB-2003.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 3945;	DB 6;	Length 720;		
Best Local Similarity	100.0%;	Pred. No. 1.5e-204;				
RESULT 12						
ID	ABU58033	standard;	protein;	720	AA.	DE Human PRO polypeptide #65.
PN	US2003027163-A1.					
PD	06-FEB-2003.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 3945;	DB 6;	Length 720;		
Best Local Similarity	100.0%;	Pred. No. 1.5e-204;				
RESULT 13						
ID	ABU59111	standard;	protein;	720	AA.	DE Novel human secreted or transmembrane protein PRO1344.
PN	US2002132252-A1.					
PD	19-SEP-2002.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 3945;	DB 6;	Length 720;		
Best Local Similarity	100.0%;	Pred. No. 1.5e-204;				
RESULT 14						
ID	ABU82623	standard;	protein;	720	AA.	DE Human secreted/transmembrane protein PRO1344.
PN	US2003032023-A1.					
PD	13-FEB-2003.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 3945;	DB 6;	Length 720;		
Best Local Similarity	100.0%;	Pred. No. 1.5e-204;				
RESULT 15						
ID	ABU82790	standard;	protein;	720	AA.	DE Human PRO polypeptide #85.
PN	US2003032113-A1.					
PD	13-FEB-2003.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 3945;	DB 6;	Length 720;		
Best Local Similarity	100.0%;	Pred. No. 1.5e-204;				
RESULT 16						
ID	ABU89911	standard;	protein;	720	AA.	DE Novel human secreted and transmembrane protein PRO1344.
PN	US2003036147-A1.					
PD	13-FEB-2003.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 3945;	DB 6;	Length 720;		
Best Local Similarity	100.0%;	Pred. No. 1.5e-204;				

PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 17
ID ABR68160 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027264-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 18
ID ABU60542 standard; protein; 720 AA.
DE Human secreted/transmembrane protein. #94.
PN US2002160384-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 19
ID ABU96213 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003036144-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 20
ID ABU92644 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036149-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 21
ID ABO08721 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003044923-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 22
ID ABO02773 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003040062-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 23
ID ABR74927 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040056-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 24
ID ABR94689 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003044926-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 25
ID ABU13924 standard; protein; 720 AA.
DE Human PRO1344 polypeptide.
PN US2002103125-A1.
PD 01-MUG-2002.
PA (GETH) GENENTECH LTD.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 26
ID ABU85662 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003036140-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 27
ID ABU98822 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003013153-A1.
PD 16-JAN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 28
ID ABU98037 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003017544-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 29
ID ABU91743 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US200302277-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 30
ID ABU89436 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003036141-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 31
ID ABU86277 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 32
ID ABU67490 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 33
ID ABU80518 standard; protein; 720 AA.
DE Human PRO protein #85.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 34
ID ABU72509 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003003531-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 35
ID ABU90894 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003018173-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 36
ID ABO33953 standard; protein; 720 AA.

DE Human secreted/transmembrane protein PRO1344.
PN US200309013-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 37
ID ABR99436 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040063-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 38
ID ABR98826 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 39
ID ABO16349 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003027267-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 40
ID ABR92449 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036160-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 41
ID ABO18890 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003044925-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 42
ID ABR78311 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054474-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 43
ID ABO171970 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003018183-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 44
ID ABO85047 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003032114-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 45
ID ABO00186 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 46
ID ABO1518 standard; protein; 720 AA.

DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 47
ID ABO02163 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 48
ID ABO8737 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003036133-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 49
ID ABO83432 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036134-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 50
ID ABO06233 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003022294-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 51
ID ABR5269 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 52
ID ABO09331 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 53
ID ABO19195 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 54
ID ABO1213 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 55
ID ABR6631 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 56
ID ABO16044 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003040060-A1.

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PD 27-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 57
ID ABO13750 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US200304916-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 58
ID ABO171524 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344.
PN US2003013855-A1.
PD 16-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 59
ID ABO5653 standard; protein; 720 AA.
DE Human secreted/transmembrane protein, SEQ ID 170.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 60
ID ABO07501 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 61
ID ABO0368 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 62
ID ABO67136 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 63
ID ABO15739 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 64
ID ABO56020 standard; protein; 720 AA.
DE Human secreted/transmembrane protein, PRO1344.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 65
ID ABO72305 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2002182638-A1.
PD 05-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 66
ID ABO65348 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003032102-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 67
ID ABO95293 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 68
ID ABO71196 standard; protein; 720 AA.
DE Human PRO1344 protein.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 69
ID ABO07806 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 70
ID ABO70047 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 71
ID ABO69380 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 72
ID ABO01521 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003008153-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 73
ID ABO81323 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 74
ID ABO60120 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003032137-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 75
ID ABO90978 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003018168-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 76
ID ABO67855 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027269-A1.
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PD 06-FEB-2003. 100.0%; Score 3945; DB 6; Length 720;
Query Match
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 77
ID ABR65243 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US200302726-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 78
ID ABR6465 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US200302727-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 79
ID ABR71877 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 80
ID ABUS9258 standard; protein; 720 AA.
DE Human secreted/transmembrane protein, #94.
PN US2003027162-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 81
ID ABUS5357 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 82
ID ABUS9047 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 83
ID ABUS3127 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003032105-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 84
ID ABUS94983 standard; protein; 720 AA.
DE Human secreted and transmembrane protein PRO1344.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 85
ID ABUS9531 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 86
ID ABUS84042 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;

Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 87
ID ABUS9693 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 88
ID ABO25955 standard; protein; 720 AA.
DE Human PRO1344 polypeptide.
PN US2002127576-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 89
ID ABR64938 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 90
ID ABO27299 standard; protein; 720 AA.
DE Human secreted/transmembrane polypeptide PRO1344.
PN US2003009012-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 91
ID ABR68770 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 92
ID ABO06586 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 93
ID ABR99131 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040068-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 94
ID ABUS7015 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003027280-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 95
ID ABUS5967 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003022300-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 96
ID ABUS2254 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003036136-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;

Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 97
ID ABU87265 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003036138-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 98
ID ABU83737 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003032109-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 99
ID ABO08111 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 100
ID ABU92494 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003045684-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 101
ID ABU81822 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 102
ID ABU65986 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 103
ID ABU81164 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344.
PN US2003027212-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 104
ID ABR59815 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 105
ID ABU94003 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003036155-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 106
ID ABU99856 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003022396-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;

RESULT 107
ID ABR66526 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 108
ID ABR90944 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 109
ID ABO5379 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003027986-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 110
ID ABU58964 standard; protein; 720 AA.
DE Human secreted/transmembrane protein, #94.
PN US2002142961-A1.
PD 03-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 111
ID ABU94371 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 112
ID ABU79253 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 113
ID ABU86582 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 114
ID ABU86887 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 115
ID ABU94676 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 116
ID ABO04603 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003032107-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;

RESULT 117
ID ABR70352 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 118
ID ABR92342 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003023187-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 119
ID ABR98517 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003022301-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 120
ID ABR65916 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036165-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 121
ID ABR64633 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036165-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 122
ID ABR9407 standard; protein; 720 AA.
DE Novel human secreted or transmembrane protein PRO1109.
PN US2003027985-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 123
ID ABR92949 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 124
ID ABR92949 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 125
ID ABR95908 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 126
ID ABR9128 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 127
ID ABR90221 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003036153-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 128
ID ABR09636 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 129
ID ABR010908 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 130
ID ABR70962 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040069-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 131
ID ABR98281 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2002183493-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 132
ID ABR87570 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003022293-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 133
ID ABR91438 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 134
ID ABR9286 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003036634-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 135
ID ABR84652 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 136
ID ABR69742 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 137
ID ABR80119 standard; protein; 720 AA.
DE Human PRO protein #85.

PN US2003036139-A1.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
Pred. No. 1.5e-204;
RESULT 138
ID AB082493 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2002183494-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
Pred. No. 1.5e-204;
RESULT 139
ID AB092173 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003017476-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
Pred. No. 1.5e-204;
RESULT 140
ID AB093388 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003017541-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
Pred. No. 1.5e-204;
RESULT 141
ID AB009941 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
Pred. No. 1.5e-204;
RESULT 142
ID AB009026 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036152-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
Pred. No. 1.5e-204;
RESULT 143
ID AB096457 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003027993-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
Pred. No. 1.5e-204;
RESULT 144
ID AB010879 standard; protein; 720 AA.
DE Human PRO polypeptide #65.
PN US2002123463-A1.
PD 05-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
Pred. No. 1.5e-204;
RESULT 145
ID AB010594 standard; protein; 720 AA.
DE Human secreted/transmembrane protein #85.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
Pred. No. 1.5e-204;
RESULT 146
ID AB081631 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2002177164-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
Pred. No. 1.5e-204;
RESULT 147

ID AB072127 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003023042-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
Pred. No. 1.5e-204;
RESULT 148
ID AB095603 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003032115-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
Pred. No. 1.5e-204;
RESULT 149
ID AB096812 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003032140-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
Pred. No. 1.5e-204;
RESULT 150
ID AB070657 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
Pred. No. 1.5e-204;
RESULT 151
ID AB005008 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
Pred. No. 1.5e-204;
RESULT 152
ID AB008416 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003044922-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
Pred. No. 1.5e-204;
RESULT 153
ID AB088570 standard; protein; 720 AA.
DE Human secreted and transmembrane polypeptide PRO1344.
PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
Pred. No. 1.5e-204;
RESULT 154
ID AB034084 standard; protein; 720 AA.
DE Human PRO1344 polypeptide.
PN US2003017981-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
Pred. No. 1.5e-204;
RESULT 155
ID AB005623 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003032118-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
Pred. No. 1.5e-204;
RESULT 156
ID AB074012 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036135-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
Pred. No. 1.5e-204;
RESULT 157

RESULT 157
ID ABR95604 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 158
ID ABR80901 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 159
ID ABR81206 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 160
ID ABM00902 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 161
ID ABR88504 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 162
ID ABM77325 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 163
ID ABO28809 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068685-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 164
ID ABO31554 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 165
ID ABM07971 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 166
ID ABO40451 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068682-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 167
ID ABO35876 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 168
ID ABO44015 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 169
ID ADA77922 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 170
ID ABM24810 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104539-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 171
ID ABO03078 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036131-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 172
ID ABR90334 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040075-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 173
ID ABM17248 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 174
ID ABR94994 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003044930-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 175
ID ABR95299 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.

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Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 176
ID ADB17095 standard; protein; 720 AA.
DE Human transmembrane PRO polypeptide (SeqID 38).
PN US2003050462-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 177
ID ABO21537 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 178
ID ABR97801 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064452-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 179
ID ABR87589 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 180
ID ABM77630 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 181
ID ABM27860 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064440-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 182
ID ABM06141 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 183
ID ABM03647 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068722-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 184
ID ABM35098 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 185
ID ABM26335 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104549-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 186
ID ABO48117 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049749-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 187
ID ABR92859 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064462-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 188
ID ABO24620 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003065159-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 189
ID ADA37742 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003008297-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 190
ID ABM11631 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064447-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 191
ID ABM02732 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073184-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 192
ID ABM16028 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064463-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 193
ID ABO27589 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 194
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ID ABM29080 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 195
ID ABM07056 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068699-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 196
ID ABM21150 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068707-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 197
ID ABM09496 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073175-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 198
ID ABO41366 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068695-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 199
ID ABO36181 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003068703-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 200
ID ABO43710 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003068732-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 201
ID ABM76410 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003082717-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 202
ID ABM76106 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104548-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 203
ID ABM25725 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.

PN US2003104542-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 204
ID ABM26030 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104543-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 205
ID ADA21428 standard; protein; 720 AA.
DE Human secreted/transmembrane polypeptide PRO1344.
PN US2003054404-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 206
ID ABO03383 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036127-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 207
ID ABO02468 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003040061-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 208
ID ABO44257 standard; protein; 720 AA.
DE Human secreted/transmembrane polypeptide PRO 1344.
PN US2003018172-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 209
ID ABR90639 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036130-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 210
ID ABR73707 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054468-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 211
ID ABO16959 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 212
ID ABR94384 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003044917-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 213
ID ABR75891 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.

PN US2003044829-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 214
ID ABR71267 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003059880-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 215
ID ABR93164 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064465-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 216
ID ABR93469 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054478-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 217
ID ADA10215 standard; protein; 720 AA.
DE Human secreted/transmembrane protein, PRO1344.
PN US2003059831-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 218
ID ABR87894 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068718-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 219
ID ABO27894 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003064454-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 220
ID ABO30029 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003064461-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 221
ID ABO33238 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 222
ID ABO4926 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 223
ID ABO0886 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 224
ID ABO36486 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 225
ID ABO35571 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003068758-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 226
ID ABO39536 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 227
ID ABO10411 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 228
ID ABO11936 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 229
ID ABO52082 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 230
ID ABO52387 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 231
ID ADA19900 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003069394-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;

Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 232
ID ABO23705 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003032134-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 233
ID ADB17283 standard; protein; 720 AA.
DE Human transmembrane PRO polypeptide (SegID 38).
PN US2003050465-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 234
ID ADH17759 standard; protein; 720 AA.
DE Human PRO1344 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 235
ID ABR97191 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054481-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 236
ID ABR86979 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049778-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 237
ID ABM11021 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049782-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 238
ID ABM28165 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054476-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 239
ID ABO32164 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068733-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 240
ID ABM15291 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068692-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 241
ID ABM06446 standard; protein; 720 AA.

DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068709-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 242
ID ABM04257 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068716-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 243
ID ABM22370 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068740-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 244
ID ABM07666 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068751-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 245
ID ABO40756 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068684-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 246
ID ABM35403 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073179-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 247
ID ABM33166 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003087374-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 248
ID ABO52692 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003048773-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 249
ID ABO50252 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049777-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 250
ID ABM9246 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003040055-A1.

PD 27-FEB-2003. 100.0%; Score 3945; DB 6; Length 720;
Query Match
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 251
ID ABO04298 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036164-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 252
ID ABO05928 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003040074-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 253
ID ABM18468 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 254
ID ADA27867 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003054359-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 255
ID AB937496 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 256
ID ABR80596 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 257
ID ABM01207 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 258
ID ABR88809 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073169-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 259
ID ABM13461 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 260
ID ABM20845 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068711-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 261
ID ABO41976 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049745-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 262
ID ABO42586 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049751-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 263
ID ABM10106 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003067478-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 264
ID ABO38621 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068773-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 265
ID ABM32861 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073185-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 266
ID ABM22675 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US200308773-A1.
PD 08-MAY-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 267
ID ABM74886 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003096353-A1.
PD 22-MAY-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 268
ID ADV79714 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003073173-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 269
ID ABR96276 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054458-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;

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Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 270
ID ABM02427 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US200305986-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 271
ID ABR86369 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049758-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 272
ID ABR8674 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 273
ID ABM1638 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064448-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 274
ID ABM29690 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064456-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 275
ID ABO29114 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068693-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 276
ID ABM23895 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 277
ID ABM23285 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 278
ID ABM22065 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 279
ID ABO22147 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003054477-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 280
ID ABM28470 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003082715-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 281
ID ABM28775 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003082716-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 282
ID ABM66419 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068737-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 283
ID ABM75801 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 284
ID ABM34081 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003066359-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 285
ID ABM34386 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003100061-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 286
ID ABO20317 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003032125-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 287
ID ABO21232 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003054454-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 288
ID ABO22147 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003054477-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
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PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 289
ID ADA20072 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003055222-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 290
ID ABO34185 standard; protein; 720 AA.
DE Human secreted/transmembrane polypeptide PRO 1344.
PN US2003060601-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 291
ID ABR96581 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 292
ID ADA94447 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003059832-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 293
ID ABR85759 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 294
ID ABR9741 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 295
ID ABM00597 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073172-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 296
ID ABM00292 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073172-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 297
ID ABO29724 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 298

ID ABM23590 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 299
ID ABM29385 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068679-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 300
ID ABO38316 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 301
ID ABO45616 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 302
ID ABM20540 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 303
ID ADA81441 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 304
ID ABO16654 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003027276-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 305
ID ABO18280 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003044920-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 306
ID ABO22707 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003027265-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 307
ID ABO23012 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003054461-A1.
PD 20-MAR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 308
ID ABR92554 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US200306446-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 309
ID ABR81511 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 310
ID ABM77935 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 311
ID ABR89724 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073171-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 312
ID ABM2640 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003032121-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 313
ID ABM13766 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 314
ID ABO28504 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003064460-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 315
ID ABO30334 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 316
ID ABM07361 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;

RESULT 317
ID ABM03952 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 318
ID ABO37096 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 319
ID ABO41671 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 320
ID ABO35266 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 321
ID ABM25115 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104540-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 322
ID ABO47507 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 323
ID ABO47812 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 324
ID ABO48422 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 325
ID ABO51472 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 326
ID ABO51777 standard; protein; 720 AA.

DE Human PRO polypeptide #85.
PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 327
ID ABO50557 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 328
ID ABR79681 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040059-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 329
ID ABM16943 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040078-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 330
ID ABO17975 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003044918-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 331
ID ABO20927 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003032132-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 332
ID ABR96686 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054462-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 333
ID ADA38672 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003059780-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 334
ID ABM12241 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064445-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 335
ID ABM16333 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064449-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;

Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 336
ID ABM24200 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064441-A1.
PD 03-APR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 337
ID ABM14681 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068696-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 338
ID ABM04562 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 339
ID ABM06751 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068730-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 340
ID ABM09191 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073174-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 341
ID ABO39231 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068775-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 342
ID ABM75496 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104545-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 343
ID ABM25420 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104541-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 344
ID ABM19930 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104554-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 345
ID ABO46636 standard; protein; 720 AA.
DE Human PRO polypeptide #85.

PN US2003049762-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 346
ID ABO47141 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 347
ID ADA83239 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 348
ID ABR71572 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003032133-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 349
ID ABR72182 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003032136-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 350
ID ABR98521 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036129-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 351
ID ABO06891 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003040053-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 352
ID ABR64644 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040057-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 353
ID ABR73402 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054467-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 354
ID ABR76496 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003044932-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 355
ID ABR73097 standard; protein; 720 AA.

DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027270-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 356
ID ABM18163 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 357
ID ABO20622 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003032126-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 358
ID ABO25365 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 359
ID ABO25670 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 360
ID ABR94079 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 361
ID ADA92793 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003060407-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 362
ID ABR79986 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049738-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 363
ID ABM13326 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064469-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 364
ID ABO32933 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;

Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 365
ID ABO30639 standard; protein; 720 AA.
DE Human secreted/cranmembrane protein (PRO) #85.
PN US2003064466-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 366
ID ABO30944 standard; protein; 720 AA.
DE Human secreted/cranmembrane protein (PRO) #85.
PN US2003064468-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 367
ID ABM27250 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068760-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 368
ID ABM29995 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068769-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 369
ID ABM05531 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003045700-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 370
ID ABM15596 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068698-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 371
ID ABM08581 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068759-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 372
ID ABO42281 standard; protein; 720 AA.
DE Human secreted/cranmembrane protein (PRO) #85.
PN US2003049748-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 373
ID ABO38011 standard; protein; 720 AA.
DE Human secreted/cranmembrane protein (PRO) #85.
PN US2003068765-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;

RESULT 374
ID ABO45921 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003049754-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 375
ID ABM66724 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068688-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 376
ID ADB20282 standard; protein; 720 AA.
DE Human secreted/cranmembrane protein (PRO) #85.
PN US2003082767-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 377
ID ABM19625 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104552-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 378
ID ABO49337 standard; protein; 720 AA.
DE Human secreted/cranmembrane protein (PRO) #85.
PN US2003049774-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 379
ID ABO49642 standard; protein; 720 AA.
DE Human secreted/cranmembrane protein (PRO) #85.
PN US2003049775-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 380
ID ADA78534 standard; protein; 720 AA.
DE Human secreted/cranmembrane protein (PRO) #85.
PN US2003049775-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 381
ID ABR88199 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068720-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 382
ID ADA00369 standard; protein; 720 AA.
DE Human secreted/cranmembrane polypeptide PRO 1344.
PN US2003027992-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 383
ID ABM26945 standard; protein; 720 AA.

DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068739-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 384
ID ABO03442 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068763-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 385
ID ABO39841 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068689-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 386
ID ABO49947 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049776-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 387
ID ABO50862 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049780-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 388
ID ABO05318 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036126-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 389
ID ABR74622 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003044924-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 390
ID ABR77101 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003044927-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 391
ID ABR17858 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040072-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 392
ID ABR95909 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040073-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;

RESULT 393
ID ABO21842 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003054475-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 394
ID ABO20012 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003032124-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 395
ID ABO24315 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003064467-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 396
ID ABR86064 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049759-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 397
ID ABR10716 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064455-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 398
ID ABR76715 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054465-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 399
ID ABR89419 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073170-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 400
ID ABR12546 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073176-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 401
ID ABR05836 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068717-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 402
ID ABO34961 standard; protein; 720 AA.
DE Human PRO polypeptide #85.

PN US2003068728-A1.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 403
ID ABR03037 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068764-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 404
ID ABR19015 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104550-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 405
ID ABR19320 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104551-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 406
ID ABO46531 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003049761-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 407
ID ABO49032 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049757-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 408
ID ABR69075 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027273-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 409
ID ABR89114 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036119-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 410
ID ABR72487 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036120-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 411
ID ABR74317 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036161-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;

Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 412
ID ABO18585 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003044921-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 413
ID ABR80291 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049739-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 414
ID ABR01512 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003059882-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 415
ID ABR02122 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003059884-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 416
ID ABR87284 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068687-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 417
ID ABR12851 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073186-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 418
ID ABR30605 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064443-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 419
ID ABR24505 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064444-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 420
ID ABR029419 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068697-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 421

ID	ABOJ1249 standard; protein; 720 AA.
DE	Human secreted/transmembrane protein (PRO) #85.
PN	US2003068710-A1.
PD	10-APR-2003.
PA	(GETH) GENENTECH INC.
Query Match	100.0%; Score 3945; DB 7;
Beet Local Similarity	100.0%; Pred. No. 1.5e-204; Length 720;
RESULT 422	
ID	ABM14376 standard; protein; 720 AA.
DE	Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN	US2003068686-A1.
PD	10-APR-2003.
PA	(GETH) GENENTECH INC.
Query Match	100.0%; Score 3945; DB 7;
Beet Local Similarity	100.0%; Pred. No. 1.5e-204; Length 720;
RESULT 423	
ID	ABM09801 standard; protein; 720 AA.
DE	Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN	US2003073178-A1.
PD	17-APR-2003.
PA	(GETH) GENENTECH INC.
Query Match	100.0%; Score 3945; DB 7;
Beet Local Similarity	100.0%; Pred. No. 1.5e-204; Length 720;
RESULT 424	
ID	ABO38926 standard; protein; 720 AA.
DE	Human secreted/transmembrane protein (PRO) #85.
PN	US2003068774-A1.
PD	10-APR-2003.
PA	(GETH) GENENTECH INC.
Query Match	100.0%; Score 3945; DB 7;
Beet Local Similarity	100.0%; Pred. No. 1.5e-204; Length 720;
RESULT 425	
ID	ABM34691 standard; protein; 720 AA.
DE	Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN	US2003104538-A1.
PD	05-JUN-2003.
PA	
Query Match	100.0%; Score 3945; DB 7;
Beet Local Similarity	100.0%; Pred. No. 1.5e-204; Length 720;
RESULT 426	
ID	ABO51167 standard; protein; 720 AA.
DE	Human secreted/transmembrane protein (PRO) #85.
PN	US2003049781-A1.
PD	13-MAR-2003.
PA	(GETH) GENENTECH INC.
Query Match	100.0%; Score 3945; DB 7;
Beet Local Similarity	100.0%; Pred. No. 1.5e-204; Length 720;
RESULT 427	
ID	ABO03993 standard; protein; 720 AA.
DE	Human secreted/transmembrane protein (PRO) #85.
PN	US2003036158-A1.
PD	20-FEB-2003.
PA	
Query Match	100.0%; Score 3945; DB 7;
Beet Local Similarity	100.0%; Pred. No. 1.5e-204; Length 720;
RESULT 428	
ID	ABOI0463 standard; protein; 720 AA.
DE	Human PRO polypeptide #85.
PN	US2003044806-A1.
PD	06-MAR-2003.
PA	
Query Match	100.0%; Score 3945; DB 7;
Beet Local Similarity	100.0%; Pred. No. 1.5e-204; Length 720;
RESULT 429	
ID	ABO53170 standard; protein; 720 AA.
DE	Human secreted/transmembrane protein PRO1344.
PN	US2003044806-A1.
PD	06-MAR-2003.
PA	
Query Match	100.0%; Score 3945; DB 7;
Beet Local Similarity	100.0%; Pred. No. 1.5e-204; Length 720;
RESULT 430	
ID	ABR77706 standard; protein; 720 AA.
DE	Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN	US2003040067-A1.
PD	27-FEB-2003.
PA	
Query Match	100.0%; Score 3945; DB 7;
Beet Local Similarity	100.0%; Pred. No. 1.5e-204; Length 720;

Beet Local Similarity	100.0%;	Pred. No.1.5e-204;
RESULT 431		
ID ABR78916 standard; protein; 720 AA.		
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.		
PN US2003054456-A1.		
PD 20-MAR-2003.		
Query Match	100.0%;	Score 3945; DB 7; Length 720;
Beet Local Similarity	100.0%;	Pred. No.1.5e-204;
RESULT 432		
ID ABO24010 standard; protein; 720 AA.		
DE Human secreted/transmembrane protein (PRO) #85.		
PN US2003054482-A1.		
PD 20-MAR-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 3945; DB 7; Length 720;
Beet Local Similarity	100.0%;	Pred. No.1.5e-204;
RESULT 433		
ID ABR33774 standard; protein; 720 AA.		
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.		
PN US2003054457-A1.		
PD 20-MAR-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 3945; DB 7; Length 720;
Beet Local Similarity	100.0%;	Pred. No.1.5e-204;
RESULT 434		
ID ABO1817 standard; protein; 720 AA.		
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.		
PN US2003059883-A1.		
PD 27-MAR-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 3945; DB 7; Length 720;
Beet Local Similarity	100.0%;	Pred. No.1.5e-204;
RESULT 435		
ID ABR78240 standard; protein; 720 AA.		
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.		
PN US2003049764-A1.		
PD 13-MAR-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 3945; DB 7; Length 720;
Beet Local Similarity	100.0%;	Pred. No.1.5e-204;
RESULT 436		
ID ABR90029 standard; protein; 720 AA.		
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.		
PN US2003073177-A1.		
PD 17-APR-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 3945; DB 7; Length 720;
Beet Local Similarity	100.0%;	Pred. No.1.5e-204;
RESULT 437		
ID ADA22354 standard; protein; 720 AA.		
DE Human secreted/transmembrane polypeptide PRO1344.		
PN US2003040473-A1.		
PD 27-FEB-2003.		
Query Match	100.0%;	Score 3945; DB 7; Length 720;
Beet Local Similarity	100.0%;	Pred. No.1.5e-204;
RESULT 438		
ID ABR27555 standard; protein; 720 AA.		
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.		
PN US2003064442-A1.		
PD 03-APR-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 3945; DB 7; Length 720;
Beet Local Similarity	100.0%;	Pred. No.1.5e-204;
RESULT 439		
ID ABR13156 standard; protein; 720 AA.		
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.		
PN US2003064450-A1.		
PD 03-APR-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 3945; DB 7; Length 720;
Beet Local Similarity	100.0%;	Pred. No.1.5e-204;
RESULT 440		
ID ABO1859 standard; protein; 720 AA.		

DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068731-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 441
ID ABR14071 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068683-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 442
ID ABR02276 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068754-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 443
ID ABO40146 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068681-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 444
ID ABR74581 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003096351-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 445
ID ABR33776 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003096358-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 446
ID ABR20235 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104556-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 447
ID ABO48727 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049756-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 448
ID ABO22540 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003017982-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 449
ID ABR72792 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036122-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;

Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 450
ID ABO15434 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036121-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 451
ID ABR85149 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040065-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 452
ID ABO15129 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003044919-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 453
ID ABO17264 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003040077-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 454
ID ABR17553 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003044928-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 455
ID ADA06520 standard; protein; 720 AA.
DE Human secreted/transmembrane PRO polypeptide #65.
PN US2003049638-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 456
ID ADA39213 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003059782-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 457
ID ABR85454 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049746-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 458
ID ABR77020 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054464-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 459
ID ABO28199 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003064459-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 460
ID ABM22980 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068757-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 461
ID ABM30300 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068723-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 462
ID ABM21760 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068741-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 463
ID ABM21455 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068744-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 464
ID ABM1986 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068766-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 465
ID ABO41061 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068694-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 466
ID ABO36791 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068715-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 467
ID ABO37401 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068726-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 468
ID ABM75191 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104544-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;

Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 469
ID ABM33471 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003096357-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 470
ID ABO46226 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003049760-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 471
ID ADA82605 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049755-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 472
ID ADB85611 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003049735-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 473
ID ADB96239 standard; protein; 720 AA.
DE Human PRO polypeptide #65.
PN US2003054403-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 474
ID ABM31825 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068680-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 475
ID ABM31215 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068762-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 476
ID ADB85913 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003054472-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 477
ID ABM32130 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068708-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 478
ID ABM32435 standard; protein; 720 AA.

DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068713-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 479
ID ADB68290 standard; protein; 720 AA.
DE Human PRO1344 protein.
PN US2003065161-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 480
ID ADB68097 standard; protein; 720 AA.
DE Human PRO1344 protein.
PN US2003060600-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 481
ID ABM31520 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068761-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 482
ID ABM30910 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068771-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 483
ID ADB90914 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003083473-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 484
ID ADC57711 standard; protein; 720 AA.
DE Human PRO polypeptide #65.
PN US2003027754-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 485
ID ADC5075 standard; protein; 720 AA.
DE Human PRO polypeptide #65.
PN US2003045463-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 486
ID ADC11942 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003049681-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 487
ID ADC06994 standard; protein; 720 AA.
DE Human PRO1344 protein.
PN US2003060602-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 488
ID ADC56364 standard; protein; 720 AA.
DE Human PRO polypeptide #65.
PN US2003064375-A1.
PD 03-APR-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 489
ID ADC17173 standard; protein; 720 AA.
DE Mammalian PRO polypeptide (SeqID 38).
PN US2003065143-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 490
ID ADC07419 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003068647-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 491
ID ADC11409 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003069403-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 492
ID ADC14871 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003073208-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 493
ID ADC52366 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003138882-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 494
ID ADC14531 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003082546-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 495
ID ADD08063 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003068623-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 496
ID ADC81888 standard; protein; 720 AA.
DE Human PRO polypeptide #65.
PN US2003083461-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 497
ID ADD07530 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2002193299-A1.
PD 19-DEC-2002.

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Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 517
ID ADH24070 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180918-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 518
ID ADH34096 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180858-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 519
ID ADH29929 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180859-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 520
ID ADH23900 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180919-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 521
ID ADH08995 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003207395-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 522
ID ADG85304 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180904-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 523
ID ADH24580 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180907-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 524
ID ADH37746 standard; protein; 720 AA.
DE Human secreted and transmembrane protein PRO1344 CDNA.
PN US2003181646-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 525
ID ADH02025 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003180837-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 526
ID ADH37606 standard; protein; 720 AA.
DE Human secreted and transmembrane protein PRO1344 CDNA.
PN US2003181648-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 527
ID ADG85644 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180905-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 528
ID ADH24240 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180914-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 529
ID ADH38534 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181643-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 530
ID ADG83655 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003180794-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 531
ID ADH29463 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180860-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 532
ID ADH27579 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180906-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 533
ID ADH37776 standard; protein; 720 AA.
DE Human secreted and transmembrane protein PRO1344 CDNA.
PN US2003181647-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 534
ID ADH37953 standard; protein; 720 AA.
DE Human secreted and transmembrane protein PRO1344 CDNA.
PN US2003181649-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 535
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ID ADH57373 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180920-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 536
ID ADH53515 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181636-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 537
ID ADH53685 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181641-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 538
ID ADH52021 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181638-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 539
ID ADH49876 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181639-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 540
ID ADI25386 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181696-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 541
ID ADH90179 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181698-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 542
ID ADI25556 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181669-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 543
ID ADH97730 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181672-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 544
ID ADI35412 standard; protein; 720 AA.

DE Human PRO polypeptide #65.
PN US2003050457-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 545
ID ADI03578 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181656-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 546
ID ADI11935 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181686-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 547
ID ADH90009 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181697-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 548
ID ADH99904 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003049682-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 549
ID ADH96410 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181707-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 550
ID ADI11085 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181682-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 551
ID ADI11595 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181684-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 552
ID ADH98240 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181709-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 553
ID ADH95580 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181708-A1.
PD 25-SEP-2003.

Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 572
ID ADH78087 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181675-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 573
ID ADI05232 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181677-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 574
ID ADH79644 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181678-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 575
ID ADI01470 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181678-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 576
ID ADI01640 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181679-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 577
ID ADI01810 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181680-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 578
ID ADH79814 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003191289-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 579
ID ADI04632 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003171550-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 580
ID ADI02768 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181651-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;

RESULT 581
ID ADH78087 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181667-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 582
ID ADI25726 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181670-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 583
ID ADI25896 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181671-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 584
ID ADK65408 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003073821-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 585
ID ADH98750 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003191284-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 586
ID ADH79991 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003191287-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 587
ID ADL32776 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003207396-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 588
ID ADM30310 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003073813-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 589
ID ADL93722 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003040013-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 590

ID ADG52176 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003130483-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 591
ID ADE74307 standard; protein; 720 AA.
DE Human secreted/cranmembrane protein (PRO) #85.
PN US2003211572-A1.
PD 13-NOV-2003.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 592
ID ADE74919 standard; protein; 720 AA.
DE Human secreted/cranmembrane protein (PRO) #85.
PN US2003211574-A1.
PD 13-NOV-2003.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 593
ID ADE35357 standard; protein; 720 AA.
DE Human PRO1344 polypeptide.
PN US2003194760-A1.
PD 16-OCT-2003.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 594
ID ADG11607 standard; protein; 720 AA.
DE Human PRO1344 polypeptide.
PN US2003228655-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 595
ID ADP96132 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003215909-A1.
PD 20-NOV-2003.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 596
ID ADG04403 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003215912-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 597
ID ADG00563 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003215911-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 598
ID ADH06608 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180852-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 599
ID ADH06318 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180853-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 600
ID ADG68859 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180855-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 601
ID ADH27749 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180912-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 602
ID ADH23090 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180913-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 603
ID ADH33722 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181645-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 604
ID ADG82819 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003215910-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 605
ID ADH02365 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003180839-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 606
ID ADH07972 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180845-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 607
ID ADG69369 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180846-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 608
ID ADH31910 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180917-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;

Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 609
ID ADH26100 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003068770-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 610
ID ADG83930 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003180842-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 611
ID ADH19477 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003228656-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 612
ID ADG85474 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003166848-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 613
ID ADH06268 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180854-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 614
ID ADH30098 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180856-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 615
ID ADH24410 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180910-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 616
ID ADH33069 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003068768-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 617
ID ADG69539 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180844-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;

RESULT 618
ID ADH07802 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180851-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 619
ID ADG85814 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180861-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 620
ID ADH39360 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180916-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 621
ID ADH33552 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181637-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 622
ID ADH33892 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181644-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 623
ID ADH01102 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003180838-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 624
ID ADG69709 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180843-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 625
ID ADH20970 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003224358-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 626
ID ADH02195 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003180841-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 627
ID ADG69199 standard; protein; 720 AA.

DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180847-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 628
ID ADH85984 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180862-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 629
ID ADH24920 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180909-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 630
ID ADH39537 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180915-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 631
ID ADH20010 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003219856-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 632
ID ADH02535 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003180840-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 633
ID ADH69029 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180849-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 634
ID ADH07632 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180850-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 635
ID ADH86154 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180863-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 636
ID ADH24750 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.

PN US2003180908-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 637
ID ADH25798 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180911-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 638
ID ADH38364 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180922-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 639
ID ADH57203 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181642-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 640
ID ADH52191 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180921-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 641
ID ADH49557 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180857-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 642
ID ADH90519 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181700-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 643
ID ADH11255 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181683-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 644
ID ADH98920 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003190698-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 645
ID ADH012150 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003190699-A1.

PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 646
ID ADH90689 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181701-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 647
ID ADJ54808 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2004023321-A1.
PD 05-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 648
ID ADJ98564 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181797-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 649
ID ADJ98734 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181728-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 650
ID ADH78893 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181703-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 651
ID ADJ99127 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003186408-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 652
ID ADJ99297 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003187196-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 653
ID ADJ98915 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003187242-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 654
ID ADH79063 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181702-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 655
ID ADK00923 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003186407-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 656
ID ADK14444 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003187229-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 657
ID ADJ64579 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2004038337-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 658
ID ADM31475 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2004048334-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 659
ID ADM36522 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2004053358-A1.
PD 18-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 660
ID ADM40327 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2004048335-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 661
ID ADM80893 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2004058411-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 662
ID ADN37935 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2004091959-A1.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 663
ID AAB70532 standard; protein; 720 AA.
DE Human PRO2 protein sequence SEQ ID NO:4.
PN WO200110902-A2.
PD 15-FEB-2001.
PA (CURA-) CURAGEN CORP.

Query Match 99.8%; Score 3939; DB 4; Length 720;
Best Local Similarity 99.7%; Pred. No. 3.1e-204;
RESULT 664
ID AAU00401 standard; protein; 720 AA.
DE Human secreted protein, POLY13.
PN W0200119856-A2.
PD 22-MAR-2001.
PA (CURA-) CURAGEN CORP.
Query Match 99.8%; Score 3939; DB 4; Length 720;
Best Local Similarity 99.7%; Pred. No. 3.1e-204;
RESULT 665
ID ADH89028 standard; protein; 720 AA.
DE Human POLYX polypeptide #13.
PN US2003198958-A1.
PD 23-OCT-2003.
PA (SHIM/) SHIMKETS R. A.
PA (FERN/) FERNANDES E.
PA (HERR/) HERRMANN J. L.
PA (LITX/) LITU X.
PA (YANG/) YANG M.
PA (BOLD/) BOLDOG F. L.
PA (SMIT/) SMITHSON G.
PA (RAST/) RASTELLI L.
Query Match 99.8%; Score 3939; DB 8; Length 720;
Best Local Similarity 99.7%; Pred. No. 3.1e-204;
RESULT 666
ID AAV88280 standard; protein; 720 AA.
DE Human TANGO 215 protein.
PN W020018904-A2.
PD 06-APR-2000.
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
Query Match 99.8%; Score 3936; DB 3; Length 720;
Best Local Similarity 99.7%; Pred. No. 4.5e-204;
RESULT 667
ID AAB85891 standard; protein; 737 AA.
DE Human serine protease-like protein (hc-PLACE1009992).
PN W0200109349-A1.
PD 08-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 99.4%; Score 3921.5; DB 4; Length 737;
Best Local Similarity 97.6%; Pred. No. 2.8e-203;
RESULT 668
ID AAB93670 standard; protein; 737 AA.
DE Human protein sequence SEQ ID NO:13202.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 99.4%; Score 3921.5; DB 4; Length 737;
Best Local Similarity 97.6%; Pred. No. 2.8e-203;
RESULT 669
ID ADJ69990 standard; protein; 737 AA.
DE Human heat mitochondrial protein as a therapeutic target SegID1796.
PN W02003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 99.4%; Score 3921.5; DB 7; Length 737;
Best Local Similarity 97.6%; Pred. No. 2.8e-203;
RESULT 670
ID ADN04640 standard; protein; 737 AA.
DE Antipsoiatic protein sequence #505.
PN W02004028479-A2.
PD 08-APR-2004.
PA (GERTH) GENENTECH INC.
Query Match 99.4%; Score 3921.5; DB 8; Length 737;
Best Local Similarity 97.6%; Pred. No. 2.8e-203;
RESULT 671
ID ADS85034 standard; protein; 737 AA.
DE Human atopic dermatitis-related protein sequence SegID36.
PN W02004031386-A1.
PD 15-APR-2004.
PA (GENO-) GENOX RES INC.
PA (UYJU-) UNIV JUNTENDO.
PA (UYJU-) UNIV JUNTENDO.

Query Match 99.4%; Score 3921.5; DB 8; Length 737;
Best Local Similarity 97.6%; Pred. No. 2.8e-203;
RESULT 672
ID ADS85022 standard; protein; 737 AA.
DE Human atopic dermatitis-related protein sequence SegID24.
PN W02004031386-A1.
PD 15-APR-2004.
PA (GENO-) GENOX RES INC.
PA (UYJU-) UNIV JUNTENDO.
Query Match 99.4%; Score 3921.5; DB 8; Length 737;
Best Local Similarity 97.6%; Pred. No. 2.8e-203;
RESULT 673
ID AAB85893 standard; protein; 762 AA.
DE Human serine protease-like protein (hc-PLACE1009992).
PN W0200109349-A1.
PD 08-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 99.4%; Score 3921.5; DB 4; Length 762;
Best Local Similarity 97.6%; Pred. No. 2.9e-203;
RESULT 674
ID AAB85892 standard; protein; 720 AA.
DE Mouse serine protease-like protein (mc-PLACE1009992).
PN W0200109349-A1.
PD 08-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 99.6%; Score 3612; DB 4; Length 720;
Best Local Similarity 90.1%; Pred. No. 1.3e-186;
RESULT 675
ID AAB09927 standard; protein; 719 AA.
DE Murine TANGO 215 protein.
PN W020018904-A2.
PD 06-APR-2000.
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
Query Match 91.3%; Score 3602.5; DB 3; Length 719;
Best Local Similarity 90.1%; Pred. No. 4.1e-186;
RESULT 676
ID AAB19180 standard; protein; 649 AA.
DE Human protease, PRPS-17 protein.
PN W0200208396-A2.
PD 31-JAN-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 88.7%; Score 3500.5; DB 5; Length 649;
Best Local Similarity 90.0%; Pred. No. 1.2e-180;
RESULT 677
ID AAB70531 standard; protein; 567 AA.
DE Human PRO1 protein sequence SEQ ID NO:2.
PN W0200110902-A2.
PD 15-FEB-2001.
PA (CURA-) CURAGEN CORP.
Query Match 78.3%; Score 3089.5; DB 4; Length 567;
Best Local Similarity 99.5%; Pred. No. 1.4e-158;
RESULT 678
ID AAB49533 standard; protein; 570 AA.
DE Clone HEPPEY75.
PN W0200061774-A2.
PD 19-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 74.7%; Score 2946.5; DB 3; Length 570;
Best Local Similarity 96.8%; Pred. No. 7.2e-151;
RESULT 679
ID ADK41485 standard; protein; 551 AA.
DE Human CD-like molecule HSKDF41, SEQ ID NO:284.
PN W0200226930-A2.
PD 04-APR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 74.6%; Score 2944; DB 5; Length 551;
Best Local Similarity 99.3%; Pred. No. 9.5e-151;
RESULT 680
ID AAM41706 standard; protein; 499 AA.
DE Human polypeptide SEQ ID NO 6637.
PN W0200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.

Query Match 65.3%; Score 2577.5; DB 4; Length 499;
Best Local Similarity 96.6%; Pred. No. 4.8e-131;
RESULT 681
ID AAE20817 standard; protein; 455 AA.
DE Human gene 5 encoded secreted protein HSLGUT5, SEQ ID NO:79.
PN WO200218435-A1.
PD 07-MAR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 61.2%; Score 2413; DB 5; Length 455;
Best Local Similarity 99.3%; Pred. No. 3.2e-122;
RESULT 682
ID ABG64652 standard; protein; 455 AA.
DE Human albumin fusion protein #1127.
PN WO200177137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 61.2%; Score 2413; DB 5; Length 455;
Best Local Similarity 99.3%; Pred. No. 3.2e-122;
RESULT 683
ID ADL77919 standard; protein; 455 AA.
DE Albumin fusion protein related therapeutic protein X, SEQ ID No 1401.
PN US2004010134-A1.
PD 15-JUN-2004.
PA (ROSE/) ROSEN C A.
Query Match 61.2%; Score 2413; DB 8; Length 455;
Best Local Similarity 99.3%; Pred. No. 3.2e-122;
RESULT 684
ID ADL06662 standard; protein; 417 AA.
DE Human 3T3 cell conversion promoter FP938.
PN CN1403477-A.
PD 19-MAR-2003.
PA (SHAN-) SHANGHAI XINSHIJI GENE TECH DEV CO LTD.
Query Match 52.2%; Score 2059; DB 7; Length 417;
Best Local Similarity 95.6%; Pred. No. 3.4e-103;
RESULT 685
ID AAM39920 standard; protein; 359 AA.
DE Human polypeptide SEQ ID NO 3065.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSIQ INC.
Query Match 48.4%; Score 1909; DB 4; Length 359;
Best Local Similarity 100.0%; Pred. No. 3.6e-95;
RESULT 686
ID AAM39957 standard; protein; 359 AA.
DE Human polypeptide SEQ ID NO 3102.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSIQ INC.
Query Match 48.4%; Score 1909; DB 4; Length 359;
Best Local Similarity 100.0%; Pred. No. 3.6e-95;
RESULT 687
ID AAE20797 standard; protein; 323 AA.
DE Human gene 5 encoded secreted protein HSLGUT5, SEQ ID NO:59.
PN WO200218435-A1.
PD 07-MAR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 43.3%; Score 1708.5; DB 5; Length 323;
Best Local Similarity 94.1%; Pred. No. 2.1e-84;
RESULT 688
ID ABG64653 standard; protein; 323 AA.
DE Human albumin fusion protein #1128.
PN WO200177137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 43.3%; Score 1708.5; DB 5; Length 323;
Best Local Similarity 94.1%; Pred. No. 2.1e-84;
RESULT 689
ID ADL77920 standard; protein; 323 AA.
DE Albumin fusion protein related therapeutic protein X, SEQ ID No 1402.
PN US2004010134-A1.
PD 15-JUN-2004.
PA (ROSE/) ROSEN C A.

PA (HASE/) HASELTINE W A.
Query Match 43.3%; Score 1708.5; DB 8; Length 323;
Best Local Similarity 94.1%; Pred. No. 2.1e-84;
RESULT 690
ID AAM24485 standard; protein; 234 AA.
DE Human EST encoded protein SEQ ID NO: 2010.
PN WO200154477-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSIQ INC.
Query Match 29.8%; Score 1175.5; DB 4; Length 234;
Best Local Similarity 91.4%; Pred. No. 7.8e-56;
RESULT 691
ID ABP72332 standard; protein; 1019 AA.
DE Horseshoe crab Factor C.
PN WO2003002976-A2.
PD 09-JAN-2003.
PA (WHIK) BIOWHITTAKER INC.
Query Match 17.0%; Score 672; DB 6; Length 1019;
Best Local Similarity 25.6%; Pred. No. 4.1e-28;
RESULT 692
ID AAM43394 standard; protein; 1019 AA.
DE Singapore horseshoe crab factor C proenzyme (CrFC 21).
PN SG42456-A1.
PD 15-AUG-1997.
PA (UYSI-) UNIV SINGAPORE NAT.
Query Match 16.9%; Score 665; DB 2; Length 1019;
Best Local Similarity 25.4%; Pred. No. 9.7e-28;
RESULT 693
ID AAY05750 standard; protein; 1019 AA.
DE Horseshoe crab Factor C.
PN WO9915676-A1.
PD 01-APR-1999.
PA (UYSI-) UNIV SINGAPORE NAT.
Query Match 16.9%; Score 665; DB 2; Length 1019;
Best Local Similarity 25.4%; Pred. No. 9.7e-28;
RESULT 694
ID AAM94302 standard; protein; 1019 AA.
DE Horseshoe crab Factor C protein #2.
PN US59858706-A.
PD 12-JAN-1999.
PA (UYSI-) UNIV SINGAPORE NAT.
Query Match 16.9%; Score 665; DB 2; Length 1019;
Best Local Similarity 25.4%; Pred. No. 9.7e-28;
RESULT 695
ID AAY42490 standard; protein; 1019 AA.
DE Recombinant N-terminally truncated Horseshoe crab Factor C protein.
PN US5985590-A.
PD 16-NOV-1999.
PA (UYSI-) UNIV SINGAPORE NAT.
Query Match 16.9%; Score 665; DB 3; Length 1019;
Best Local Similarity 25.4%; Pred. No. 9.7e-28;
RESULT 696
ID AAB60935 standard; protein; 1019 AA.
DE Horseshoe crab recombinant Factor C #2.
PN WO200127289-A2.
PD 19-APR-2001.
PA (UYSI-) UNIV SINGAPORE NAT.
Query Match 16.9%; Score 665; DB 4; Length 1019;
Best Local Similarity 25.4%; Pred. No. 9.7e-28;
RESULT 697
ID ABP72334 standard; protein; 1019 AA.
DE Horseshoe crab Factor C.
PN WO2003002976-A2.
PD 09-JAN-2003.
PA (WHIK) BIOWHITTAKER INC.
Query Match 16.9%; Score 665; DB 6; Length 1019;
Best Local Similarity 25.4%; Pred. No. 9.7e-28;
RESULT 698
ID AAM43393 standard; protein; 1083 AA.
DE Singapore horseshoe crab factor C proenzyme (CrFC 26).
PN SG42456-A1.
PD 15-AUG-1997.
PA (UYSI-) UNIV SINGAPORE NAT.

Query Match 16.9%; Score 665; DB 2; Length 1083;
Best Local Similarity 25.4%; Pred. No. 1e-27;
RESULT 699
ID AAY05749 standard; protein; 1083 AA.
DE Horsehoe crab Factor C.
PN WO9915676-A1.
PD 01-APR-1999.
PA (UYSI-) UNIV SINGAPORE NAT.
Query Match 16.9%; Score 665; DB 2; Length 1083;
Best Local Similarity 25.4%; Pred. No. 1e-27;
RESULT 700
ID AAY94301 standard; protein; 1083 AA.
DE Horsehoe crab Factor C protein #1.
PN US5858706-A.
PD 12-JAN-1999.
PA (UYSI-) UNIV SINGAPORE NAT.
Query Match 16.9%; Score 665; DB 2; Length 1083;
Best Local Similarity 25.4%; Pred. No. 1e-27;
RESULT 701
ID AAY42489 standard; protein; 1083 AA.
DE Horsehoe crab recombinant Factor C protein.
PN US5985590-A.
PD 16-NOV-1999.
PA (UYSI-) UNIV SINGAPORE NAT.
Query Match 16.9%; Score 665; DB 3; Length 1083;
Best Local Similarity 25.4%; Pred. No. 1e-27;
RESULT 702
ID AAB60934 standard; protein; 1083 AA.
DE Horsehoe crab recombinant Factor C #1.
PN WO200127289-A2.
PD 19-APR-2001.
PA (UYSI-) UNIV SINGAPORE NAT.
Query Match 16.9%; Score 665; DB 4; Length 1083;
Best Local Similarity 25.4%; Pred. No. 1e-27;
RESULT 703
ID AAB7233 standard; protein; 1083 AA.
DE Horsehoe crab Factor C.
PN WO200302976-A2.
PD 09-JAN-2003.
PA (WHIK) BIONITTAKER INC.
Query Match 16.9%; Score 665; DB 6; Length 1083;
Best Local Similarity 25.4%; Pred. No. 1e-27;
RESULT 704
ID AAM41743 standard; protein; 146 AA.
DE Human polypeptide SEQ ID NO 6674.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 16.8%; Score 662; DB 4; Length 146;
Best Local Similarity 85.4%; Pred. No. 2.3e-28;
RESULT 705
ID AAY11743 standard; protein; 103 AA.
DE Human 5' EST secreted protein SEQ ID No: 343.
PN WO9906550-A2.
PD 11-FEB-1999.
PA (GENST) GENSET.
Query Match 14.7%; Score 580; DB 2; Length 103;
Best Local Similarity 97.1%; Pred. No. 4.3e-24;
RESULT 706
ID ADE87459 standard; protein; 699 AA.
DE Human MBL-associated serine protease-1 protein.
PN EP1344533-A1.
PD 17-SEP-2003.
PA (NATL-) NATLMUNE AS.
Query Match 12.1%; Score 476; DB 7; Length 699;
Best Local Similarity 24.6%; Pred. No. 1e-17;
RESULT 707
ID ADL91028 standard; protein; 699 AA.
DE Human mannose binding lectin amino acid sequence SEQ ID NO:14.
PN WO2004024925-A2.
PD 25-MAR-2004.
PA (NATL-) NATLMUNE AS.
Query Match 12.0%; Score 475; DB 8; Length 699;

Best Local Similarity 24.6%; Pred. No. 1.2e-17;
RESULT 708
ID AAM83722 standard; protein; 698 AA.
DE Human diagnostic and therapeutic proteoin SEQ ID NO:3971.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 12.0%; Score 474.5; DB 8; Length 698;
Best Local Similarity 24.4%; Pred. No. 1.2e-17;
RESULT 709
ID AAB85060 standard; protein; 728 AA.
DE Human serine protease MASP-3 polypeptide.
PN WO200140451-A2.
PD 07-JUN-2001.
PA (JENS/) JENSENIUS J C.
PA (THIE/) THIEL S.
Query Match 11.9%; Score 471; DB 4; Length 728;
Best Local Similarity 25.0%; Pred. No. 2e-17;
RESULT 710
ID ADE87461 standard; protein; 728 AA.
DE Human MBL-associated serine protease-4 protein.
PN EP1344533-A1.
PD 17-SEP-2003.
PA (NATL-) NATLMUNE AS.
Query Match 11.9%; Score 468; DB 7; Length 728;
Best Local Similarity 25.0%; Pred. No. 2.9e-17;
RESULT 711
ID ADL91027 standard; protein; 728 AA.
DE Human mannose binding lectin amino acid sequence SEQ ID NO:13.
PN WO2004024925-A2.
PD 25-MAR-2004.
PA (NATL-) NATLMUNE AS.
Query Match 11.9%; Score 468; DB 8; Length 728;
Best Local Similarity 25.0%; Pred. No. 2.9e-17;
RESULT 712
ID AAB47559 standard; protein; 728 AA.
DE Protease PRPS-1.
PN WO200171004-A2.
PD 27-SEP-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 11.7%; Score 461; DB 4; Length 728;
Best Local Similarity 24.9%; Pred. No. 6.9e-17;
RESULT 713
ID AAG80756 standard; protein; 707 AA.
DE Murine C1r protein.
PN KR2001077614-A.
PD 20-AUG-2001.
PA (BIOC-) BIO CLUE & SOLUTION CO LTD.
PA (KIMT/) KIM T Y.
Query Match 10.9%; Score 429; DB 5; Length 707;
Best Local Similarity 22.3%; Pred. No. 3.6e-15;
RESULT 714
ID AAB50288 standard; protein; 705 AA.
DE Complement component 1 r ovarian tumour marker protein, SEQ ID NO:66.
PN WO200175177-A2.
PD 11-OCT-2001.
PA (USHS) US DEPT HEALTH & HUMAN SERVICES.
Query Match 10.2%; Score 403.5; DB 4; Length 705;
Best Local Similarity 22.9%; Pred. No. 8.4e-14;
RESULT 715
ID AAG80757 standard; protein; 705 AA.
DE Human C1r protein.
PN KR2001077614-A.
PD 20-AUG-2001.
PA (BIOC-) BIO CLUE & SOLUTION CO LTD.
PA (KIMT/) KIM T Y.
Query Match 10.2%; Score 403.5; DB 5; Length 705;
Best Local Similarity 22.9%; Pred. No. 8.4e-14;
RESULT 716
ID ADP65211 standard; protein; 705 AA.
DE Human complement component 1, r subcomponent.
PN WO2003072827-A1.
PD 04-SEP-2003.

PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
 Query Match 10.2%; Score 403.5; DB 7; Length 705;
 Best Local Similarity 22.6%; Pred. No. 8.4e-14;
 RESULT 717
 ID ABG31619 standard; protein; 686 AA.
 DE Human mannin-binding lectin associated serine protease-2 protein.
 PN US2002082208-A1.
 PD 27-JUN-2002.
 PA (JENS/) JENSENIUS J C.
 (THIE/) THIEL S.
 Query Match 10.2%; Score 401.5; DB 5; Length 686;
 Best Local Similarity 22.7%; Pred. No. 1.1e-13;
 RESULT 718
 ID AAE14564 standard; protein; 686 AA.
 DE Human MASP-2 protein.
 PN WO200206460-A2.
 PD 24-JUN-2002.
 PA (JENS/) JENSENIUS J C.
 (THIE/) THIEL S.
 Query Match 10.2%; Score 401.5; DB 5; Length 686;
 Best Local Similarity 22.7%; Pred. No. 1.1e-13;
 RESULT 719
 ID ABG3115 standard; protein; 686 AA.
 DE Mannan-binding lectin associated serine protease-2 (MASP-2).
 PN US2002082209-A1.
 PD 27-JUN-2002.
 PA (JENS/) JENSENIUS J C.
 (THIE/) THIEL S.
 Query Match 10.2%; Score 401.5; DB 5; Length 686;
 Best Local Similarity 22.7%; Pred. No. 1.1e-13;
 RESULT 720
 ID ADL91025 standard; protein; 686 AA.
 DE Human mannose binding lectin amino acid sequence SEQ ID NO:11.
 PN WO2004024925-A2.
 PD 25-MAR-2004.
 PA (NATL-) NATIMONE AS.
 Query Match 10.2%; Score 401.5; DB 8; Length 686;
 Best Local Similarity 22.7%; Pred. No. 1.1e-13;
 RESULT 721
 ID AAE1568 standard; protein; 686 AA.
 DE Human MASP-2 protein, alternative version.
 PN WO200206460-A2.
 PD 24-JUN-2002.
 PA (JENS/) JENSENIUS J C.
 (THIE/) THIEL S.
 Query Match 10.2%; Score 400.5; DB 5; Length 686;
 Best Local Similarity 22.7%; Pred. No. 1.2e-13;
 RESULT 722
 ID ADE87460 standard; protein; 686 AA.
 DE Human MB1-associated serine protease-2 protein.
 PN EP1344533-A1.
 PD 17-SEP-2003.
 PA (NATL-) NATIMONE AS.
 Query Match 10.2%; Score 400.5; DB 7; Length 686;
 Best Local Similarity 22.7%; Pred. No. 1.2e-13;
 RESULT 723
 ID ADQ27010 standard; protein; 671 AA.
 DE Human MASP-2 mature polypeptide.
 PN WO2004050907-A2.
 PD 17-JUN-2004.
 PA (UYAA-) UNIV AARHUS.
 (AARH) AARHUS AMT.
 Query Match 10.1%; Score 399.5; DB 8; Length 671;
 Best Local Similarity 22.8%; Pred. No. 1.3e-13;
 RESULT 724
 ID AAE14565 standard; peptide; 671 AA.
 DE Human mature MASP-2 protein.
 PN WO200206460-A2.
 PD 24-JUN-2002.
 PA (JENS/) JENSENIUS J C.
 (THIE/) THIEL S.
 Query Match 10.1%; Score 398.5; DB 5; Length 671;
 Best Local Similarity 22.8%; Pred. No. 1.5e-13;

RESULT 725
 ID ADE56422 standard; protein; 694 AA.
 DE Rat Protein BAA25797, SEQ ID NO 2275.
 PN WO2003016475-A2.
 PD 27-FEB-2003.
 PA (GEHO) GEN HOSPITAL CORP.
 (FARB) BAYER AG.
 Query Match 8.6%; Score 340.5; DB 7; Length 694;
 Best Local Similarity 21.2%; Pred. No. 2e-10;
 RESULT 726
 ID ADE83526 standard; protein; 694 AA.
 DE Rat Protein BAA25797, SEQ ID NO 11123.
 PN WO2003016475-A2.
 PD 27-FEB-2003.
 PA (GEHO) GEN HOSPITAL CORP.
 (FARB) BAYER AG.
 Query Match 8.6%; Score 340.5; DB 7; Length 694;
 Best Local Similarity 21.2%; Pred. No. 2e-10;
 RESULT 727
 ID ADE56418 standard; protein; 695 AA.
 DE Rat Protein D88250, SEQ ID NO 2271.
 PN WO2003016475-A2.
 PD 27-FEB-2003.
 PA (GEHO) GEN HOSPITAL CORP.
 (FARB) BAYER AG.
 Query Match 8.6%; Score 340.5; DB 7; Length 695;
 Best Local Similarity 21.2%; Pred. No. 2.1e-10;
 RESULT 728
 ID ADD45338 standard; protein; 695 AA.
 DE Rat Protein D88250, SEQ ID NO 10771.
 PN WO2003016475-A2.
 PD 27-FEB-2003.
 PA (GEHO) GEN HOSPITAL CORP.
 (FARB) BAYER AG.
 Query Match 8.6%; Score 340.5; DB 7; Length 695;
 Best Local Similarity 21.2%; Pred. No. 2.1e-10;
 RESULT 729
 ID ABA43579 standard; protein; 760 AA.
 DE Human cancer associated protein sequence SEQ ID NO:1024.
 PN WO200055350-A1.
 PD 21-SEP-2000.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 8.5%; Score 336; DB 3; Length 760;
 Best Local Similarity 21.7%; Pred. No. 3.9e-10;
 RESULT 730
 ID ADD45340 standard; protein; 688 AA.
 DE Human Protein Q9UCV3, SEQ ID NO 10773.
 PN WO2003016475-A2.
 PD 27-FEB-2003.
 PA (GEHO) GEN HOSPITAL CORP.
 (FARB) BAYER AG.
 Query Match 8.5%; Score 334; DB 7; Length 688;
 Best Local Similarity 21.7%; Pred. No. 4.6e-10;
 RESULT 731
 ID ADE56420 standard; protein; 688 AA.
 DE Human Protein Q9UCV3, SEQ ID NO 2273.
 PN WO2003016475-A2.
 PD 27-FEB-2003.
 PA (GEHO) GEN HOSPITAL CORP.
 (FARB) BAYER AG.
 Query Match 8.5%; Score 334; DB 7; Length 688;
 Best Local Similarity 21.7%; Pred. No. 4.6e-10;
 RESULT 732
 ID ADP65315 standard; protein; 688 AA.
 DE Human complement C1s component precursor (c1 esterase).
 PN WO2003072827-A1.
 PD 04-SEP-2003.
 PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
 Query Match 8.5%; Score 334; DB 7; Length 688;
 Best Local Similarity 21.7%; Pred. No. 4.6e-10;
 RESULT 733
 ID ADJ75392 standard; protein; 688 AA.
 DE Marker gene related amino acid sequence SEQ ID NO:644.

PN EPI394274-A2.
 PD 03-MAR-2004.
 PA (GENO-) GENOX RES INC.
 Query Match
 Best Local Similarity 8.5%; Score 334; DB 8; Length 688;
 RESULT 734
 ID ADU91020 standard; protein; 688 AA.
 DE Human mannosyl binding lectin amino acid sequence SEQ ID NO:6.
 PN WO2004024925-A2.
 PD 25-MAR-2004.
 PA (NATI-) NATIMUNE AS.
 Query Match
 Best Local Similarity 8.5%; Score 334; DB 8; Length 688;
 RESULT 735
 ID AEM81337 standard; protein; 688 AA.
 DE Tumour-associated antigenic target (TAT) polypeptide PRO2660, SEQ:3453.
 PN WO2004030615-A2.
 PD 15-APR-2004.
 PA (SETH-) GENENTECH INC.
 Query Match
 Best Local Similarity 8.5%; Score 334; DB 8; Length 688;
 RESULT 736
 ID ADI16884 standard; protein; 655 AA.
 DE Human NOVX protein homologue SegID 420.
 PN WO200268649-A2.
 PD 06-SEP-2002.
 PA (CURA-) CURAGEN CORP.
 Query Match
 Best Local Similarity 8.4%; Score 332; DB 5; Length 855;
 RESULT 737
 ID ADI16818 standard; protein; 855 AA.
 DE Human NOVX protein homologue SegID 354.
 PN WO200268649-A2.
 PD 06-SEP-2002.
 PA (CURA-) CURAGEN CORP.
 Query Match
 Best Local Similarity 8.4%; Score 332; DB 5; Length 855;
 RESULT 738
 ID AAE06940 standard; protein; 1019 AA.
 DE Human enterokinase protein.
 PN WO200157194-A2.
 PD 09-AUG-2001.
 PA (CORV-) CORVAS INT INC.
 Query Match
 Best Local Similarity 8.4%; Score 331.5; DB 4; Length 1019;
 RESULT 739
 ID ADA83985 standard; protein; 1019 AA.
 DE Human PRSS7 protein.
 PN WO2002103028-A2.
 PD 27-DEC-2002.
 PA (BIOM-) BIOMEDICAL CENT.
 Query Match
 Best Local Similarity 8.4%; Score 331.5; DB 6; Length 1019;
 RESULT 740
 ID ADI10400 standard; protein; 1019 AA.
 DE Human cell surface protease #16.
 PN WO200295007-A2.
 PD 28-NOV-2002.
 PA (CORV-) CORVAS INT INC.
 Query Match
 Best Local Similarity 8.4%; Score 331.5; DB 7; Length 1019;
 RESULT 741
 ID ADU46924 standard; protein; 1019 AA.
 DE Human transmembrane serine protease (MTSP)-related polypeptide #6.
 PN US2004001801-A1.
 PD 01-JAN-2004.
 PA (CORV-) CORVAS INT INC.
 Query Match
 Best Local Similarity 8.4%; Score 331.5; DB 8; Length 1019;
 RESULT 742
 ID ADU70437 standard; protein; 1019 AA.
 DE Human heat mitochondrial protein as a therapeutic target SegID2243.
 PN WO2003087768-A2.

PD 23-OCT-2003.
 PA (MITO-) MITOKOR.
 PA (BUCK-) BUCK INST AGE RES.
 Query Match
 Best Local Similarity 8.4%; Score 330.5; DB 7; Length 1019;
 RESULT 743
 ID ADU70480 standard; protein; 3389 AA.
 DE Human heat mitochondrial protein as a therapeutic target SegID2286.
 PN WO2003087768-A2.
 PD 23-OCT-2003.
 PA (MITO-) MITOKOR.
 PA (BUCK-) BUCK INST AGE RES.
 Query Match
 Best Local Similarity 8.4%; Score 329.5; DB 7; Length 3389;
 RESULT 744
 ID ADH72216 standard; protein; 3567 AA.
 DE Human protein of the invention NOV54b SEQ ID NO:1112.
 PN WO2003102155-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match
 Best Local Similarity 8.4%; Score 329.5; DB 8; Length 3567;
 RESULT 745
 ID AAR13623 standard; protein; 460 AA.
 DE Human Protein C zymogen SC.
 PN EP43875-A.
 PD 28-AUG-1991.
 PA (ELIL) LILLY & CO ELI.
 Query Match
 Best Local Similarity 8.3%; Score 329; DB 2; Length 460;
 RESULT 746
 ID ABG76507 standard; protein; 1274 AA.
 DE DNA encoding protein modification and maintenance molecule #11.
 PN WO200260942-A2.
 PD 08-AUG-2002.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match
 Best Local Similarity 8.3%; Score 328.5; DB 5; Length 1274;
 RESULT 747
 ID AUI1815 standard; protein; 1783 AA.
 DE Cancer and neurogenesis associated gene, variant 5G-3V3.
 PN WO200190354-A1.
 PD 29-NOV-2001.
 PA (UYLE-) UNIV LEEDS.
 Query Match
 Best Local Similarity 8.3%; Score 328.5; DB 5; Length 1783;
 RESULT 748
 ID AUI1813 standard; protein; 1800 AA.
 DE Cancer and neurogenesis associated gene, variant 5G-3V1.
 PN WO200190354-A1.
 PD 29-NOV-2001.
 PA (UYLE-) UNIV LEEDS.
 Query Match
 Best Local Similarity 8.3%; Score 328.5; DB 5; Length 1800;
 RESULT 749
 ID AUI1812 standard; protein; 1826 AA.
 DE Cancer and neurogenesis associated gene.
 PN WO200190354-A1.
 PD 29-NOV-2001.
 PA (UYLE-) UNIV LEEDS.
 Query Match
 Best Local Similarity 8.3%; Score 328.5; DB 5; Length 1826;
 RESULT 750
 ID AUI1814 standard; protein; 2008 AA.
 DE Cancer and neurogenesis associated gene, variant 5G-3V2.
 PN WO200190354-A1.
 PD 29-NOV-2001.
 PA (UYLE-) UNIV LEEDS.
 Query Match
 Best Local Similarity 8.3%; Score 328.5; DB 5; Length 2008;
 RESULT 751
 ID AUI1817 standard; protein; 2306 AA.
 DE Cancer and neurogenesis associated gene, variant 5R23V2.

PN W0200190354-A1.
PD 29-NOV-2001.
PA (UYLE-) UNIV LEBDS.
Query Match
Best Local Similarity 8.3%; Score 328.5; DB 5; Length 2306;
RESULT 752
ID AAV1816 standard; protein; 2352 AA.
DE Cancer and neurogenesis associated gene, variant 5R-3V2.
PN W0200190354-A1.
PD 29-NOV-2001.
PA (UYLE-) UNIV LEBDS.
Query Match
Best Local Similarity 8.3%; Score 328.5; DB 5; Length 2352;
RESULT 753
ID AAB19551 standard; protein; 683 AA.
DE Human matrixase (truncated form).
PN W0200053232-A1.
PD 14-SEP-2000.
PA (GEOU) UNIV GEORGETOWN.
Query Match
Best Local Similarity 8.3%; Score 328; DB 3; Length 683;
RESULT 754
ID AAY90284 standard; protein; 762 AA.
DE Human peptidase, HPEP-1 protein sequence.
PN W0200042201-A2.
PD 20-JUL-2000.
PA (INCY-) INCYTE PHARM INC.
Query Match
Best Local Similarity 8.3%; Score 328; DB 3; Length 762;
RESULT 755
ID AAM25628 standard; protein; 851 AA.
DE Human protein sequence SEQ ID NO:1143.
PN W0200153455-A2.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 8.3%; Score 328; DB 4; Length 851;
RESULT 756
ID AAB11428 standard; peptide; 851 AA.
DE Human membrane-type Ser Kinase homologue, SEQ ID NO:1798.
PN W0200157188-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 8.3%; Score 328; DB 4; Length 851;
RESULT 757
ID AAO55145 standard; protein; 853 AA.
DE Protein #47 with increased gene expression in renal cell carcinoma.
PN W02004032842-A2.
PD 23-APR-2004.
PA (VAND-) VAN ANDEL INST.
Query Match
Best Local Similarity 8.3%; Score 328; DB 8; Length 853;
RESULT 758
ID AAB19552 standard; protein; 855 AA.
DE Human matrixase.
PN W0200053232-A1.
PD 14-SEP-2000.
PA (GEOU) UNIV GEORGETOWN.
Query Match
Best Local Similarity 8.3%; Score 328; DB 3; Length 855;
RESULT 759
ID AAB35465 standard; protein; 855 AA.
DE Human membrane-type serine protease MT-SPL.
PN W0200123524-A2.
PD 05-APR-2001.
PA (REGC) UNIV CALIFORNIA.
Query Match
Best Local Similarity 8.3%; Score 328; DB 4; Length 855;
RESULT 760
ID AD11617 standard; protein; 855 AA.
DE Human NOVX protein homologue SeqID 353.
PN W0200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 8.3%; Score 328; DB 5; Length 855;
RESULT 761
ID AD116893 standard; protein; 855 AA.
DE Human NOVX protein homologue SeqID 419.
PN W0200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 8.3%; Score 328; DB 5; Length 855;
RESULT 762
ID AD116876 standard; protein; 855 AA.
DE Human NOVX protein homologue SeqID 412.
PN W0200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 8.3%; Score 328; DB 5; Length 855;
RESULT 763
ID ADN39867 standard; protein; 855 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C237.
PN W02003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match
Best Local Similarity 8.3%; Score 328; DB 7; Length 855;
RESULT 764
ID ADN04754 standard; protein; 855 AA.
DE Antipsoriatic protein sequence #558.
PN W02004028479-A2.
PD 08-APR-2004.
PA (GETH-) GENENTECH INC.
Query Match
Best Local Similarity 8.3%; Score 328; DB 8; Length 855;
RESULT 765
ID ADP23334 standard; protein; 855 AA.
DE PRO polypeptide SEQ ID NO:428.
PN W02004041170-A2.
PD 21-MAY-2004.
PA (GETH-) GENENTECH INC.
Query Match
Best Local Similarity 8.3%; Score 328; DB 8; Length 855;
RESULT 766
ID ADR66721 standard; protein; 863 AA.
DE Human prostatic carcinoma derived protein SEQ ID 233 #3.
PN W02004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
Query Match
Best Local Similarity 8.3%; Score 328; DB 8; Length 863;
RESULT 767
ID ADR66379 standard; protein; 863 AA.
DE Human prostatic carcinoma derived protein SEQ ID 233 #2.
PN W02004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
Query Match
Best Local Similarity 8.3%; Score 328; DB 8; Length 863;
RESULT 768
ID AAB58274 standard; protein; 449 AA.
DE Lung cancer associated polypeptide sequence SEQ ID: 612.
PN W0200055180-A2.
PD 21-SEP-2000.

PA (HUMA-) HUMAN GENOME SCI INC.
 PA (ROSE/) ROSEN C A.
 Query Match 8.3%; Score 327.5; DB 3; Length 449;
 Best Local Similarity 23.3%; Pred. No. 6.8e-10;
 RESULT 769
 ID AD64961 standard; protein; 688 AA.
 DE Human complement component 1 protein , CIS.
 PN US2004033582-A1.
 PD 19-FEB-2004.
 PA (EDMO/) EDMONDS M.
 PA (HUI/) HUI L.
 PA (PERR/) PERRONE M.
 PA (POWE/) POWELL J R.
 PA (RAMA/) RAMANATHAN C S.
 PA (SWAN/) SWANSON B.
 PA (TSUC/) TSUCHIHASHI Z.
 PA (ZERB/) ZERBA K.
 Query Match 8.3%; Score 327; DB 8; Length 688;
 Best Local Similarity 21.7%; Pred. No. 1.1e-09;
 RESULT 770
 ID AD116508 standard; protein; 757 AA.
 DE Human NOVX protein to treat human pathological conditions SegID44.
 PN WO200268649-A2.
 PD 06-SEP-2002.
 PA (CURA-) CURAGEN CORP.
 Query Match 8.3%; Score 327; DB 5; Length 757;
 Best Local Similarity 21.6%; Pred. No. 1.2e-09;
 RESULT 771
 ID AAY06671 standard; protein; 855 AA.
 DE Tumour antigen derived gene-15 (TADG-15) protein.
 PN WO9942120-A1.
 PD 26-AUG-1999.
 PA (UYAR-) UNIV ARKANSAS.
 Query Match 8.3%; Score 327; DB 2; Length 855;
 Best Local Similarity 21.6%; Pred. No. 1.3e-09;
 RESULT 772
 ID AAB98500 standard; protein; 855 AA.
 DE Human TADG-15.
 PN WO200129056-A1.
 PD 26-APR-2001.
 PA (UYAR-) UNIV ARKANSAS.
 Query Match 8.3%; Score 327; DB 4; Length 855;
 Best Local Similarity 21.6%; Pred. No. 1.3e-09;
 RESULT 773
 ID AAE06930 standard; protein; 855 AA.
 DE Human membrane-type serine protease (MTSP) 1.
 PN WO200157194-A2.
 PD 09-AUG-2001.
 PA (CORV-) CORVAS INT INC.
 Query Match 8.3%; Score 327; DB 4; Length 855;
 Best Local Similarity 21.6%; Pred. No. 1.3e-09;
 RESULT 774
 ID AAO29292 standard; protein; 855 AA.
 DE Type II transmembrane serine protease 1 protein SEQ ID NO 2.
 PN WO200272786-A2.
 PD 19-SEP-2002.
 PA (CORV-) CORVAS INT INC.
 Query Match 8.3%; Score 327; DB 5; Length 855;
 Best Local Similarity 21.6%; Pred. No. 1.3e-09;
 RESULT 775
 ID AD116816 standard; protein; 855 AA.
 DE Human NOVX protein homologue SegID 352.
 PN WO200268649-A2.
 PD 06-SEP-2002.
 PA (CURA-) CURAGEN CORP.
 Query Match 8.3%; Score 327; DB 5; Length 855;
 Best Local Similarity 21.6%; Pred. No. 1.3e-09;
 RESULT 776
 ID AD116882 standard; protein; 855 AA.
 DE Human NOVX protein homologue SegID 418.
 PN WO200268649-A2.
 PD 06-SEP-2002.
 PA (CURA-) CURAGEN CORP.

Query Match 8.3%; Score 327; DB 5; Length 855;
 Best Local Similarity 21.6%; Pred. No. 1.3e-09;
 RESULT 777
 ID AD116875 standard; protein; 855 AA.
 DE Human NOVX protein homologue SegID 411.
 PN WO200268649-A2.
 PD 06-SEP-2002.
 PA (CURA-) CURAGEN CORP.
 Query Match 8.3%; Score 327; DB 5; Length 855;
 Best Local Similarity 21.6%; Pred. No. 1.3e-09;
 RESULT 778
 ID AAB56619 standard; protein; 855 AA.
 DE Human membrane-type serine protease MTSP1 protein SEQ ID NO:2.
 PN WO200292841-A2.
 PD 21-NOV-2002.
 PA (CORV-) CORVAS INT INC.
 Query Match 8.3%; Score 327; DB 6; Length 855;
 Best Local Similarity 21.6%; Pred. No. 1.3e-09;
 RESULT 779
 ID AAO30146 standard; protein; 855 AA.
 DE Human membrane-type serine protease MTSP1 protein.
 PN WO2003044179-A2.
 PD 30-MAY-2003.
 PA (CORV-) CORVAS INT INC.
 Query Match 8.3%; Score 327; DB 6; Length 855;
 Best Local Similarity 21.6%; Pred. No. 1.3e-09;
 RESULT 780
 ID AAE29820 standard; protein; 855 AA.
 DE Human membrane-type serine protease 1 (MTSP1).
 PN WO20027267-A2.
 PD 03-OCT-2002.
 PA (CORV-) CORVAS INT INC.
 Query Match 8.3%; Score 327; DB 6; Length 855;
 Best Local Similarity 21.6%; Pred. No. 1.3e-09;
 RESULT 781
 ID AAE29791 standard; protein; 855 AA.
 DE Human membrane-type serine protease, MTSP1.
 PN WO20027263-A2.
 PD 03-OCT-2002.
 PA (CORV-) CORVAS INT INC.
 Query Match 8.3%; Score 327; DB 6; Length 855;
 Best Local Similarity 21.6%; Pred. No. 1.3e-09;
 RESULT 782
 ID ABE72376 standard; protein; 855 AA.
 DE Transmembrane serine protease 1 (MTSP1).
 PN WO2003004681-A2.
 PD 16-JAN-2003.
 PA (CORV-) CORVAS INT INC.
 Query Match 8.3%; Score 327; DB 6; Length 855;
 Best Local Similarity 21.6%; Pred. No. 1.3e-09;
 RESULT 783
 ID ADB97551 standard; protein; 855 AA.
 DE Human MTSP1, SEQ ID NO:2.
 PN WO2003031585-A2.
 PD 17-APR-2003.
 PA (CORV-) CORVAS INT INC.
 Query Match 8.3%; Score 327; DB 7; Length 855;
 Best Local Similarity 21.6%; Pred. No. 1.3e-09;
 RESULT 784
 ID AD110371 standard; protein; 855 AA.
 DE Human cell surface protease #1.
 PN WO200295007-A2.
 PD 28-NOV-2002.
 PA (CORV-) CORVAS INT INC.
 Query Match 8.3%; Score 327; DB 7; Length 855;
 Best Local Similarity 21.6%; Pred. No. 1.3e-09;
 RESULT 785
 ID ADG65326 standard; protein; 855 AA.
 DE Human MTSP1.
 PN WO2003104394-A2.
 PD 18-DEC-2003.
 PA (DENND-) DENNDREON SAN DIEGO LLC.
 Query Match 8.3%; Score 327; DB 8; Length 855;

Best Local Similarity 21.6%; Pred. No. 1.3e-09;
RESULT 786
ID AD128661 standard; protein; 855 AA.
DE Human matrixinase (MTSP1) serine protease.
PN WO2004005471-A2.
PD 15-JAN-2004.
PA (DEND-) DENDREON SAN DIEGO LLC.
Query Match 8.3%; Score 327; DB 8; Length 855;
Best Local Similarity 21.6%; Pred. No. 1.3e-09;
RESULT 787
ID AD446895 standard; protein; 855 AA.
DE Human transmembrane serine protease (MTSP) polypeptide #1.
PN US2004001801-A1.
PD 01-JAN-2004.
PA (CORV-) CORVAS INT INC.
Query Match 8.3%; Score 327; DB 8; Length 855;
Best Local Similarity 21.6%; Pred. No. 1.3e-09;
RESULT 788
ID AAE20788 standard; protein; 3095 AA.
DE Rat C3b/C4b complement receptor like protein.
PN WO200210199-A2.
PD 07-FEB-2002.
PA (AMGE-) AMGEN INC.
Query Match 8.2%; Score 324; DB 5; Length 3095;
Best Local Similarity 20.1%; Pred. No. 6.4e-09;
RESULT 789
ID AD42162 standard; protein; 757 AA.
DE Human novel protein NOV 8.
PN US2004033493-A1.
PD 19-FEB-2004.
PA (TCHE/) TCHERNEV V. T.
PA (SPYT/) SPYTEK K. A.
PA (ZERR/) ZERRHUSEN B. D.
PA (PATT/) PATTURAJAN M.
PA (SHIM/) SHIMKETS R. A.
PA (LILL/) LI L.
PA (GANG/) GANGGOLI E. A.
PA (PADI/) PADIGARU M.
PA (ANDE/) ANDERSON D. W.
PA (RAST/) RASTELI L.
PA (MILL/) MILLER C. E.
PA (GERL/) GERLACH V.
PA (TAUP/) TAUPIER R. J.
PA (GUSE/) GUSEV V. Y.
PA (COLM/) COLMAN S. D.
PA (WOLE/) WOLENC A. R.
PA (PENA/) PENA C. E. A.
PA (FURT/) FURTAK K.
PA (GROS/) GROSSE W. M.
PA (ALSO/) ALSOBROOK J. P.
PA (LEPL/) LEPLER D. M.
PA (RIEG/) RIEGER D. K.
PA (BURG/) BURGESS C. E.
Query Match 8.2%; Score 323; DB 8; Length 757;
Best Local Similarity 21.6%; Pred. No. 1.9e-09;
RESULT 790
ID ADH71146 standard; protein; 3130 AA.
DE Human protein of the invention NOV46 SEQ ID NO:42.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 8.1%; Score 321; DB 8; Length 3130;
Best Local Similarity 22.6%; Pred. No. 9.4e-09;
RESULT 791
ID ADH71144 standard; protein; 3483 AA.
DE Human protein of the invention NOV4e SEQ ID NO:40.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 8.1%; Score 321; DB 8; Length 3483;
Best Local Similarity 22.6%; Pred. No. 1e-08;
RESULT 792
ID ADH71136 standard; protein; 3546 AA.
DE Human protein of the invention NOV4a SEQ ID NO:32.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 8.1%; Score 321; DB 8; Length 3546;
Best Local Similarity 22.6%; Pred. No. 1.1e-08;
RESULT 793
ID AAE20787 standard; protein; 3069 AA.
DE Human C3b/C4b complement receptor like protein #1.
PN WO200210199-A2.
PD 07-FEB-2002.
PA (AMGE-) AMGEN INC.
Query Match 8.1%; Score 320.5; DB 5; Length 3069;
Best Local Similarity 20.7%; Pred. No. 9.8e-09;
RESULT 794
ID AAE20789 standard; protein; 3100 AA.
DE Human C3b/C4b complement receptor like protein #2.
PN WO200210199-A2.
PD 07-FEB-2002.
PA (AMGE-) AMGEN INC.
Query Match 8.1%; Score 320.5; DB 5; Length 3100;
Best Local Similarity 20.7%; Pred. No. 9.9e-09;
RESULT 795
ID AAU99088 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant G383N/G385T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 8.1%; Score 319.5; DB 5; Length 419;
Best Local Similarity 24.7%; Pred. No. 1.7e-09;
RESULT 796
ID AAU99080 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant L349N/D351T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 8.1%; Score 319.5; DB 5; Length 419;
Best Local Similarity 24.7%; Pred. No. 1.7e-09;
RESULT 797
ID ADG83836 standard; protein; 455 AA.
DE Rough scale snake venom protease.
PN WO2003082914-A1.
PD 09-OCT-2003.
PA (UYQU) UNIV QUEENSLAND.
Query Match 8.1%; Score 319.5; DB 8; Length 455;
Best Local Similarity 23.4%; Pred. No. 1.9e-09;
RESULT 798
ID AAU99078 standard; protein; 419 AA.
DE Human protein C zymogen protein mutant I348N/G350T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 8.1%; Score 318.5; DB 5; Length 419;
Best Local Similarity 24.7%; Pred. No. 2e-09;
RESULT 799
ID ADH71142 standard; protein; 2612 AA.
DE Human protein of the invention NOV4d SEQ ID NO:38.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 8.1%; Score 318; DB 8; Length 2612;
Best Local Similarity 22.6%; Pred. No. 1.2e-08;
RESULT 800
ID ABG79169 standard; protein; 2669 AA.
DE Human cub and sushi domain containing protein #2.
PN WO200264791-A2.
PD 22-AUG-2002.
PA (CURA-) CURAGEN CORP.
Query Match 8.1%; Score 318; DB 5; Length 2669;
Best Local Similarity 22.6%; Pred. No. 1.2e-08;

RESULT 801
ID ADH71140 standard; protein; 2669 AA.
DE Human protein of the invention NOV4c SEQ ID NO:36.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 8.1%; Score 318; DB 8; Length 2669;
Best Local Similarity 22.6%; Pred. No. 1.2e-08;
RESULT 802
ID ABG79168 standard; protein; 3104 AA.
DE Human cub and sushi domain containing protein #1.
PN WO200264791-A2.
PD 22-AUG-2002.
PA (CURA-) CURAGEN CORP.
Query Match 8.1%; Score 318; DB 5; Length 3104;
Best Local Similarity 22.6%; Pred. No. 1.4e-08;
RESULT 803
ID ADH71168 standard; protein; 3104 AA.
DE Human protein of the invention NOV4q SEQ ID NO:64.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 8.1%; Score 318; DB 8; Length 3104;
Best Local Similarity 22.6%; Pred. No. 1.4e-08;
RESULT 804
ID ADH71166 standard; protein; 3104 AA.
DE Human protein of the invention NOV4p SEQ ID NO:62.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 8.1%; Score 318; DB 8; Length 3104;
Best Local Similarity 22.6%; Pred. No. 1.4e-08;
RESULT 805
ID ADH71138 standard; protein; 3104 AA.
DE Human protein of the invention NOV4b SEQ ID NO:34.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 8.1%; Score 318; DB 8; Length 3104;
Best Local Similarity 22.6%; Pred. No. 1.4e-08;
RESULT 806
ID AAU99006 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant D189N/K191T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 8.0%; Score 317.5; DB 5; Length 419;
Best Local Similarity 24.4%; Pred. No. 2.2e-09;
RESULT 807
ID AAU99066 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant T315N/V317T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 8.0%; Score 317.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 2.2e-09;
RESULT 808
ID AAB57283 standard; protein; 798 AA.
DE Bovine enterokinase.
PN WO9416083-A1.
PD 21-JUL-1994.
PA (GENY-) GENETICS INST INC.
Query Match 8.0%; Score 317.5; DB 2; Length 798;
Best Local Similarity 24.6%; Pred. No. 4e-09;
RESULT 809
ID AAE20900 standard; protein; 3069 AA.
DE Human C3b/C4b complement receptor like protein #1, alternative version.
PN WO200210199-A2.
PD 07-FEB-2002.
PA (AMGE-) AMGEN INC.
Query Match 8.0%; Score 317.5; DB 5; Length 3069;
Best Local Similarity 24.5%; Pred. No. 2.8e-09;

Best Local Similarity 20.7%; Pred. No. 1.4e-08;
RESULT 810
ID AAE20901 standard; protein; 3100 AA.
DE Human C3b/C4b complement receptor like protein #2, alternative version.
PN WO200210199-A2.
PD 07-FEB-2002.
PA (AMGE-) AMGEN INC.
Query Match 8.0%; Score 317.5; DB 5; Length 3100;
Best Local Similarity 20.7%; Pred. No. 1.4e-08;
RESULT 811
ID AAU99076 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant M338N/S340T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 8.0%; Score 316.5; DB 5; Length 419;
Best Local Similarity 24.7%; Pred. No. 2.5e-09;
RESULT 812
ID AAU99022 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant K217N/L219T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 8.0%; Score 316.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 2.5e-09;
RESULT 813
ID AAU99026 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant L220N/R222T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 8.0%; Score 315.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 2.8e-09;
RESULT 814
ID AAU99081 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant D351N/Q353S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 8.0%; Score 315.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 2.8e-09;
RESULT 815
ID AAU99071 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant S336N/W338S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 8.0%; Score 315.5; DB 5; Length 419;
Best Local Similarity 24.7%; Pred. No. 2.8e-09;
RESULT 816
ID AAU99087 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant G383N/G385S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 8.0%; Score 315.5; DB 5; Length 419;
Best Local Similarity 24.7%; Pred. No. 2.8e-09;
RESULT 817
ID AAU99079 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant L349N/D351S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 8.0%; Score 315.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 2.8e-09;
RESULT 818
ID AAU99079 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant L349N/D351S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 8.0%; Score 315.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 2.8e-09;

ID AAR62653 standard; protein; 461 AA.
 DE Human protein C.
 PN US5358932-A.
 PD 25-OCT-1994.
 PA (ZYMO) ZYMOGENETICS INC.
 Query Match 8.0%; Score 315.5; DB 2; Length 461;
 Best Local Similarity 24.5%; Pred. No. 3.1e-09;
 RESULT 819
 ID AAR5760 standard; protein; 419 AA.
 DE Protein C (PC).
 PN WO9309804-A1.
 PD 27-MAY-1993.
 PA (SCRI) SCRIPPS RES INST.
 Query Match 8.0%; Score 314.5; DB 2; Length 419;
 Best Local Similarity 23.3%; Pred. No. 3.2e-09;
 RESULT 820
 ID AAU99053 standard; protein; 419 AA.
 DE Human Protein C zymogen protein mutant R306N/K308S.
 PN WO200232461-A2.
 PD 25-APR-2002.
 PA (MAXY-) MAXYGEN APS.
 Query Match 8.0%; Score 314.5; DB 5; Length 419;
 Best Local Similarity 24.7%; Pred. No. 3.2e-09;
 RESULT 821
 ID AAU99007 standard; protein; 419 AA.
 DE Human Protein C zymogen protein mutant S190N/K192S.
 PN WO200232461-A2.
 PD 25-APR-2002.
 PA (MAXY-) MAXYGEN APS.
 Query Match 8.0%; Score 314.5; DB 5; Length 419;
 Best Local Similarity 24.4%; Pred. No. 3.2e-09;
 RESULT 822
 ID AAU99077 standard; protein; 419 AA.
 DE Human Protein C zymogen protein mutant I348N/G350S.
 PN WO200232461-A2.
 PD 25-APR-2002.
 PA (MAXY-) MAXYGEN APS.
 Query Match 8.0%; Score 314.5; DB 5; Length 419;
 Best Local Similarity 24.5%; Pred. No. 3.2e-09;
 RESULT 823
 ID AAU99043 standard; protein; 419 AA.
 DE Human Protein C zymogen protein mutant L296N.
 PN WO200232461-A2.
 PD 25-APR-2002.
 PA (MAXY-) MAXYGEN APS.
 Query Match 8.0%; Score 314.5; DB 5; Length 419;
 Best Local Similarity 24.5%; Pred. No. 3.2e-09;
 RESULT 824
 ID ADG83832 standard; protein; 454 AA.
 DE Red belly black snake venom protease.
 PN WO2003082914-A1.
 PD 09-OCT-2003.
 PA (UYOU) UNIV QUEENSLAND.
 Query Match 8.0%; Score 314.5; DB 8; Length 454;
 Best Local Similarity 23.0%; Pred. No. 3.5e-09;
 RESULT 825
 ID AAM77504 standard; protein; 461 AA.
 DE Human protein C variant #2 amino acid sequence.
 PN WO2003106666-A2.
 PD 24-DEC-2003.
 PA (MAXY-) MAXYGEN APS.
 Query Match 8.0%; Score 314.5; DB 8; Length 461;
 Best Local Similarity 24.5%; Pred. No. 3.5e-09;
 RESULT 826
 ID AAE23083 standard; protein; 855 AA.
 DE Epithin protein.
 PN WO200203787-A2.
 PD 17-JAN-2002.

PA (DELT-) DELTAGEN INC.
 Query Match 8.0%; Score 314; DB 5; Length 855;
 Best Local Similarity 21.4%; Pred. No. 6.7e-09;
 RESULT 827
 ID AD16819 standard; protein; 855 AA.
 DE Murine NOVX protein homologue Segid 355.
 PN WO200268649-A2.
 PD 06-SEP-2002.
 PA (CURA-) CURAGEN CORP.
 Query Match 8.0%; Score 314; DB 5; Length 855;
 Best Local Similarity 21.4%; Pred. No. 6.7e-09;
 RESULT 828
 ID AD16877 standard; protein; 855 AA.
 DE Murine NOVX protein homologue Segid 413.
 PN WO200268649-A2.
 PD 06-SEP-2002.
 PA (CURA-) CURAGEN CORP.
 Query Match 8.0%; Score 314; DB 5; Length 855;
 Best Local Similarity 21.4%; Pred. No. 6.7e-09;
 RESULT 829
 ID AAM72753 standard; protein; 419 AA.
 DE Primary structure of activated human protein C.
 PN EP875563-A2.
 PD 04-NOV-1998.
 PA (BLIL) LILLY & CO ELI.
 Query Match 7.9%; Score 313.5; DB 2; Length 419;
 Best Local Similarity 23.3%; Pred. No. 3.6e-09;
 RESULT 830
 ID AAU99005 standard; protein; 419 AA.
 DE Human Protein C zymogen protein mutant D189N/K191S.
 PN WO200232461-A2.
 PD 25-APR-2002.
 PA (MAXY-) MAXYGEN APS.
 Query Match 7.9%; Score 313.5; DB 5; Length 419;
 Best Local Similarity 24.2%; Pred. No. 3.6e-09;
 RESULT 831
 ID AAU99025 standard; protein; 419 AA.
 DE Human Protein C zymogen protein mutant L220N/R222S.
 PN WO200232461-A2.
 PD 25-APR-2002.
 PA (MAXY-) MAXYGEN APS.
 Query Match 7.9%; Score 313.5; DB 5; Length 419;
 Best Local Similarity 24.5%; Pred. No. 3.6e-09;
 RESULT 832
 ID AAU99065 standard; protein; 419 AA.
 DE Human Protein C zymogen protein mutant T315N/V317S.
 PN WO200232461-A2.
 PD 25-APR-2002.
 PA (MAXY-) MAXYGEN APS.
 Query Match 7.9%; Score 313.5; DB 5; Length 419;
 Best Local Similarity 24.3%; Pred. No. 3.6e-09;
 RESULT 833
 ID AAU99016 standard; protein; 419 AA.
 DE Human Protein C zymogen protein mutant D214N/S216T.
 PN WO200232461-A2.
 PD 25-APR-2002.
 PA (MAXY-) MAXYGEN APS.
 Query Match 7.9%; Score 313.5; DB 5; Length 419;
 Best Local Similarity 24.7%; Pred. No. 3.6e-09;
 RESULT 834
 ID AAU99023 standard; protein; 419 AA.
 DE Human Protein C zymogen protein mutant K218N/L220S.
 PN WO200232461-A2.
 PD 25-APR-2002.
 PA (MAXY-) MAXYGEN APS.
 Query Match 7.9%; Score 313.5; DB 5; Length 419;
 Best Local Similarity 24.5%; Pred. No. 3.6e-09;
 RESULT 835

ID AAR13083 standard; protein: 509 AA.
DE PAP-I-Protein C fusion construct.
PN WO9109953-A.
PD 11-JUL-1991.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 7.9%; Score 313; DB 2; Length 509;
Best Local Similarity 23.5%; Pred. No. 4.6e-09;
RESULT 836
ID AD116820 standard; protein: 855 AA.
DE Rat NOVX protein homologue SeqID 356.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 7.9%; Score 313; DB 5; Length 855;
Best Local Similarity 21.4%; Pred. No. 7.5e-09;
RESULT 837
ID AD116881 standard; protein: 855 AA.
DE Rat NOVX protein homologue SeqID 417.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 7.9%; Score 313; DB 5; Length 855;
Best Local Similarity 21.4%; Pred. No. 7.5e-09;
RESULT 838
ID AD116878 standard; protein: 855 AA.
DE Rat NOVX protein homologue SeqID 414.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 7.9%; Score 313; DB 5; Length 855;
Best Local Similarity 21.4%; Pred. No. 7.5e-09;
RESULT 839
ID AAU99072 standard; protein: 419 AA.
DE Human Protein C zymogen protein mutant S336N/M338T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 4.1e-09;
RESULT 840
ID AAU99097 standard; protein: 419 AA.
DE Human Protein C zymogen protein mutant D189N/K191N.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.2%; Pred. No. 4.1e-09;
RESULT 841
ID AAU99009 standard; protein: 419 AA.
DE Human Protein C zymogen protein mutant K191N/K193S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.2%; Pred. No. 4.1e-09;
RESULT 842
ID AAU99064 standard; protein: 419 AA.
DE Human Protein C zymogen protein mutant R312N/R314T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.9%; Pred. No. 4.1e-09;
RESULT 843
ID AAU99069 standard; protein: 419 AA.
DE Human Protein C zymogen protein mutant V334N.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.

PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 4.1e-09;
RESULT 844
ID AAU99082 standard; protein: 419 AA.
DE Human Protein C zymogen protein mutant D351N/Q353T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 4.1e-09;
RESULT 845
ID AAU99096 standard; protein: 419 AA.
DE Human Protein C zymogen protein mutant M338A.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 4.1e-09;
RESULT 846
ID AAU99091 standard; protein: 419 AA.
DE Human Protein C zymogen protein mutant L387N/N389S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 4.1e-09;
RESULT 847
ID AAU99024 standard; protein: 419 AA.
DE Human Protein C zymogen protein mutant K218N/L220T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 4.1e-09;
RESULT 848
ID AAU99048 standard; protein: 419 AA.
DE Human Protein C zymogen protein mutant H303N/S305T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.3%; Pred. No. 4.1e-09;
RESULT 849
ID AAU99067 standard; protein: 419 AA.
DE Human Protein C zymogen protein mutant F316N/L318S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 4.1e-09;
RESULT 850
ID AAU99075 standard; protein: 419 AA.
DE Human Protein C zymogen protein mutant M338N.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 4.1e-09;
RESULT 851
ID AAU99092 standard; protein: 419 AA.
DE Human Protein C zymogen protein mutant L387N/N389T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 4.1e-09;
RESULT 852
ID AAU99092 standard; protein: 419 AA.
DE Human Protein C zymogen protein mutant L387N/N389T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN HOLDINGS LTD.

Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 4.1e-09;
RESULT 852
ID AAU99011 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant K192N/L194S.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 4.1e-09;
RESULT 853
ID AAU99032 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant S250N/S252T.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 4.1e-09;
RESULT 854
ID ADM77507 standard; protein; 461 AA.
DE Human protein C variant #5 amino acid sequence.
PN W02003106666-A2.
PD 24-DEC-2003.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 312.5; DB 8; Length 461;
Best Local Similarity 24.3%; Pred. No. 4.5e-09;
RESULT 855
ID ADM77505 standard; protein; 461 AA.
DE Human protein C variant #3 amino acid sequence.
PN W02003106666-A2.
PD 24-DEC-2003.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 312.5; DB 8; Length 461;
Best Local Similarity 24.5%; Pred. No. 4.5e-09;
RESULT 856
ID AAB82677 standard; protein; 419 AA.
DE Human protein C derivative (H10Q/S11G/Q32E/N33D/L194S).
PN W0200157193-A2.
PD 09-AUG-2001.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 312; DB 4; Length 419;
Best Local Similarity 24.5%; Pred. No. 4.4e-09;
RESULT 857
ID AAR13537 standard; protein; 460 AA.
DE Human Protein C zymogen N.
PN EP443875-A.
PD 28-AUG-1991.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 312; DB 2; Length 460;
Best Local Similarity 24.7%; Pred. No. 4.8e-09;
RESULT 858
ID ADG83630 standard; protein; 467 AA.
DE Coesetal taipan venom protease.
PN W02003082914-A1.
PD 09-OCT-2003.
PA (UYOU) UNIV QUEENSLAND.
Query Match 7.9%; Score 312; DB 8; Length 467;
Best Local Similarity 23.0%; Pred. No. 4.9e-09;
RESULT 859
ID AAB60993 standard; protein; 1031 AA.
DE Novel human protein. SEQ ID 80.
PN W0200250105-A1.
PD 27-JUN-2002.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (GLAX) GLAXO GROUP LTD.
Query Match 7.9%; Score 312; DB 5; Length 1031;
Best Local Similarity 22.6%; Pred. No. 1e-08;
RESULT 860

ID AAU99008 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant S190N/K192T.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 311.5; DB 5; Length 419;
Best Local Similarity 24.2%; Pred. No. 4.7e-09;
RESULT 861
ID AAU99039 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant T254N/N256S.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 311.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 4.7e-09;
RESULT 862
ID AAU99047 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant H303N.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 311.5; DB 5; Length 419;
Best Local Similarity 24.3%; Pred. No. 4.7e-09;
RESULT 863
ID AAU99070 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant V334N/S336T.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 311.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 4.7e-09;
RESULT 864
ID AAU99017 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant E215N/K217S.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 311.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 4.7e-09;
RESULT 865
ID AAU99044 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant L296N/T298S.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 311.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 4.7e-09;
RESULT 866
ID AAU99014 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant K193N/A195T.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 311.5; DB 5; Length 419;
Best Local Similarity 24.2%; Pred. No. 4.7e-09;
RESULT 867
ID AAU99031 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant S250N.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 311.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 4.7e-09;
RESULT 868
ID AAU99057 standard; protein; 419 AA.

DE Human Protein C zymogen protein mutant K306N/A310S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.9%; Score 311.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 4.7e-09;
RESULT 869
ID AAU99054 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant R306N/K308T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.9%; Score 311.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 4.7e-09;
RESULT 870
ID AAU99095 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant D214N.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.9%; Score 311.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 4.7e-09;
RESULT 871
ID AAU99015 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant D214N.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.9%; Score 311.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 4.7e-09;
RESULT 872
ID AAP81205 standard; protein; 461 AA.
DE Human protein C.
PN EP266190-A.
PD 04-MAY-1988.
PA (ZVMO) ZYMOGENETICS INC.
Query Match 7.9%; Score 311.5; DB 1; Length 461;
Best Local Similarity 24.5%; Pred. No. 5.1e-09;
RESULT 873
ID AAR13539 standard; protein; 461 AA.
DE Human Protein C zymogen LIN.
PN EP443875-A.
PD 28-AUG-1991.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 311.5; DB 2; Length 461;
Best Local Similarity 24.5%; Pred. No. 5.1e-09;
RESULT 874
ID AAR13997 standard; protein; 461 AA.
DE Human protein C zymogen Q329.
PN EP443874-A.
PD 28-AUG-1991.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 311.5; DB 2; Length 461;
Best Local Similarity 24.5%; Pred. No. 5.1e-09;
RESULT 875
ID ADM77503 standard; protein; 461 AA.
DE Human protein C variant #1 amino acid sequence.
PN WO2003106666-A2.
PD 24-DEC-2003.
PA (MAXY-) MAXYGEN APS.
Query Match 7.9%; Score 311.5; DB 8; Length 461;
Best Local Similarity 24.5%; Pred. No. 5.1e-09;
RESULT 876
ID AAB82678 standard; protein; 419 AA.
DE Human protein C derivative (H10Q/S11G/Q32E/N33D/L194S/T254S).
PN WO200157193-A2.
PD 09-AUG-2001.
PA (ELIL) LILLY & CO ELI.

Query Match 7.9%; Score 311; DB 4; Length 419;
Best Local Similarity 24.5%; Pred. No. 5e-09;
RESULT 877
ID AAB82675 standard; protein; 419 AA.
DE Human protein C derivative (S11G/Q32E/N33D/L194S).
PN WO200157193-A2.
PD 09-AUG-2001.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 311; DB 4; Length 419;
Best Local Similarity 24.5%; Pred. No. 5e-09;
RESULT 878
ID ADC40013 standard; protein; 409 AA.
DE Human activated protein C-related protein #2.
PN WO2003075834-A2.
PD 18-SEP-2003.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 310.5; DB 7; Length 409;
Best Local Similarity 24.5%; Pred. No. 5.2e-09;
RESULT 879
ID ADC40012 standard; protein; 410 AA.
DE Human activated protein C-related protein #1.
PN WO2003075834-A2.
PD 18-SEP-2003.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 310.5; DB 7; Length 410;
Best Local Similarity 24.5%; Pred. No. 5.2e-09;
RESULT 880
ID AAY56803 standard; protein; 415 AA.
DE Truncated human protein C polypeptide.
PN WO9963070-A1.
PD 09-DEC-1999.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 310.5; DB 3; Length 415;
Best Local Similarity 24.5%; Pred. No. 5.2e-09;
RESULT 881
ID AAB82673 standard; protein; 419 AA.
DE Wild-type human protein C.
PN WO200157193-A2.
PD 09-AUG-2001.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 310.5; DB 4; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.3e-09;
RESULT 882
ID AAB36896 standard; protein; 419 AA.
DE Human protein C derivative 3.
PN WO200066754-A1.
PD 09-NOV-2000.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 310.5; DB 4; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.3e-09;
RESULT 883
ID AAB36894 standard; protein; 419 AA.
DE Human protein C derivative 1.
PN WO200066754-A1.
PD 09-NOV-2000.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 310.5; DB 4; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.3e-09;
RESULT 884
ID AAB06625 standard; protein; 419 AA.
DE Human mature wild type protein C.
PN WO200159084-A1.
PD 16-AUG-2001.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 310.5; DB 4; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.3e-09;
RESULT 885
ID AAU99063 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant R312N/R314S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.9%; Score 310.5; DB 4; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.3e-09;
RESULT 886
ID AAB82678 standard; protein; 419 AA.
DE Human protein C derivative (H10Q/S11G/Q32E/N33D/L194S/T254S).
PN WO200157193-A2.
PD 09-AUG-2001.
PA (ELIL) LILLY & CO ELI.

Query Match 7.9%; Score 310.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.3e-09;
RESULT 886
ID AAU99012 standard; protein: 419 AA.
DE Human Protein C zymogen protein mutant K192N/L194T.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.3e-09;
RESULT 887
ID AAU99050 standard; protein: 419 AA.
DE Human Protein C zymogen protein mutant S304N/E306T.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.3e-09;
RESULT 888
ID AAU99010 standard; protein: 419 AA.
DE Human Protein C zymogen protein mutant K191N/K193T.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 5; Length 419;
Best Local Similarity 24.2%; Pred. No. 5.3e-09;
RESULT 889
ID AAU99040 standard; protein: 419 AA.
DE Human Protein C zymogen protein mutant T254N/N256T.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.3e-09;
RESULT 890
ID AAU99060 standard; protein: 419 AA.
DE Human Protein C zymogen protein mutant E309N/K311T.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.3e-09;
RESULT 891
ID AAU99055 standard; protein: 419 AA.
DE Human Protein C zymogen protein mutant E307N/E309S.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.3e-09;
RESULT 892
ID AAU99056 standard; protein: 419 AA.
DE Human Protein C zymogen protein mutant E307N/E309T.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.3e-09;
RESULT 893
ID AAU99059 standard; protein: 419 AA.
DE Human Protein C zymogen protein mutant E309N/K311S.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.3e-09;
RESULT 894
ID AAU99052 standard; protein: 419 AA.
DE Human Protein C zymogen protein mutant S305N/E307T.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.3e-09;
RESULT 895
ID AAU99051 standard; protein: 419 AA.
DE Human Protein C zymogen protein mutant S305N/E307S.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.3e-09;
RESULT 896
ID AAU99052 standard; protein: 419 AA.
DE Human Protein C zymogen protein mutant S305N/E307T.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.3e-09;
RESULT 897
ID ABR55547 standard; protein: 419 AA.
DE Amino acid sequence of mature human protein C (PC).
PN FR2831170-A1.
PD 25-APR-2003.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
Query Match 7.9%; Score 310.5; DB 6; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.3e-09;
RESULT 898
ID ADC40014 standard; protein: 419 AA.
DE Human activated protein C-related protein #3.
PN W02003075834-A2.
PD 18-SEP-2003.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 310.5; DB 7; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.3e-09;
RESULT 899
ID APO18786 standard; protein: 419 AA.
DE Mature human zymogen-like protein C.
PN W02004044190-A2.
PD 27-MAY-2004.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 8; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.3e-09;
RESULT 900
ID ADG83834 standard; protein: 453 AA.
DE Mainland tiger snake venom protease.
PN W02003082914-A1.
PD 09-OCT-2003.
PA (UYOU) UNIV QUEBENS LAND.
Query Match 7.9%; Score 310.5; DB 8; Length 453;
Best Local Similarity 22.8%; Pred. No. 5.7e-09;
RESULT 901
ID AAP81104 standard; protein: 460 AA.
DE Sequence of human protein C.
PN JF63263083-A.
PD 31-OCT-1988.
PA (FARH) HOECHST JAPAN LTD.
Query Match 7.9%; Score 310.5; DB 1; Length 460;
Best Local Similarity 24.5%; Pred. No. 5.8e-09;
RESULT 902
ID AAW25086 standard; protein: 460 AA.
DE Human protein C.
PN W09720043-A1.

Best Local Similarity 24.5%; Pred. No. 5.3e-09;
RESULT 894
ID AAU99002 standard; protein: 419 AA.
DE Human Protein C zymogen protein.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.3e-09;
RESULT 895
ID AAU99051 standard; protein: 419 AA.
DE Human Protein C zymogen protein mutant S305N/E307S.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.3e-09;
RESULT 896
ID AAU99052 standard; protein: 419 AA.
DE Human Protein C zymogen protein mutant S305N/E307T.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.3e-09;
RESULT 897
ID ABR55547 standard; protein: 419 AA.
DE Amino acid sequence of mature human protein C (PC).
PN FR2831170-A1.
PD 25-APR-2003.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
Query Match 7.9%; Score 310.5; DB 6; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.3e-09;
RESULT 898
ID ADC40014 standard; protein: 419 AA.
DE Human activated protein C-related protein #3.
PN W02003075834-A2.
PD 18-SEP-2003.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 310.5; DB 7; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.3e-09;
RESULT 899
ID APO18786 standard; protein: 419 AA.
DE Mature human zymogen-like protein C.
PN W02004044190-A2.
PD 27-MAY-2004.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 8; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.3e-09;
RESULT 900
ID ADG83834 standard; protein: 453 AA.
DE Mainland tiger snake venom protease.
PN W02003082914-A1.
PD 09-OCT-2003.
PA (UYOU) UNIV QUEBENS LAND.
Query Match 7.9%; Score 310.5; DB 8; Length 453;
Best Local Similarity 22.8%; Pred. No. 5.7e-09;
RESULT 901
ID AAP81104 standard; protein: 460 AA.
DE Sequence of human protein C.
PN JF63263083-A.
PD 31-OCT-1988.
PA (FARH) HOECHST JAPAN LTD.
Query Match 7.9%; Score 310.5; DB 1; Length 460;
Best Local Similarity 24.5%; Pred. No. 5.8e-09;
RESULT 902
ID AAW25086 standard; protein: 460 AA.
DE Human protein C.
PN W09720043-A1.

PD 05-JUN-1997.
PA (ZYMO) ZYMOGENETICS INC.
PA (PBLT-) PPL THERAPEUTICS.
Query Match 7.9%; Score 310.5; DB 2; Length 460;
Best Local Similarity 24.5%; Pred. No. 5.8e-09;
RESULT 903
ID AAB60001 standard; protein; 461 AA.
DE Sequence of polypeptide with human protein C activity.
PN EPI91606-A.
PD 20-AUG-1986.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 310.5; DB 1; Length 461;
Best Local Similarity 24.5%; Pred. No. 5.8e-09;
RESULT 904
ID AAE70855 standard; protein; 461 AA.
DE Human protein C.
PN EPI15548-A.
PD 25-MAR-1987.
PA (ZYMO) ZYMOGENETICS INC.
PA (UNIV) UNIV WASHINGTON.
Query Match 7.9%; Score 310.5; DB 1; Length 461;
Best Local Similarity 24.5%; Pred. No. 5.8e-09;
RESULT 905
ID AAP90401 standard; protein; 461 AA.
DE Zymogen form of human protein C.
PN EP323149-A.
PD 05-JUL-1989.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 310.5; DB 1; Length 461;
Best Local Similarity 24.5%; Pred. No. 5.8e-09;
RESULT 906
ID AAR13622 standard; protein; 461 AA.
DE Human protein C.
PN WO9109953-A.
PD 11-JUL-1991.
PA (ZYMO) ZYMOGENETICS INC.
PA (TEIJ) TEIJIN LTD.
Query Match 7.9%; Score 310.5; DB 2; Length 461;
Best Local Similarity 24.5%; Pred. No. 5.8e-09;
RESULT 907
ID AAR13081 standard; protein; 461 AA.
DE Human protein C.
PN WO9109953-A.
PD 11-JUL-1991.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 7.9%; Score 310.5; DB 2; Length 461;
Best Local Similarity 24.5%; Pred. No. 5.8e-09;
RESULT 908
ID AAR13074 standard; protein; 461 AA.
DE Protein C precursor.
PN WO9109951-A.
PD 11-JUL-1991.
PA (ZYMO) ZYMOGENETICS INC.
PA (TEIJ) TEIJIN LTD.
Query Match 7.9%; Score 310.5; DB 2; Length 461;
Best Local Similarity 24.5%; Pred. No. 5.8e-09;
RESULT 909
ID AAR34295 standard; protein; 461 AA.
DE Protein C.
PN JP05064588-A.
PD 19-MAR-1993.
PA (TEIJ) TEIJIN LTD.
Query Match 7.9%; Score 310.5; DB 2; Length 461;
Best Local Similarity 24.5%; Pred. No. 5.8e-09;
RESULT 910
ID AAM02600 standard; protein; 461 AA.
DE Human protein C.
PN USS516650-A.
PD 14-MAY-1996.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 7.9%; Score 310.5; DB 2; Length 461;
Best Local Similarity 24.5%; Pred. No. 5.8e-09;
RESULT 911

ID AAY9561 standard; protein; 461 AA.
DE Human lecithin cholesterol acyltransferase protein sequence.
PN WO9950454-A2.
PD 07-OCT-1999.
PA (WHEB) WIREHEAD INST BIOMEDICAL RES.
Query Match 7.9%; Score 310.5; DB 2; Length 461;
Best Local Similarity 24.5%; Pred. No. 5.8e-09;
RESULT 912
ID AAB82674 standard; protein; 461 AA.
DE Wild-type human protein C.
PN WO200157193-A2.
PD 09-AUG-2001.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 310.5; DB 4; Length 461;
Best Local Similarity 24.5%; Pred. No. 5.8e-09;
RESULT 913
ID AAB36895 standard; protein; 461 AA.
DE Human protein C derivative 2.
PN WO200066754-A1.
PD 09-NOV-2000.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 310.5; DB 4; Length 461;
Best Local Similarity 24.5%; Pred. No. 5.8e-09;
RESULT 914
ID AAB08626 standard; protein; 461 AA.
DE Human wild type protein C.
PN WO200159084-A1.
PD 16-AUG-2001.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 310.5; DB 4; Length 461;
Best Local Similarity 24.5%; Pred. No. 5.8e-09;
RESULT 915
ID AAU99001 standard; protein; 461 AA.
DE Human Protein C precursor protein.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 5; Length 461;
Best Local Similarity 24.5%; Pred. No. 5.8e-09;
RESULT 916
ID ADW77502 standard; protein; 461 AA.
DE Human protein C wild-type amino acid sequence.
PN WO2003106666-A2.
PD 24-DEC-2003.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 8; Length 461;
Best Local Similarity 24.5%; Pred. No. 5.8e-09;
RESULT 917
ID ADO18787 standard; protein; 461 AA.
DE Human zymogen-like protein C.
PN WO2004044190-A2.
PD 27-MAY-2004.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 8; Length 461;
Best Local Similarity 24.5%; Pred. No. 5.8e-09;
RESULT 918
ID AAB82676 standard; protein; 419 AA.
DE Human protein C derivative (S11G/Q32E/N33D/L194S/T234S).
PN WO200157193-A2.
PD 09-AUG-2001.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 310; DB 4; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.6e-09;
RESULT 919
ID AAE08630 standard; protein; 419 AA.
DE Human protein C derivative #4.
PN WO200159084-A1.
PD 16-AUG-2001.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 310; DB 4; Length 419;
Query Match 7.9%; Score 310; DB 4; Length 419;

Best Local Similarity 24.5%; Pred. No. 5.6e-09;
RESULT 920
ID AAR13538 standard; protein; 460 AA.
DE Human Protein C zymogen FN.
PN EP443875-A.
PD 28-AUG-1991.
PA (ELIL) LILLY & CO ELI.
Query Match 7.8%; Score 310; DB 2; Length 460;
Best Local Similarity 24.7%; Pred. No. 6.1e-09;
RESULT 921
ID AAB36897 standard; protein; 419 AA.
DE Human protein C derivative 4.
PN WO20006754-A1.
PD 09-NOV-2000.
PA (ELIL) LILLY & CO ELI.
Query Match 7.8%; Score 309.5; DB 4; Length 419;
Best Local Similarity 24.5%; Pred. No. 6e-09;
RESULT 922
ID AAB36898 standard; protein; 419 AA.
DE Human protein C derivative 5.
PN WO20006754-A1.
PD 09-NOV-2000.
PA (ELIL) LILLY & CO ELI.
Query Match 7.8%; Score 309.5; DB 4; Length 419;
Best Local Similarity 24.5%; Pred. No. 6e-09;
RESULT 923
ID AAU99018 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant E215N/K217T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.8%; Score 309.5; DB 5; Length 419;
Best Local Similarity 24.4%; Pred. No. 6e-09;
RESULT 924
ID AAU99033 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant K251N.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.8%; Score 309.5; DB 5; Length 419;
Best Local Similarity 24.4%; Pred. No. 6e-09;
RESULT 925
ID AAU99013 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant K193N/A195S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.8%; Score 309.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 6e-09;
RESULT 926
ID AAU99068 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant F316N/K318T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.8%; Score 309.5; DB 5; Length 419;
Best Local Similarity 24.2%; Pred. No. 6e-09;
RESULT 927
ID AAU99062 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant A310N/K312T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.8%; Score 309.5; DB 5; Length 419;
Best Local Similarity 24.8%; Pred. No. 6e-09;
RESULT 928
ID AAU99020 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant S216N/K218T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.8%; Score 309.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 6e-09;
RESULT 929
ID AAU99035 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant S252N.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.8%; Score 309.5; DB 5; Length 419;
Best Local Similarity 24.4%; Pred. No. 6e-09;
RESULT 930
ID AAU99085 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant E357N/D359S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.8%; Score 309.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 6e-09;
RESULT 931
ID AAU99058 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant K308N/A310T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.8%; Score 309.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 6e-09;
RESULT 932
ID AAU99019 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant S216N/K218S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.8%; Score 309.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 6e-09;
RESULT 933
ID AAU99094 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant H388N/Y390T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.8%; Score 309.5; DB 5; Length 419;
Best Local Similarity 24.4%; Pred. No. 6e-09;
RESULT 934
ID AAU99089 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant L386N/H388S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.8%; Score 309.5; DB 5; Length 419;
Best Local Similarity 24.7%; Pred. No. 6e-09;
RESULT 935
ID AAP90070 standard; protein; 461 AA.
DE Human protein C.
PN EP319312-A.
PD 07-JUN-1989.
PA (ELIL) LILLY & CO ELI.
Query Match 7.8%; Score 309.5; DB 1; Length 461;
Best Local Similarity 24.5%; Pred. No. 6.5e-09;
RESULT 936
ID AAR13540 standard; protein; 461 AA.
DE Human Protein C zymogen FLIN.
PN EP443875-A.
PD 28-AUG-1991.

PA (ELIL) LILLY & CO ELI.
Query Match 7.8%; Score 309.5; DB 2; Length 461;
Best Local Similarity 24.5%; Pred. No. 6.5e-09;
RESULT 937
ID AD16874 standard; protein; 799 AA.
DE Murine NOVX protein homologue SegID 410.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 7.8%; Score 309.5; DB 5; Length 799;
Best Local Similarity 21.6%; Pred. No. 1.1e-08;
RESULT 938
ID AD16880 standard; protein; 799 AA.
DE Murine NOVX protein homologue SegID 416.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 7.8%; Score 309.5; DB 5; Length 799;
Best Local Similarity 21.6%; Pred. No. 1.1e-08;
RESULT 939
ID AAE08627 standard; protein; 419 AA.
DE Human protein C derivative #1.
PN WO200159084-A1.
PD 16-AUG-2001.
PA (ELIL) LILLY & CO ELI.
Query Match 7.8%; Score 309; DB 4; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.4e-09;
RESULT 940
ID AAE08629 standard; protein; 419 AA.
DE Human protein C derivative #3.
PN WO200159084-A1.
PD 16-AUG-2001.
PA (ELIL) LILLY & CO ELI.
Query Match 7.8%; Score 309; DB 4; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.4e-09;
RESULT 941
ID AAU99049 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant S304N/R310S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.8%; Score 308.5; DB 5; Length 419;
Best Local Similarity 24.1%; Pred. No. 6.8e-09;
RESULT 942
ID AAU99061 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant A310N/R312S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.8%; Score 308.5; DB 5; Length 419;
Best Local Similarity 24.1%; Pred. No. 6.8e-09;
RESULT 943
ID AAU99090 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant L386N/H388T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.8%; Score 308.5; DB 5; Length 419;
Best Local Similarity 24.1%; Pred. No. 6.8e-09;
RESULT 944
ID AAU99096 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant E357N/D359T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.8%; Score 308.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.8e-09;
RESULT 945
ID AAU99036 standard; protein; 419 AA.

DE Human Protein C zymogen protein mutant S252N/T254S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.8%; Score 308.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.8e-09;
RESULT 946
ID AAU99045 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant Y302N.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.8%; Score 308.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.8e-09;
RESULT 947
ID AAU99034 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant K251N/T253S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.8%; Score 308.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.8e-09;
RESULT 948
ID ADM77506 standard; protein; 461 AA.
DE Human protein C variant #4 amino acid sequence.
PN WO200310666-A2.
PD 24-DEC-2003.
PA (MAXY-) MAXYGEN APS.
Query Match 7.8%; Score 308.5; DB 8; Length 461;
Best Local Similarity 24.5%; Pred. No. 7.4e-09;
RESULT 949
ID AAE08628 standard; protein; 419 AA.
DE Human protein C derivative #2.
PN WO200159084-A1.
PD 16-AUG-2001.
PA (ELIL) LILLY & CO ELI.
Query Match 7.8%; Score 308; DB 4; Length 419;
Best Local Similarity 24.5%; Pred. No. 7.2e-09;
RESULT 950
ID AAU99084 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant R352N/D354T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.8%; Score 307.5; DB 5; Length 419;
Best Local Similarity 24.6%; Pred. No. 7.7e-09;
RESULT 951
ID AAU99021 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant K217N/L219S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.8%; Score 307.5; DB 5; Length 419;
Best Local Similarity 24.4%; Pred. No. 7.7e-09;
RESULT 952
ID AAU99046 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant Y302N/S304T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.8%; Score 307.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 7.7e-09;
RESULT 953
ID AAU99093 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant H388N/Y390S.
PN WO200232461-A2.

PD 25-APR-2002.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match
Best Local Similarity 24.7%; Pred. No. 7.7e-09; Length 419;
RESULT 954
ID AAU99083 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant R352N/D354S.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match
Best Local Similarity 7.8%; Score 306.5; DB 5; Length 419;
RESULT 955
ID AAU99074 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant V339T.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match
Best Local Similarity 7.8%; Score 306.5; DB 5; Length 419;
RESULT 956
ID AAU99003 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant D172N/K174S.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match
Best Local Similarity 7.8%; Score 306.5; DB 5; Length 419;
RESULT 957
ID AAR13585 standard; protein; 461 AA.
DE Human protein C zymogen Q313.
PN EP43874-A.
PD 28-AUG-1991.
PA (ELIL) LILLY & CO ELI.
Query Match
Best Local Similarity 7.8%; Score 306.5; DB 2; Length 461;
RESULT 958
ID AAM83654 standard; protein; 495 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:3903.
PN W02004023973-A2.
PD 25-MAR-2004.
PA (TNCY-) INCYTE CORP.
Query Match
Best Local Similarity 7.8%; Score 306.5; DB 8; Length 495;
RESULT 959
ID AAU99004 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant D172N/K174T.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match
Best Local Similarity 7.7%; Score 305.5; DB 5; Length 419;
RESULT 960
ID AAU99073 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant V339S.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match
Best Local Similarity 7.7%; Score 305.5; DB 5; Length 419;
RESULT 961
ID AAR13582 standard; protein; 461 AA.
DE Human protein C zymogen Q097.
PN EP43874-A.
PD 28-AUG-1991.
PA (ELIL) LILLY & CO ELI.
Query Match
7.7%; Score 304.5; DB 2; Length 461;

Best Local Similarity 24.4%; Pred. No. 1.2e-08;
RESULT 962
ID AAR13584 standard; protein; 461 AA.
DE Human protein C zymogen Q248.
PN EP43874-A.
PD 28-AUG-1991.
PA (ELIL) LILLY & CO ELI.
Query Match
Best Local Similarity 7.7%; Score 304.5; DB 2; Length 461;
RESULT 963
ID AAU99037 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant T253N/D255S.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match
Best Local Similarity 7.7%; Score 302.5; DB 5; Length 419;
RESULT 964
ID AAU99028 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant V243N/V245T.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match
Best Local Similarity 7.7%; Score 302.5; DB 5; Length 419;
RESULT 965
ID AAU99027 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant V243N/V245S.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match
Best Local Similarity 7.7%; Score 301.5; DB 5; Length 419;
RESULT 966
ID AAU99038 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant T253N/D255T.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match
Best Local Similarity 7.6%; Score 301.5; DB 5; Length 419;
RESULT 967
ID AAP93714 standard; protein; 461 AA.
DE Hybrid protein of protein-C and Factor-X.
PN EP296413-A.
PD 28-DEC-1988.
PA (PARH) HOECHST JAPAN LTD.
Query Match
Best Local Similarity 7.6%; Score 301.5; DB 1; Length 461;
RESULT 968
ID AAU99041 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant D255N/D257S.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match
Best Local Similarity 7.6%; Score 299.5; DB 5; Length 419;
RESULT 969
ID AAU99029 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant V245N/P247S.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match
Best Local Similarity 7.6%; Score 298.5; DB 5; Length 419;
RESULT 970
ID AAU99030 standard; protein; 419 AA.

DE Human Protein C zymogen protein mutant V245N/E247T.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match
Best Local Similarity 7.6%; Score 298.5; DB 5; Length 419;
24.4%; Pred. No. 2.3e-08;
RESULT 971
ID AAU9042 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant D255N/D257T.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match
Best Local Similarity 7.6%; Score 298.5; DB 5; Length 419;
24.2%; Pred. No. 2.3e-08;
RESULT 972
ID ADB65750 standard; protein; 397 AA.
DE Human protein encoded by clone UTERU20087070.
PN EPI308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match
Best Local Similarity 7.6%; Score 298; DB 7; Length 397;
24.1%; Pred. No. 2.4e-08;
RESULT 973
ID ADI17268 standard; protein; 230 AA.
DE Polypeptide homologous to a human NOVX domain Segid 804.
PN W0200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 7.5%; Score 296; DB 5; Length 230;
32.3%; Pred. No. 1.8e-08;
RESULT 974
ID ADI17276 standard; protein; 230 AA.
DE Polypeptide homologous to a human NOVX domain Segid 812.
PN W0200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 7.5%; Score 296; DB 5; Length 230;
32.3%; Pred. No. 1.8e-08;
RESULT 975
ID AD83075 standard; protein; 230 AA.
DE Trypsin-like serine protease protein - SEQ ID 66.
PN US2003170630-A1.
PD 11-SEP-2003.
PA (ALSO/) ALSOBROOK J. P.
PA (TCHS/) TCHERNEV V. T.
PA (LITX/) LIT X.
PA (SEYT/) SPYTEK K. A.
PA (ZERH/) ZERHUSEN B. D.
PA (PATY/) PATYUSAN M.
PA (LEPL/) LEPLAY D. M.
PA (BURG/) BURGESS C. E.
PA (SHIM/) SHIMKETS R. A.
PA (GROS/) GROSSE W. M.
PA (SZEK/) SZEKERES E. S.
PA (VERN/) VERNER C. A. M.
PA (LITL/) LI L.
PA (CASM/) CASMAN S. J.
PA (BOLD/) BOLDOS F. L.
PA (GORG/) GORGAN L.
PA (GANG/) GANGOLLI E. A.
PA (PERN/) FERNANDES E. R.
PA (RIEG/) RIEGER D. K.
PA (EDIN/) EDINGER S. R.
PA (GUNT/) GUNTHER E.
PA (MILT/) MILLER I.
PA (SCIO/) SCIORE P.
PA (ELLE/) ELLERMAN K.
PA (MACD/) MACDOUGALL J. R.
PA (SMIT/) SMITHSON G.
Query Match 7.5%; Score 296; DB 7; Length 230;

Best Local Similarity 32.3%; Pred. No. 1.8e-08;
RESULT 976
ID ABG21442 standard; protein; 932 AA.
DE Novel human diagnostic protein #21433.
PN W0200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 7.5%; Score 296; DB 4; Length 932;
21.0%; Pred. No. 6.7e-08;
RESULT 977
ID AAR09290 standard; protein; 562 AA.
DE Sequence of tissue plasminogen activator analogue GPe (Leu 66, Asp 67,
DE Thr 68, Gln 117).
PN W08912681-A.
PD 28-DEC-1989.
PA (BRBI-) BRIT BIO-TECHN LTD.
Query Match
Best Local Similarity 7.5%; Score 294; DB 2; Length 562;
23.3%; Pred. No. 5.4e-08;
RESULT 978
ID ABU12065 standard; protein; 986 AA.
DE Human NOV12a CG92293-01 protein SEQ ID 50.
PN W0200281625-A2.
PD 17-OCT-2002.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 7.4%; Score 293; DB 6; Length 986;
23.1%; Pred. No. 1e-07;
RESULT 979
ID AAR70903 standard; protein; 527 AA.
DE Human t-PA variant (N103,A432,A434).
PN US3385732-A.
PD 31-JAN-1995.
PA (GETH-) GENENTECH INC.
Query Match
Best Local Similarity 7.4%; Score 292; DB 2; Length 527;
23.4%; Pred. No. 6.5e-08;
RESULT 980
ID AAR70895 standard; protein; 527 AA.
DE Human t-PA variant (N103,A331,A332).
PN US3385732-A.
PD 31-JAN-1995.
PA (GETH-) GENENTECH INC.
Query Match
Best Local Similarity 7.4%; Score 292; DB 2; Length 527;
23.5%; Pred. No. 6.5e-08;
RESULT 981
ID ADV03787 standard; protein; 516 AA.
DE Antipeptidic protein sequence #90.
PN W02004028479-A2.
PD 08-APR-2004.
PA (GETH-) GENENTECH INC.
Query Match
Best Local Similarity 7.4%; Score 291.5; DB 8; Length 516;
23.1%; Pred. No. 6.8e-08;
RESULT 982
ID AEM80985 standard; protein; 516 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO81669, SEQ:2539.
PN W02004030615-A2.
PD 15-APR-2004.
PA (GETH-) GENENTECH INC.
Query Match
Best Local Similarity 7.4%; Score 291.5; DB 8; Length 516;
23.1%; Pred. No. 6.8e-08;
RESULT 983
ID ADQ39246 standard; protein; 516 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 909.
PN W02004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match
Best Local Similarity 7.4%; Score 291.5; DB 8; Length 516;
23.1%; Pred. No. 6.8e-08;
RESULT 984
ID ARI13921 standard; protein; 522 AA.
DE Delta (466-470) tPA variant with H432A and R434A substns.
PN W09113149-A.
PD 05-SEP-1991.
PA (GETH-) GENENTECH INC.
Query Match 7.4%; Score 291.5; DB 2; Length 522;

Best Local Similarity 22.7%; Pred. No. 6.8e-08;
RESULT 985
ID AAR70475 standard; protein: 564 AA.
DE Sequence of tissue plasminogen (TPA) analogue.
PN W08703906-A.
PD 02-JUL-1987.
PA (UPJO) UPJOHN CO.
PA (MARO/) MAROTTI K R.
Query Match
Best Local Similarity 22.9%; Pred. No. 7.4e-08; Length 564;
RESULT 986
ID A068338 standard; protein: 376 AA.
DE Rough scale snake venom prothrombin activator, crocacin.
PN W02003082914-A1.
PD 09-OCT-2003.
PA (UYOU) UNIV QUEENSLAND.
Query Match
Best Local Similarity 22.4%; Score 291; DB 8; Length 376;
RESULT 987
ID AAR60614 standard; protein: 516 AA.
DE Plasmid pDAP3 encoded sequence.
PN JP61139386-A.
PD 26-JUN-1986.
PA (TOYU) TOYO SODA MFG CO LTD.
PA (SAGA) SAGAMI CHEM RES CENTRE.
PA (CENG) CENTRAL GLASS CO LTD.
PA (HODO) HODOGAYA CHEM IND CO LTD.
Query Match
Best Local Similarity 23.1%; Score 290.5; DB 1; Length 516;
RESULT 988
ID AAR70257 standard; protein: 516 AA.
DE Sequence of human tissue plasminogen activator (TPA) and leader.
PN EP211883-A.
PD 12-AUG-1987.
PA (SAGA) SAGAMI CHEM RES CENTRE.
PA (NIPS) NIPPON SODA CO.
PA (CENG) CENTRAL GLASS CO LTD.
PA (TOYU) TOYO SODA MFG CO LTD.
PA (NISC) NISSAN CHEM IND LTD.
PA (NISC) NISSAN CHEMICAL IND K.K.
Query Match
Best Local Similarity 7.4%; Score 290.5; DB 1; Length 516;
RESULT 989
ID AAR70878 standard; protein: 483 AA.
DE Human tissue PA variant (delcal-44,N103,D184,E275).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 23.3%; Pred. No. 7.7e-08; Length 483;
RESULT 990
ID AAR70885 standard; protein: 483 AA.
DE Human tissue PA variant (delcal-44,N103,D184,E275).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 23.3%; Pred. No. 7.7e-08; Length 483;
RESULT 991
ID AAR70894 standard; protein: 527 AA.
DE Human t-PA variant (N103,A303,A304).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.4%; Score 290; DB 2; Length 527;
RESULT 992
ID AD100357 standard; protein: 520 AA.
DE Human tissue type plasminogen activator (h-TPA) mutant polypeptide.
PN CN1397564-A.
PD 19-FEB-2003.
PA (LIRB/) LI B.
Query Match
7.3%; Score 289.5; DB 7; Length 520;

Best Local Similarity 23.2%; Pred. No. 8.7e-08;
RESULT 993
ID AAR12340 standard; protein: 559 AA.
DE T-PA variant contg. fibrinogen for thrombosis lysis (1).
PN JP03061482-A.
PD 18-MAR-1991.
PA (FUJI) FUJISAWA PHARM CO LTD.
Query Match
Best Local Similarity 22.2%; Pred. No. 9.4e-08; Length 559;
RESULT 994
ID AAR22664 standard; protein: 564 AA.
DE tPA analogue KRZA.
PN US106741-A.
PD 21-APR-1992.
PA (UPJO) UPJOHN CO.
Query Match
Best Local Similarity 23.4%; Score 289.5; DB 2; Length 564;
RESULT 995
ID AAR06934 standard; protein: 658 AA.
DE Human membrane-type serine protease (MTSP) 4-S splice variant.
PN W0200157194-A2.
PD 09-AUG-2001.
PA (CORV-) CORVAS INT INC.
Query Match
Best Local Similarity 7.3%; Score 289.5; DB 4; Length 658;
RESULT 996
ID AD110379 standard; protein: 658 AA.
DE Human cell surface protease #5.
PN W0200295007-A2.
PD 28-NOV-2002.
PA (CORV-) CORVAS INT INC.
Query Match
Best Local Similarity 7.3%; Score 289.5; DB 7; Length 658;
RESULT 997
ID ADJ46903 standard; protein: 658 AA.
DE Human transmembrane serine protease (MTSP) polypeptide #5.
PN US2004001801-A1.
PD 01-JUN-2004.
PA (CORV-) CORVAS INT INC.
Query Match
Best Local Similarity 7.3%; Score 289.5; DB 8; Length 658;
RESULT 998
ID AAR06933 standard; protein: 802 AA.
DE Human membrane-type serine protease (MTSP) 4-L splice variant.
PN W0200157194-A2.
PD 09-AUG-2001.
PA (CORV-) CORVAS INT INC.
Query Match
Best Local Similarity 7.3%; Score 289.5; DB 4; Length 802;
RESULT 999
ID AD110377 standard; protein: 802 AA.
DE Human cell surface protease #4.
PN W0200295007-A2.
PD 28-NOV-2002.
PA (CORV-) CORVAS INT INC.
Query Match
Best Local Similarity 22.7%; Pred. No. 1.3e-07; Length 802;
RESULT 1000
ID ADJ46901 standard; protein: 802 AA.
DE Human transmembrane serine protease (MTSP) polypeptide #4.
PN US2004001801-A1.
PD 01-JUN-2004.
PA (CORV-) CORVAS INT INC.
Query Match
Best Local Similarity 7.3%; Score 289.5; DB 8; Length 802;
RESULT 1001
ID AAR21598 standard; protein: 527 AA.
DE tPA variant - T103W, D236A, D238A, K240A.
PN W09202612-A.
PD 20-FEB-1992.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 23.4%; Score 289; DB 2; Length 527;

RESULT 1002
ID AAR09217 standard; protein; 529 AA.
DE t-PA insertion variant 1304 HR.
PN MO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 289; DB 2; Length 529;
Best Local Similarity 23.4%; Pred. No. 9.5e-08;
RESULT 1003
ID AAB85076 standard; peptide; 296 AA.
DE Amino acid sequence of MASP-1 polypeptide.
PN MO200140451-A2.
PD 07-JUN-2001.
PA (JENS/) JENSENIUS J C.
PA (THIE/) THIEL S.
Query Match 7.3%; Score 288.5; DB 4; Length 296;
Best Local Similarity 29.3%; Pred. No. 5.9e-06;
RESULT 1004
ID AAY41710 standard; protein; 802 AA.
DE Human PRO618 protein sequence.
PN MO9946281-A2.
PD 16-SEP-1999.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 2; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1005
ID AAB44266 standard; protein; 802 AA.
DE Human PRO618 (UNQ354) protein sequence SEQ ID NO:169.
PN MO200053756-A2.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 3; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1006
ID AAB24052 standard; protein; 802 AA.
DE Human PRO618 protein sequence SEQ ID NO:24.
PN MO200053754-A1.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 3; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1007
ID AAB82755 standard; protein; 802 AA.
DE Amino acid sequence of novel human protease #54.
PN MO200200860-A2.
PD 03-JAN-2002.
PA (SUGE-) SUGEN INC.
Query Match 7.3%; Score 288.5; DB 5; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1008
ID ABO25212 standard; protein; 802 AA.
DE Novel human secreted and transmembrane protein PRO618.
PN US2003050239-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 6; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1009
ID ABO72218 standard; protein; 802 AA.
DE Novel human secreted and transmembrane protein PRO618.
PN US2002192706-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 6; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1010
ID ABO84898 standard; protein; 802 AA.
DE Human secreted and transmembrane polypeptide PRO618.
PN US2002177553-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 6; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;

RESULT 1011
ID ABO61096 standard; protein; 802 AA.
DE Human PRO618 polypeptide.
PN US2002169284-A1.
PD 14-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 6; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1012
ID ABO80365 standard; protein; 802 AA.
DE Human secreted/transmembrane protein PRO618.
PN US2003004102-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 6; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1013
ID ADA24708 standard; protein; 802 AA.
DE Novel human secreted and transmembrane protein PRO618.
PN US2003050241-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 6; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1014
ID ABO19667 standard; protein; 802 AA.
DE Novel human secreted and transmembrane protein PRO618.
PN US2003050240-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 6; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1015
ID ADA12369 standard; protein; 802 AA.
DE Human secreted/transmembrane polypeptide PRO618.
PN US2003055216-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 6; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1016
ID ABO19558 standard; protein; 802 AA.
DE Novel human secreted and transmembrane polypeptide #26.
PN US2003049633-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 6; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1017
ID ADB73675 standard; protein; 802 AA.
DE Human PRO polypeptide #26.
PN US2003045462-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1018
ID ADB76391 standard; protein; 802 AA.
DE Human PRO polypeptide #26.
PN US2003083248-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1019
ID ADC43817 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003054986-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1020
ID ADC61577 standard; protein; 802 AA.

DE Human secreted/transmembrane protein, PRO618.
PN US2003049684-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1021
ID ADC63541 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003054405-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1022
ID ADC66641 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003060406-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1023
ID ADC68765 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003064407-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1024
ID ADC62825 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003068648-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1025
ID ADC67890 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003069178-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1026
ID ADC41210 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003072745-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1027
ID ADC67265 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003073131-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1028
ID ADC62201 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003073624-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1029
ID ADC41834 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.

PN US2003104998-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1030
ID ADB49203 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003096744-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1031
ID ADB35257 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003203434-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1032
ID ADB16371 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003203435-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1033
ID ADD72986 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003203436-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1034
ID ADD72344 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003194781-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1035
ID ADB16995 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003203433-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1036
ID ADF47009 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003195333-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1037
ID ADC52766 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003216561-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1038
ID ADC60086 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003206915-A1.

PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1039
ID AD160846 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US200307700-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1040
ID ADE48503 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003104536-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1041
ID ADE89604 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US200310181-A1.
PD 10-JUL-2003.
PA (ASHK/) ASHKENAZI A J.
PA (BAKE/) BAKER K P.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOVERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FLIV/) FLIVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GIRM/) GIRMALDI J C.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (KUOS/) KUO S S.
PA (NAPI/) NAPIER W A.
PA (PANT/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (SHEL/) SHELTON D L.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1042
ID ADF61244 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003195345-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1043
ID ADF39936 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003198994-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1044
ID ADF45732 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.

PN US2003195148-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1045
ID ADF24128 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003204055-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1046
ID ADF40560 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003199021-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1047
ID ADF23504 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003203402-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1048
ID ADF33487 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003194780-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1049
ID ADF26954 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003199436-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1050
ID ADF27590 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003198437-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1051
ID ADF41184 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003199435-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1052
ID ADF32863 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003211091-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1053
ID ADF25229 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003211092-A1.

PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1054
ID ADF26330 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003199674-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1055
ID ADF34119 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003194410-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1056
ID ADF46356 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003195344-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1057
ID ADF50342 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003207803-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1058
ID ADF49718 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003215905-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1059
ID ADF51590 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003215908-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1060
ID ADF49094 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003216305-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1061
ID ADF46470 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003216560-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1062
ID ADF50966 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2004005312-A1.
PD 08-JAN-2004.

PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1063
ID ADF58910 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2004005657-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1064
ID ADF62366 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2004006219-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1065
ID ADH25391 standard; protein; 802 AA.
DE Human neurocrinin homologue related protein sequence SEQ ID NO:169.
PN EP1386931-A1.
PD 04-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1066
ID ADM17168 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2004048332-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1067
ID ADL07002 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2004063921-A1.
PD 01-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1068
ID ADP91615 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2004063921-A1.
PD 01-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1069
ID ADF91615 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2004063921-A1.
PD 01-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1070
ID AAB98507 standard; protein; 902 AA.
DE Murine epithin.
PN WO200129056-A1.
PD 26-APR-2001.
PA (UYAR-) UNIV ARKANSAS.
Query Match 7.3%; Score 288.5; DB 4; Length 902;
Best Local Similarity 21.4%; Pred. No. 1.7e-07;
RESULT 1071
ID AAU80517 standard; protein; 902 AA.
DE Mouse epithin-like serine protease.
PN WO200196378-A2.
PD 20-DEC-2001.
PA (FARB) BAYER AG.
Query Match 7.3%; Score 288.5; DB 5; Length 902;
Best Local Similarity 21.4%; Pred. No. 1.7e-07;
RESULT 1072
ID AAU77549 standard; protein; 902 AA.
DE Murine type II membrane serine protease, epithin.
PN WO200212461-A2.
PD 14-FEB-2002.
PA (FARB) BAYER AG.

Query Match 7.3%; Score 288.5; DB 5; Length 902;
Best Local Similarity 21.4%; Pred. No. 1.7e-07;
RESULT 1072
ID AAR05489 standard; protein; 527 AA.
DE tPA024 precursor protein.
PN EP373896-A.
PD 20-JUN-1990.
PA (YAMA) YAMANOUCHI PHARM CO LTD.
Query Match 7.3%; Score 288; DB 2; Length 527;
Best Local Similarity 23.6%; Pred. No. 1.1e-07;
RESULT 1073
ID AAR21599 standard; protein; 527 AA.
DE tPA variant - N117Q, D236A, D238A, K240A.
PN WO9202612-A.
PD 20-FEB-1992.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288; DB 2; Length 527;
Best Local Similarity 23.4%; Pred. No. 1.1e-07;
RESULT 1074
ID AAR20220 standard; protein; 527 AA.
DE t-PA analogue expressed by pCDM8-012.
PN JP03285680-A.
PD 16-DEC-1991.
PA (SUMU) SUMITOMO SEIYAKU KK.
Query Match 7.3%; Score 288; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 1.1e-07;
RESULT 1075
ID AAR20219 standard; protein; 527 AA.
DE t-PA analogue expressed by pCDM8-011.
PN JP03285680-A.
PD 16-DEC-1991.
PA (SUMU) SUMITOMO SEIYAKU KK.
Query Match 7.3%; Score 288; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 1.1e-07;
RESULT 1076
ID AAR20217 standard; protein; 527 AA.
DE t-PA analogue expressed by pCDM8-009.
PN JP03285680-A.
PD 16-DEC-1991.
PA (SUMU) SUMITOMO SEIYAKU KK.
Query Match 7.3%; Score 288; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 1.1e-07;
RESULT 1077
ID AAR20218 standard; protein; 527 AA.
DE t-PA analogue expressed by pCDM8-010.
PN JP03285680-A.
PD 16-DEC-1991.
PA (SUMU) SUMITOMO SEIYAKU KK.
Query Match 7.3%; Score 288; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 1.1e-07;
RESULT 1078
ID AAR70901 standard; protein; 527 AA.
DE Human t-PA variant (N103,A416,A417,A418).
PN US3385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288; DB 2; Length 527;
Best Local Similarity 23.5%; Pred. No. 1.1e-07;
RESULT 1079
ID AAR70904 standard; protein; 527 AA.
DE Human t-PA variant (N103,A440).
PN US3385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288; DB 2; Length 527;
Best Local Similarity 23.4%; Pred. No. 1.1e-07;
RESULT 1080
ID AAY49558 standard; protein; 356 AA.
DE Human protein C protein sequence.
PN WO9950454-A2.
PD 07-OCT-1999.
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.

Query Match 7.3%; Score 287.5; DB 2; Length 356;
Best Local Similarity 24.5%; Pred. No. 7.9e-08;
RESULT 1081
ID AAM52187 standard; protein; 406 AA.
DE Human FVII mutant K143N/N145T/R315N/V317T.
PN WO200158935-A2.
PD 16-AUG-2001.
PA (MAXY-) MAXYGEN APS.
Query Match 7.3%; Score 287.5; DB 4; Length 406;
Best Local Similarity 23.0%; Pred. No. 8.9e-08;
RESULT 1082
ID ADJ56078 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant K143N/ N145T/ R290N/ A292T.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.3%; Score 287.5; DB 8; Length 406;
Best Local Similarity 23.0%; Pred. No. 8.9e-08;
RESULT 1083
ID AAR1318 standard; protein; 522 AA.
DE Delta (466-470) tPA variant with K416A, H417A and E418A subctms.
PN WO9113149-A.
PD 05-SEP-1991.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 287.5; DB 2; Length 522;
Best Local Similarity 22.9%; Pred. No. 1.1e-07;
RESULT 1084
ID ABP43952 standard; protein; 795 AA.
DE Human PRO618.
PN WO200231111-A2.
PD 18-APR-2002.
PA (HYSE-) HYSEQ INC.
Query Match 7.3%; Score 287.5; DB 5; Length 795;
Best Local Similarity 22.7%; Pred. No. 1.7e-07;
RESULT 1085
ID ADG83828 standard; protein; 467 AA.
DE Coxsack talipan venom protease.
PN WO2003082914-A1.
PD 09-OCT-2003.
PA (UYOU) UNIV QUEENSLAND.
Query Match 7.3%; Score 287; DB 8; Length 467;
Best Local Similarity 22.5%; Pred. No. 1.1e-07;
RESULT 1086
ID AAR70879 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N103,S184,E275).
PN US3385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 483;
Best Local Similarity 23.4%; Pred. No. 1.1e-07;
RESULT 1087
ID AAR70883 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N103,K210,E275).
PN US3385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 483;
Best Local Similarity 23.4%; Pred. No. 1.1e-07;
RESULT 1088
ID AAR70884 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N103,E275,I277).
PN US3385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 483;
Best Local Similarity 23.4%; Pred. No. 1.1e-07;
RESULT 1089
ID AAR70886 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N103,S184,E275,I277).
PN US3385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 483;


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Best Local Similarity 23.4%; Pred. No. 1.1e-07;
RESULT 1090
ID AAR70874 standard; protein: 483 AA.
DE Human tissue PA variant (delta1-44,N103,E275).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 483;
Best Local Similarity 23.4%; Pred. No. 1.1e-07;
RESULT 1091
ID AAR70887 standard; protein: 483 AA.
DE Human tissue PA variant (delta1-44,N103,K213,E275,I277).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 483;
Best Local Similarity 23.4%; Pred. No. 1.1e-07;
RESULT 1092
ID AAR70881 standard; protein: 483 AA.
DE Human tissue PA variant (delta1-44,N103,R210,A211,R212,R213,E275).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 483;
Best Local Similarity 23.1%; Pred. No. 1.1e-07;
RESULT 1093
ID AAR70882 standard; protein: 483 AA.
DE Human tissue PA variant (delta1-44,N103,R252,E275).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 483;
Best Local Similarity 23.4%; Pred. No. 1.1e-07;
RESULT 1094
ID AAR70889 standard; protein: 483 AA.
DE Human tissue PA variant (delta1-44,N103,R252,E275,O277).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 483;
Best Local Similarity 23.4%; Pred. No. 1.1e-07;
RESULT 1095
ID AAR70888 standard; protein: 483 AA.
DE Human tissue PA variant (delta1-44,N103,K210,E275,I277).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 483;
Best Local Similarity 23.1%; Pred. No. 1.1e-07;
RESULT 1096
ID AAR70890 standard; protein: 483 AA.
DE Human tissue PA variant (delta1-44,N103,K210,E275,I277).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 483;
Best Local Similarity 23.4%; Pred. No. 1.1e-07;
RESULT 1097
ID AAR70880 standard; protein: 483 AA.
DE Human tissue PA variant (delta1-44,N103,K213,E275).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 483;
Best Local Similarity 23.4%; Pred. No. 1.1e-07;
RESULT 1098
ID AAR70907 standard; protein: 527 AA.
DE Human t-PA variant (N103,A460,A462).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 527;
Best Local Similarity 23.4%; Pred. No. 1.2e-07;
RESULT 1099
ID AAR70874 standard; protein: 527 AA.
DE Human t-PA variant (N67,N103).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 527;
Best Local Similarity 23.4%; Pred. No. 1.2e-07;
RESULT 1100
ID AAR70892 standard; protein: 527 AA.
DE Human t-PA variant (N103,A283,A287).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 527;
Best Local Similarity 23.4%; Pred. No. 1.2e-07;
RESULT 1101
ID AAR52182 standard; protein: 406 AA.
DE Human FVII mutant K143N/N145T.
PN WO200158935-A2.
PD 16-AUG-2001.
PA (MAXY-) MAXYGEN APS.
Query Match 7.3%; Score 286.5; DB 4; Length 406;
Best Local Similarity 23.0%; Pred. No. 1e-07;
RESULT 1102
ID ADJ56073 standard; protein: 406 AA.
DE Human factor VII polypeptide mutant K143N/ N145T.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO ) NOVO NORDISK AS.
Query Match 7.3%; Score 286.5; DB 8; Length 406;
Best Local Similarity 23.0%; Pred. No. 1e-07;
RESULT 1103
ID ADO10589 standard; protein: 406 AA.
DE Human factor VII/VIII protein mutant #25.
PN WO2004029091-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN APS.
Query Match 7.3%; Score 286.5; DB 8; Length 406;
Best Local Similarity 23.0%; Pred. No. 1e-07;
RESULT 1104
ID ADG83826 standard; protein: 467 AA.
DE Brown snake venom protease.
PN WO2003082914-A1.
PD 09-OCT-2003.
PA (VYQU ) UNIV QUEENSLAND.
Query Match 7.3%; Score 286.5; DB 8; Length 467;
Best Local Similarity 22.2%; Pred. No. 1.1e-07;
RESULT 1105
ID AAR14486 standard; protein: 522 AA.
DE Delta (466-470) tPA variant with Y67N substitution.
PN WO9113149-A.
PD 05-SEP-1991.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 286.5; DB 2; Length 522;
Best Local Similarity 22.7%; Pred. No. 1.3e-07;
RESULT 1106
ID AAR44816 standard; protein: 527 AA.
DE Human tPA variant (N67,N103).
PN US5270198-A.
PD 14-DEC-1993.
PA (GETH ) GENENTECH INC.
Query Match 7.2%; Score 286; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 1.4e-07;
RESULT 1107
ID AAR44812 standard; protein: 527 AA.
DE Human tPA variant N103.
PN US5270198-A.
PD 14-DEC-1993.
PA (GETH ) GENENTECH INC.
Query Match 7.2%; Score 286; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 1.4e-07;
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RESULT 1108
ID AAR70868 standard; protein; 527 AA.
DE Human t-PA variant (N67,A432,A434).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 286; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 1.4e-07;
RESULT 1109
ID AAR70860 standard; protein; 527 AA.
DE Human t-PA variant (N67,A331,A332).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 286; DB 2; Length 527;
Best Local Similarity 23.4%; Pred. No. 1.4e-07;
RESULT 1110
ID AAR70900 standard; protein; 527 AA.
DE Human t-PA variant (N103,A410).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 286; DB 2; Length 527;
Best Local Similarity 23.1%; Pred. No. 1.4e-07;
RESULT 1111
ID AAR09220 standard; protein; 529 AA.
DE t-PA insertion variant 1304H, 1305H.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 286; DB 2; Length 529;
Best Local Similarity 23.2%; Pred. No. 1.4e-07;
RESULT 1112
ID AAP70449 standard; protein; 530 AA.
DE Sequence encoded by of synthetic gene for mature human tissue plasminogen activator (tPA).
PN WO8705934-A.
PD 08-OCT-1987.
PA (CREA/) CREA R.
Query Match 7.2%; Score 286; DB 1; Length 530;
Best Local Similarity 22.9%; Pred. No. 1.4e-07;
RESULT 1113
ID AAB12342 standard; protein; 561 AA.
DE T-PA with -ve charged finger and/or kringle domain (1).
PN JP03061483-A.
PD 18-MAR-1991.
PA (FUJI) FUJISAWA PHARM CO LTD.
Query Match 7.2%; Score 286; DB 2; Length 561;
Best Local Similarity 22.1%; Pred. No. 1.4e-07;
RESULT 1114
ID AAR09289 standard; protein; 562 AA.
DE Sequence of tissue plasminogen activator analogue BBN12 (Aep 67, Thr 68).
PN WO8912681-A.
PD 28-DEC-1989.
PA (BRBI-) BRIT BIO-TECHN LTD.
Query Match 7.2%; Score 286; DB 2; Length 562;
Best Local Similarity 23.3%; Pred. No. 1.5e-07;
RESULT 1115
ID AAP70860 standard; protein; 527 AA.
DE Thrombolytic proteins 1-9-11 having t-PA activity and R275 is deleted or replaced and containing a modified N-linked glycosylation site.
PN WO8704722-A.
PD 13-AUG-1987.
PA (GENY) GENETICS INST INC.
Query Match 7.2%; Score 285.5; DB 1; Length 527;
Best Local Similarity 23.1%; Pred. No. 1.5e-07;
RESULT 1116
ID AAP91683 standard; protein; 527 AA.
DE Sequence of tissue plasminogen activator (tPA).
PN WO8911531-A.
PD 30-NOV-1989.
PA (GETH) GENENTECH INC.

PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 285; DB 1; Length 527;
Best Local Similarity 23.2%; Pred. No. 1.5e-07;
RESULT 1117
ID AAR09270 standard; protein; 527 AA.
DE t-PA variant H331A, H332A.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 285; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 1.5e-07;
RESULT 1118
ID AAR09278 standard; protein; 527 AA.
DE t-PA variant H432A, R434A.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 285; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 1.5e-07;
RESULT 1119
ID AAP71449 standard; protein; 528 AA.
DE Modified human tissue plasminogen activator.
PN EP238304-A.
PD 23-SEP-1987.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 285; DB 1; Length 528;
Best Local Similarity 23.4%; Pred. No. 1.6e-07;
RESULT 1120
ID AAR13148 standard; protein; 556 AA.
DE T-PA variant contg. fibronectin for thrombosis lysis (2).
PN JP03061482-A.
PD 18-MAR-1991.
PA (FUJI) FUJISAWA PHARM CO LTD.
Query Match 7.2%; Score 285; DB 2; Length 556;
Best Local Similarity 21.9%; Pred. No. 1.6e-07;
RESULT 1121
ID AAB11710 standard; protein; 264 AA.
DE Human serine protease BSSPS (hBSSPS) SEQ ID NO:2.
PN WO200031243-A1.
PD 02-JUN-2000.
PA (FUSO) FUSO PHARM IND LTD.
Query Match 7.2%; Score 284.5; DB 3; Length 264;
Best Local Similarity 28.0%; Pred. No. 8.6e-08;
RESULT 1122
ID AAP91961 standard; protein; 518 AA.
DE Sequence of des 1-44E275 t-PA mutant.
PN WO8909266-A.
PD 05-OCT-1989.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 284.5; DB 1; Length 518;
Best Local Similarity 22.9%; Pred. No. 1.6e-07;
RESULT 1123
ID ABW84749 standard; protein; 629 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:4998.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 7.2%; Score 284.5; DB 8; Length 629;
Best Local Similarity 19.5%; Pred. No. 1.9e-07;
RESULT 1124
ID ABW82817 standard; protein; 629 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:3066.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 7.2%; Score 284.5; DB 8; Length 629;
Best Local Similarity 19.5%; Pred. No. 1.9e-07;
RESULT 1125
ID AAR70851 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N67,D184,E275,I277).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.

Query Match 7.2%; Score 284; DB 2; Length 483;
Best Local Similarity 23.1%; Pred. No. 1.6e-07;
RESULT 1126
ID AAR70844 standard; protein; 483 AA.
DE Human tissue PA variant (delcal-44,N67,D184,E275).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 284; DB 2; Length 483;
Best Local Similarity 23.1%; Pred. No. 1.6e-07;
RESULT 1127
ID AAR44809 standard; protein; 527 AA.
DE Human cPA variant (N65, S67).
PN US5270198-A.
PD 14-DEC-1993.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 284; DB 2; Length 527;
Best Local Similarity 23.1%; Pred. No. 1.8e-07;
RESULT 1128
ID AAR70908 standard; protein; 527 AA.
DE Human c-PA variant (N103,A477).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 284; DB 2; Length 527;
Best Local Similarity 23.4%; Pred. No. 1.8e-07;
RESULT 1129
ID AAR70859 standard; protein; 527 AA.
DE Human c-PA variant (N67,A303,A304).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 284; DB 2; Length 527;
Best Local Similarity 23.8%; Pred. No. 1.8e-07;
RESULT 1130
ID AAR70893 standard; protein; 527 AA.
DE Human c-PA variant (N103,A296,A297,A298,A299).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 284; DB 2; Length 527;
Best Local Similarity 23.5%; Pred. No. 1.8e-07;
RESULT 1131
ID AAR70891 standard; protein; 527 AA.
DE Human c-PA variant (N103,A267).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 284; DB 2; Length 527;
Best Local Similarity 23.7%; Pred. No. 1.8e-07;
RESULT 1132
ID AAP70474 standard; protein; 562 AA.
DE Sequence of tissue plasminogen (TPA) analogue.
PN W08703906-A.
PD 02-JUL-1987.
PA (UPJO) UPJOHN CO.
PA (MARO) MAROTTI K R.
Query Match 7.2%; Score 284; DB 1; Length 562;
Best Local Similarity 23.0%; Pred. No. 1.9e-07;
RESULT 1133
ID AAR09286 standard; protein; 562 AA.
DE Sequence of tissue plasminogen activator analogue BBNTS (Ser 67, Ser 68).
PN W06912681-A.
PD 28-DEC-1989.
PA (BRBI) BRIT BIO-TECHN LTD.
Query Match 7.2%; Score 284; DB 2; Length 562;
Best Local Similarity 23.1%; Pred. No. 1.9e-07;
RESULT 1134
ID AAR23807 standard; protein; 562 AA.
DE c-PA (Tyr 297) mutant.
PN W09206203-A.
PD 16-APR-1992.
PA (TEXA) UNIV TEXAS SYSTEM.

Query Match 7.2%; Score 284; DB 2; Length 562;
Best Local Similarity 23.2%; Pred. No. 1.9e-07;
RESULT 1135
ID ABB80068 standard; protein; 406 AA.
DE Human coagulation factor VII mutant L305V/M306D/D309S.
PN W0200183725-A1.
PD 08-NOV-2001.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.2%; Score 283.5; DB 5; Length 406;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1136
ID AEG73125 standard; protein; 406 AA.
DE Human coagulation factor VII mutant polypeptide L305V/M306D/D309S.
PN W0200277218-A1.
PD 03-OCT-2002.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.2%; Score 283.5; DB 6; Length 406;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1137
ID ADJ55852 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant L305V/M306D/D309S.
PN W02004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.2%; Score 283.5; DB 8; Length 406;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1138
ID ADE83543 standard; protein; 482 AA.
DE Rat Protein NP_058639, SEQ ID NO 11161.
PN W02003016475-A2.
PD 27-FEB-2003.
PA (GENO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 7.2%; Score 283.5; DB 7; Length 482;
Best Local Similarity 22.8%; Pred. No. 1.7e-07;
RESULT 1139
ID AAR13917 standard; peptide; 522 AA.
DE Delta (466-470) cPA variant with K296A, H297A, R298A and R299A
DE substitutions.
PN W09113148-A.
PD 05-SEP-1991.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 283.5; DB 2; Length 522;
Best Local Similarity 22.8%; Pred. No. 1.8e-07;
RESULT 1140
ID AAP90169 standard; peptide; 571 AA.
DE Tissue plasminogen activator mutant 2G.
PN W08907146-A.
PD 10-AUG-1989.
PA (INTE) INTEG GENETICS INC.
Query Match 7.2%; Score 283.5; DB 1; Length 571;
Best Local Similarity 22.4%; Pred. No. 2e-07;
RESULT 1141
ID AAR09257 standard; protein; 483 AA.
DE c-PA variant dl-44, N184D, I210R, G211A, K212R, V213R, T252R, F305H.
PN W09002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 283; DB 2; Length 483;
Best Local Similarity 23.2%; Pred. No. 1.8e-07;
RESULT 1142
ID AAR09269 standard; protein; 527 AA.
DE c-PA variant E303A, R304A.
PN W09002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 283; DB 2; Length 527;
Best Local Similarity 23.7%; Pred. No. 2e-07;
RESULT 1143
ID AAR44810 standard; protein; 527 AA.
DE Human cPA variant (N65, T67).
PN US5270198-A.
PD 14-DEC-1993.

PA (GETH) GENENTECH INC. 7.2%; Score 283; DB 2; Length 527;
 Query Match
 Best Local Similarity 23.1%; Pred. No. 2e-07;
 RESULT 1144
 ID AAR44817 standard; protein; 527 AA.
 DE Human tPA variant (N67,A236,A297,A298,A299).
 PN US5270198-A.
 PD 14-DEC-1993.
 PA (GETH) GENENTECH INC. 7.2%; Score 283; DB 2; Length 527;
 Query Match
 Best Local Similarity 23.4%; Pred. No. 2e-07;
 RESULT 1145
 ID AAR4814 standard; protein; 527 AA.
 DE Human tPA variant (N105,T107).
 PN US5270198-A.
 PD 14-DEC-1993.
 PA (GETH) GENENTECH INC. 7.2%; Score 283; DB 2; Length 527;
 Query Match
 Best Local Similarity 23.6%; Pred. No. 2e-07;
 RESULT 1146
 ID AAR70899 standard; protein; 527 AA.
 DE Human t-PA variant (N103,A408).
 PN US5385732-A.
 PD 31-JAN-1995.
 PA (GETH) GENENTECH INC. 7.2%; Score 283; DB 2; Length 527;
 Query Match
 Best Local Similarity 22.9%; Pred. No. 2e-07;
 RESULT 1147
 ID AAR12341 standard; protein; 560 AA.
 DE t-PA variant congl. fibrinectin for chromobasis lysis (3).
 PN JP03061482-A.
 PD 18-MAR-1991.
 PA (FUJI) FUJISAWA PHARM CO LTD. 7.2%; Score 283; DB 2; Length 560;
 Query Match
 Best Local Similarity 22.1%; Pred. No. 2.1e-07;
 RESULT 1148
 ID AAR12367 standard; protein; 561 AA.
 DE T-PA with -ve charged finger and/or kringle domain (7).
 PN JP03061483-A.
 PD 18-MAR-1991.
 PA (FUJI) FUJISAWA PHARM CO LTD. 7.2%; Score 283; DB 2; Length 561;
 Query Match
 Best Local Similarity 22.1%; Pred. No. 2.1e-07;
 RESULT 1149
 ID AAR09231 standard; protein; 524 AA.
 DE t-PA deletion variant d297-299.
 PN WO9002798-A.
 PD 22-MAR-1990.
 PA (GETH) GENENTECH INC. 7.2%; Score 282.5; DB 2; Length 524;
 Query Match
 Best Local Similarity 22.8%; Pred. No. 2.1e-07;
 RESULT 1150
 ID AAR09246 standard; protein; 483 AA.
 DE t-PA variant d1-44, N184D, F305H.
 PN WO9002798-A.
 PD 22-MAR-1990.
 PA (GETH) GENENTECH INC. 7.1%; Score 282; DB 2; Length 483;
 Query Match
 Best Local Similarity 23.0%; Pred. No. 2.1e-07;
 RESULT 1151
 ID AAR09254 standard; protein; 483 AA.
 DE t-PA variant d1-44, I210R, G211H, K212Q, V213K, F305H.
 PN WO9002798-A.
 PD 22-MAR-1990.
 PA (GETH) GENENTECH INC. 7.1%; Score 282; DB 2; Length 483;
 Query Match
 Best Local Similarity 22.8%; Pred. No. 2.1e-07;
 RESULT 1152
 ID AAR09230 standard; protein; 525 AA.
 DE t-PA deletion variant d297-298.
 PN WO9002798-A.
 PD 22-MAR-1990.
 PA (GETH) GENENTECH INC. 7.1%; Score 282; DB 2; Length 525;
 Query Match
 Best Local Similarity 23.4%; Pred. No. 2.2e-07;
 RESULT 1153
 ID AAR09255 standard; protein; 527 AA.
 DE t-PA variant I210R, G211H, K212Q, V213K, F305H.
 PN WO9002798-A.
 PD 22-MAR-1990.
 PA (GETH) GENENTECH INC. 7.1%; Score 282; DB 2; Length 527;
 Query Match
 Best Local Similarity 22.8%; Pred. No. 2.2e-07;
 RESULT 1154
 ID AAR21600 standard; protein; 527 AA.
 DE tPA variant - B94A, D95A, T103N.
 PN WO9202612-A.
 PD 20-FEB-1992.
 PA (GETH) GENENTECH INC. 7.1%; Score 282; DB 2; Length 527;
 Query Match
 Best Local Similarity 23.2%; Pred. No. 2.2e-07;
 RESULT 1155
 ID AAR70866 standard; protein; 527 AA.
 DE Human t-PA variant (N67,A416,A417,A418).
 PN US5385732-A.
 PD 31-JAN-1995.
 PA (GETH) GENENTECH INC. 7.1%; Score 282; DB 2; Length 527;
 Query Match
 Best Local Similarity 23.4%; Pred. No. 2.2e-07;
 RESULT 1156
 ID AAR70902 standard; protein; 527 AA.
 DE Human t-PA variant (N103,A426,A427,A429,A430).
 PN US5385732-A.
 PD 31-JAN-1995.
 PA (GETH) GENENTECH INC. 7.1%; Score 282; DB 2; Length 527;
 Query Match
 Best Local Similarity 23.4%; Pred. No. 2.2e-07;
 RESULT 1157
 ID AAR70869 standard; protein; 527 AA.
 DE Human t-PA variant (N67,A440).
 PN US5385732-A.
 PD 31-JAN-1995.
 PA (GETH) GENENTECH INC. 7.1%; Score 282; DB 2; Length 527;
 Query Match
 Best Local Similarity 23.2%; Pred. No. 2.2e-07;
 RESULT 1158
 ID AAR82582 standard; protein; 562 AA.
 DE Tissue plasminogen activator with S-119 substd for M and QG196-98 substd
 DE for NGT.
 PN JP63230083-A.
 PD 26-SEP-1988.
 PA (ETSA) ETSAI CO LTD. 7.1%; Score 282; DB 2; Length 527;
 Query Match
 Best Local Similarity 23.2%; Pred. No. 2.2e-07;
 RESULT 1159
 ID AAR09287 standard; protein; 562 AA.
 DE Sequence of tissue plasminogen activator analogue BBNT6 (Thr 67, Asp 68).
 PN WO8912681-A.
 PD 28-DEC-1989.
 PA (BRBI-) BRIT BIO-TECHN LTD. 7.1%; Score 282; DB 2; Length 562;
 Query Match
 Best Local Similarity 23.1%; Pred. No. 2.4e-07;
 RESULT 1160
 ID AAR23808 standard; protein; 562 AA.
 DE t-PA (Glu 298) mutant.
 PN WO9206203-A.
 PD 16-APR-1992.
 PA (TEXA) UNIV TEXAS SYSTEM. 7.1%; Score 282; DB 2; Length 562;
 Query Match
 Best Local Similarity 23.5%; Pred. No. 2.4e-07;
 RESULT 1161
 ID AAR23810 standard; protein; 562 AA.
 DE t-PA (Gly 301) mutant.
 PN WO9206203-A.
 PD 16-APR-1992.
 PA (TEXA) UNIV TEXAS SYSTEM.

Query Match	7.1%;	Score 282;	DB 2;	Length 562;
Best Local Similarity	23.6%;	Pred. No. 2.4e-07;		
RESULT 1162				
ID AAB84869 standard; protein; 406 AA.				
DE Mutant blood coagulant factor VII (FVII-30).				
PN JP2001061479-A.				
PD 13-MAR-2001.				
PA (KAGA) ZH KAGAKU & KESSSEI RYOH KENKYUSHO.				
Query Match	7.1%;	Score 281.5;	DB 4;	Length 406;
Best Local Similarity	22.8%;	Pred. No. 1.9e-07;		
RESULT 1163				
ID AAM52185 standard; protein; 406 AA.				
DE Human FVII mutant G291N.				
PN WO200158935-A2.				
PD 16-AUG-2001.				
PA (MAXY-) MAXYGEN APS.				
Query Match	7.1%;	Score 281.5;	DB 4;	Length 406;
Best Local Similarity	22.8%;	Pred. No. 1.9e-07;		
RESULT 1164				
ID AAO30584 standard; protein; 406 AA.				
DE Human coagulation factor VII variant (S314E/L305V/V158D/K337A/M298Q).				
PN WO2003037932-A2.				
PD 08-MAY-2003.				
PA (NOVO) NOVO NORDISK AS.				
Query Match	7.1%;	Score 281.5;	DB 6;	Length 406;
Best Local Similarity	22.5%;	Pred. No. 1.9e-07;		
RESULT 1165				
ID AAO30626 standard; protein; 406 AA.				
DE Human coagulation factor VII variant (K316Q/L305V/V158T/K337A/M298Q).				
PN WO2003037932-A2.				
PD 08-MAY-2003.				
PA (NOVO) NOVO NORDISK AS.				
Query Match	7.1%;	Score 281.5;	DB 6;	Length 406;
Best Local Similarity	22.5%;	Pred. No. 1.9e-07;		
RESULT 1166				
ID AAO30582 standard; protein; 406 AA.				
DE Human coagulation factor VII variant (S314E/L305V/V158T/K337A/M298Q).				
PN WO2003037932-A2.				
PD 08-MAY-2003.				
PA (NOVO) NOVO NORDISK AS.				
Query Match	7.1%;	Score 281.5;	DB 6;	Length 406;
Best Local Similarity	22.5%;	Pred. No. 1.9e-07;		
RESULT 1167				
ID AAO30616 standard; protein; 406 AA.				
DE Human coagulation factor VII variant (K316Q/L305V/K337A/M298Q).				
PN WO2003037932-A2.				
PD 08-MAY-2003.				
PA (NOVO) NOVO NORDISK AS.				
Query Match	7.1%;	Score 281.5;	DB 6;	Length 406;
Best Local Similarity	22.5%;	Pred. No. 1.9e-07;		
RESULT 1168				
ID AAO30572 standard; protein; 406 AA.				
DE Human coagulation factor VII variant (S314E/L305V/K337A/M298Q).				
PN WO2003037932-A2.				
PD 08-MAY-2003.				
PA (NOVO) NOVO NORDISK AS.				
Query Match	7.1%;	Score 281.5;	DB 6;	Length 406;
Best Local Similarity	22.5%;	Pred. No. 1.9e-07;		
RESULT 1169				
ID AAO30628 standard; protein; 406 AA.				
DE Human coagulation factor VII variant (K316Q/L305V/V158D/K337A/M298Q).				
PN WO2003037932-A2.				
PD 08-MAY-2003.				
PA (NOVO) NOVO NORDISK AS.				
Query Match	7.1%;	Score 281.5;	DB 6;	Length 406;
Best Local Similarity	22.5%;	Pred. No. 1.9e-07;		
RESULT 1170				
ID ADU55926 standard; protein; 406 AA.				
DE Human factor VII polypeptide mutant V158T/ M298Q/ L305V/ S314E/ K337A.				
PN WO2004000366-A1.				
PD 31-DEC-2003.				
PA (NOVO) NOVO NORDISK AS.				
Query Match	7.1%;	Score 281.5;	DB 8;	Length 406;
Best Local Similarity	22.5%;	Pred. No. 1.9e-07;		
RESULT 1171				
ID ADU55926 standard; protein; 406 AA.				
DE Human factor VII polypeptide mutant V158T/ M298Q/ L305V/ S314E/ K337A.				
PN WO2004000366-A1.				
PD 31-DEC-2003.				
PA (NOVO) NOVO NORDISK AS.				
Query Match	7.1%;	Score 281.5;	DB 8;	Length 406;
Best Local Similarity	22.5%;	Pred. No. 1.9e-07;		
RESULT 1172				
ID ADU55926 standard; protein; 406 AA.				
DE Human factor VII polypeptide mutant V158T/ M298Q/ L305V/ S314E/ K337A.				
PN WO2004000366-A1.				
PD 31-DEC-2003.				
PA (NOVO) NOVO NORDISK AS.				
Query Match	7.1%;	Score 281.5;	DB 8;	Length 406;
Best Local Similarity	22.5%;	Pred. No. 1.9e-07;		
RESULT 1173				
ID ADU55926 standard; protein; 406 AA.				
DE Human factor VII polypeptide mutant V158T/ M298Q/ L30				

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Best Local Similarity 22.5%; Pred. No. 1.9e-07;
RESULT 1171
ID ADJ55927 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158D/ M298Q/ L305V/ S314E/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO ) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 1.9e-07;
RESULT 1172
ID ADJ55915 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant M298Q/ L305V/ S314E/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO ) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 1.9e-07;
RESULT 1173
ID ADJ55970 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158T/ M298Q/ L305V/ K316Q/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO ) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 1.9e-07;
RESULT 1174
ID ADJ56063 standard; protein; 406 AA.
DE Human factor VII protein mutant F374Y/ V158D/ M298Q/ L305V/ S314E/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO ) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 1.9e-07;
RESULT 1175
ID ADJ55959 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant M298Q/ L305V/ K316Q/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO ) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 1.9e-07;
RESULT 1176
ID ADJ56067 standard; protein; 406 AA.
DE Human factor VII protein mutant F374Y/ V158T/ M298Q/ L305V/ S314E/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO ) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 1.9e-07;
RESULT 1177
ID ADJ55971 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158D/ M298Q/ L305V/ K316Q/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO ) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 1.9e-07;
RESULT 1178
ID ADJ56033 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant F374Y/ S314E/ M298Q/ L305V/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO ) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 1.9e-07;
RESULT 1179
ID ADJ56076 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant G291N.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO ) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 1.9e-07;
RESULT 1180
ID ADJ56076 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant G291N.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO ) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 1.9e-07;

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RESULT 1180
ID ADOI0585 standard; protein; 406 AA.
DE Human factor VII/VIIIa protein mutant #21.
PN WO2004029091-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN APS.
Query Match 7.1%; Score 281.5; DB 8; Length 406;
Best Local Similarity 22.8%; Pred. No. 1.9e-07;
RESULT 1181
ID ADOI0626 standard; protein; 406 AA.
DE Human factor VII/VIIIa protein mutant #62.
PN WO2004029091-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN APS.
Query Match 7.1%; Score 281.5; DB 8; Length 406;
Best Local Similarity 22.6%; Pred. No. 1.9e-07;
RESULT 1182
ID AD512886 standard; protein; 406 AA.
DE Human factor VII G237L mutant.
PN WO2004083361-A2.
PD 30-SEP-2004.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.1%; Score 281.5; DB 8; Length 406;
Best Local Similarity 22.6%; Pred. No. 1.9e-07;
RESULT 1183
ID AAR09233 standard; protein; 522 AA.
DE t-PA deletion variant d397-301.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH ) GENENTECH INC.
Query Match 7.1%; Score 281.5; DB 2; Length 522;
Best Local Similarity 23.4%; Pred. No. 2.4e-07;
RESULT 1184
ID AAR13919 standard; protein; 522 AA.
DE Delta (466-470) tPA variant with E426A, R427A, K429A and E430A
DE substitutions.
PN WO9113149-A.
PD 05-SEP-1991.
PA (GETH ) GENENTECH INC.
Query Match 7.1%; Score 281.5; DB 2; Length 522;
Best Local Similarity 22.7%; Pred. No. 2.4e-07;
RESULT 1185
ID AAR09239 standard; protein; 524 AA.
DE t-PA deletion variant d300-302.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH ) GENENTECH INC.
Query Match 7.1%; Score 281.5; DB 2; Length 524;
Best Local Similarity 23.2%; Pred. No. 2.4e-07;
RESULT 1186
ID AAR12366 standard; protein; 562 AA.
DE T-PA with -ve charged finger and/or kringles domain (5).
PN JPO3061483-A.
PD 18-MAR-1991.
PA (FUJI ) FUJISAWA PHARM CO LTD.
Query Match 7.1%; Score 281.5; DB 2; Length 562;
Best Local Similarity 21.9%; Pred. No. 2.5e-07;
RESULT 1187
ID AAR09249 standard; protein; 483 AA.
DE t-PA variant d1-44, I210R, G211A, K212R, V213K, F305H.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH ) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 483;
Best Local Similarity 23.3%; Pred. No. 2.3e-07;
RESULT 1188
ID AAR70855 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N67,K210,E275,I277).
PN US3385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 483;
Best Local Similarity 23.2%; Pred. No. 2.3e-07;
RESULT 1189
ID AAR70845 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N67,S184,E275).
PN US3385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 483;
Best Local Similarity 23.2%; Pred. No. 2.3e-07;
RESULT 1190
ID AAR70848 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N67,R252,E275).
PN US3385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 483;
Best Local Similarity 23.2%; Pred. No. 2.3e-07;
RESULT 1191
ID AAR70849 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N67,K210,E275).
PN US3385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 483;
Best Local Similarity 23.2%; Pred. No. 2.3e-07;
RESULT 1192
ID AAR70854 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N67,R252,E275,I277).
PN US3385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 483;
Best Local Similarity 23.2%; Pred. No. 2.3e-07;
RESULT 1193
ID AAR70843 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N67,E275).
PN US3385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 483;
Best Local Similarity 23.2%; Pred. No. 2.3e-07;
RESULT 1194
ID AAR70846 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N67,K213,E275).
PN US3385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 483;
Best Local Similarity 23.2%; Pred. No. 2.3e-07;
RESULT 1195
ID AAR79144 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N67,S184,E275,I277).
PN US3385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 483;
Best Local Similarity 23.2%; Pred. No. 2.3e-07;
RESULT 1196
ID AAR70850 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N67,E275,I277).
PN US3385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 483;
Best Local Similarity 23.2%; Pred. No. 2.3e-07;
RESULT 1197
ID AAR70852 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N67,K213,E275,I277).
PN US3385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
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Query Match 7.1%; Score 281; DB 2; Length 483;
Best Local Similarity 23.2%; Pred. No. 2.3e-07;
RESULT 1198
ID AAR70847 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N67,R210,A211,R212,R213,E275).
PN US3385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 483;
Best Local Similarity 23.0%; Pred. No. 2.3e-07;
RESULT 1199
ID AAR70853 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N67,R210,A211,R212,R213,E275,1277).
PN US3385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 483;
Best Local Similarity 23.0%; Pred. No. 2.3e-07;
RESULT 1200
ID AAR60518 standard; protein; 487 AA.
DE Cattle Factor-Xa.
PN WO9418227-A2.
PD 18-AUG-1994.
PA (DENZ-) DENZYME APS.
Query Match 7.1%; Score 281; DB 2; Length 487;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1201
ID AAR76216 standard; protein; 488 AA.
DE Human Factor X protein.
PN WO9838317-A1.
PD 03-SEP-1998.
PA (IMMO) IMMUNO AG.
Query Match 7.1%; Score 281; DB 2; Length 488;
Best Local Similarity 24.0%; Pred. No. 2.4e-07;
RESULT 1202
ID AAR76217 standard; protein; 488 AA.
DE Human Factor X protein analogue.
PN WO9838317-A1.
PD 03-SEP-1998.
PA (IMMO) IMMUNO AG.
Query Match 7.1%; Score 281; DB 2; Length 488;
Best Local Similarity 22.6%; Pred. No. 2.4e-07;
RESULT 1203
ID AAR76218 standard; protein; 488 AA.
DE Human Factor X protein.
PN WO9838318-A1.
PD 03-SEP-1998.
PA (IMMO) IMMUNO AG.
Query Match 7.1%; Score 281; DB 2; Length 488;
Best Local Similarity 24.0%; Pred. No. 2.4e-07;
RESULT 1204
ID AAR70411 standard; protein; 488 AA.
DE Human factor X protein sequence SEQ ID NO:2.
PN WO200110896-A2.
PD 15-FEB-2001.
PA (BAXT) BAXTER AG.
Query Match 7.1%; Score 281; DB 4; Length 488;
Best Local Similarity 24.0%; Pred. No. 2.4e-07;
RESULT 1205
ID AAR60502 standard; protein; 492 AA.
DE Serine protease for fusion protein cleavage.
PN WO9418227-A2.
PD 18-AUG-1994.
PA (DENZ-) DENZYME APS.
Query Match 7.1%; Score 281; DB 2; Length 492;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1206
ID AAR09238 standard; protein; 525 AA.
DE t-PA deletion variant d300-301.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 525;

Best Local Similarity 22.8%; Pred. No. 2.5e-07;
RESULT 1207
ID AAR09276 standard; protein; 527 AA.
DE t-PA variant K416A, H417A, E418A.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 2.5e-07;
RESULT 1208
ID AAR09279 standard; protein; 527 AA.
DE t-PA variant R440A.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 2.5e-07;
RESULT 1209
ID AAR70875 standard; protein; 527 AA.
DE Human t-PA variant (N60,N103).
PN US3385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 2.5e-07;
RESULT 1210
ID AAR70876 standard; protein; 527 AA.
DE Human t-PA variant (N60,N67,N103).
PN US3385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 2.5e-07;
RESULT 1211
ID AAR70857 standard; protein; 527 AA.
DE Human t-PA variant (N67,A283,A287).
PN US3385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 2.5e-07;
RESULT 1212
ID AAR70898 standard; protein; 527 AA.
DE Human t-PA variant (N103,A364,A365,A366).
PN US3385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 2.5e-07;
RESULT 1213
ID AAR70906 standard; protein; 527 AA.
DE Human t-PA variant (N103,A449,A453).
PN US3385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 2.5e-07;
RESULT 1214
ID AAR70872 standard; protein; 527 AA.
DE Human t-PA variant (N67,A460,A462).
PN US3385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 2.5e-07;
RESULT 1215
ID AAR70842 standard; protein; 527 AA.
DE Wild type tissue plasminogen activator protein.
PN US3385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 2.5e-07;

RESULT 1216
ID AAI3150 standard; protein; 558 AA.
DE T-PA with -ve charged finger and/or kringle domain (3).
PN JP03061483-A.
PD 18-MAR-1991.
PA (FUJII) FUJISAWA PHARM CO LTD.
Query Match 7.1%; Score 281; DB 2; Length 558;
Best Local Similarity 23.0%; Pred. No. 2.7e-07;
RESULT 1217
ID AAI3152 standard; protein; 559 AA.
DE T-PA with -ve charged finger and/or kringle domain (6).
PN JP03061483-A.
PD 18-MAR-1991.
PA (FUJII) FUJISAWA PHARM CO LTD.
Query Match 7.1%; Score 281; DB 2; Length 559;
Best Local Similarity 23.0%; Pred. No. 2.7e-07;
RESULT 1218
ID AAP0691 standard; protein; 1087 AA.
DE Hybrid plasminogen/-C-PA compound 1.
PN EP292326-A.
PD 23-NOV-1988.
PA (BEEC) BEECHAM GROUP PLC.
Query Match 7.1%; Score 281; DB 1; Length 1087;
Best Local Similarity 22.3%; Pred. No. 5e-07;
RESULT 1219
ID ABM1778 standard; protein; 264 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO2719, SEQ.4580.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GENTH) GENTECH INC.
Query Match 7.1%; Score 280.5; DB 8; Length 264;
Best Local Similarity 27.2%; Pred. No. 1.4e-07;
RESULT 1220
ID ABM84054 standard; protein; 279 AA.
DE Human diagnostic and therapeutic protein SEQ ID NO:4303.
PN WO2004023873-A2.
PD 25-MAR-2004.
PA (INCYT) INCYTE CORP.
Query Match 7.1%; Score 280.5; DB 8; Length 279;
Best Local Similarity 27.2%; Pred. No. 1.5e-07;
RESULT 1221
ID AAO30575 standard; protein; 406 AA.
DE Human coagulation factor VII variant (S314E/L305V/V158T/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.1e-07;
RESULT 1222
ID AAO30604 standard; protein; 406 AA.
DE Human coagulation factor VII variant (K316H/L305V/V158T/K337A/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.1e-07;
RESULT 1223
ID AAO30577 standard; protein; 406 AA.
DE Human coagulation factor VII variant (S314E/L305V/V158T/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.1e-07;
RESULT 1224
ID AAO30594 standard; protein; 406 AA.
DE Human coagulation factor VII variant (K316H/L305V/K337A/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.1e-07;
RESULT 1225

ID AAO30569 standard; protein; 406 AA.
DE Human coagulation factor VII variant (S314E/L305V/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.1e-07;
RESULT 1226
ID AAO30606 standard; protein; 406 AA.
DE Human coagulation factor VII variant (K316H/L305V/V158D/K337A/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.1e-07;
RESULT 1227
ID AAO30613 standard; protein; 406 AA.
DE Human coagulation factor VII variant (K316Q/L305V/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.1e-07;
RESULT 1228
ID AAO30621 standard; protein; 406 AA.
DE Human coagulation factor VII variant (K316Q/L305V/V158T/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.1e-07;
RESULT 1229
ID AAO30619 standard; protein; 406 AA.
DE Human coagulation factor VII variant (K316Q/L305V/V158D/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.1e-07;
RESULT 1230
ID ADJ55876 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant / M298Q/L305V/K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.1e-07;
RESULT 1231
ID ADJ55937 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant M298Q/L305V/K316H/K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.1e-07;
RESULT 1232
ID ADJ56047 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant F374Y/V158D/M298Q/L305V/S314E.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.1e-07;
RESULT 1233
ID ADJ55949 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158D/M298Q/L305V/K316H/K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.1e-07;
RESULT 1234
ID ADJ55965 standard; protein; 406 AA.

DE Human factor VII polypeptide mutant V158T/ M298Q/ L305V/ K316Q.
 PN W02004000366-A1.
 PD 31-DEC-2003.
 PA (NOVO) NOVO NORDISK AS.
 Query Match 7.1%; Score 280.5; DB 8; Length 406;
 Best Local Similarity 22.5%; Pred. No. 2.1e-07;
 RESULT 1235
 ID ADJ55948 standard; protein; 406 AA.
 DE Human factor VII polypeptide mutant V158T/ M298Q/ L305V/ K316H/ K337A.
 PN W02004000366-A1.
 PD 31-DEC-2003.
 PA (NOVO) NOVO NORDISK AS.
 Query Match 7.1%; Score 280.5; DB 8; Length 406;
 Best Local Similarity 22.5%; Pred. No. 2.1e-07;
 RESULT 1236
 ID ADJ556057 standard; protein; 406 AA.
 DE Human factor VII polypeptide mutant F374Y V158T M298Q L305V S314E.
 PN W02004000366-A1.
 PD 31-DEC-2003.
 PA (NOVO) NOVO NORDISK AS.
 Query Match 7.1%; Score 280.5; DB 8; Length 406;
 Best Local Similarity 22.5%; Pred. No. 2.1e-07;
 RESULT 1237
 ID ADJ55885 standard; protein; 406 AA.
 DE Human factor VII polypeptide mutant V158T/ M298Q/ L305V/ K337A.
 PN W02004000366-A1.
 PD 31-DEC-2003.
 PA (NOVO) NOVO NORDISK AS.
 Query Match 7.1%; Score 280.5; DB 8; Length 406;
 Best Local Similarity 22.5%; Pred. No. 2.1e-07;
 RESULT 1238
 ID ADJ55921 standard; protein; 406 AA.
 DE Human factor VII polypeptide mutant V158T/ M298Q/ L305V/ S314E.
 PN W02004000366-A1.
 PD 31-DEC-2003.
 PA (NOVO) NOVO NORDISK AS.
 Query Match 7.1%; Score 280.5; DB 8; Length 406;
 Best Local Similarity 22.5%; Pred. No. 2.1e-07;
 RESULT 1239
 ID ADJ55958 standard; protein; 406 AA.
 DE Human factor VII polypeptide mutant M298Q/ L305V/ K316Q.
 PN W02004000366-A1.
 PD 31-DEC-2003.
 PA (NOVO) NOVO NORDISK AS.
 Query Match 7.1%; Score 280.5; DB 8; Length 406;
 Best Local Similarity 22.5%; Pred. No. 2.1e-07;
 RESULT 1240
 ID ADJ55963 standard; protein; 406 AA.
 DE Human factor VII polypeptide mutant V158D/ M298Q/ L305V/ K316Q.
 PN W02004000366-A1.
 PD 31-DEC-2003.
 PA (NOVO) NOVO NORDISK AS.
 Query Match 7.1%; Score 280.5; DB 8; Length 406;
 Best Local Similarity 22.5%; Pred. No. 2.1e-07;
 RESULT 1241
 ID ADJ56016 standard; protein; 406 AA.
 DE Human factor VII polypeptide mutant F374Y/ L305V/ M298Q/ S314E.
 PN W02004000366-A1.
 PD 31-DEC-2003.
 PA (NOVO) NOVO NORDISK AS.
 Query Match 7.1%; Score 280.5; DB 8; Length 406;
 Best Local Similarity 22.5%; Pred. No. 2.1e-07;
 RESULT 1242
 ID ADJ56046 standard; protein; 406 AA.
 DE Human factor VII polypeptide mutant F374Y/ V158D/ M298Q/ L305V/ K337A.
 PN W02004000366-A1.
 PD 31-DEC-2003.
 PA (NOVO) NOVO NORDISK AS.
 Query Match 7.1%; Score 280.5; DB 8; Length 406;
 Best Local Similarity 22.5%; Pred. No. 2.1e-07;
 RESULT 1243
 ID ADJ55919 standard; protein; 406 AA.
 DE Human factor VII polypeptide mutant V158D/ M298Q/ L305V/ S314E.

PN W02004000366-A1.
 PD 31-DEC-2003.
 PA (NOVO) NOVO NORDISK AS.
 Query Match 7.1%; Score 280.5; DB 8; Length 406;
 Best Local Similarity 22.5%; Pred. No. 2.1e-07;
 RESULT 1244
 ID ADJ56056 standard; protein; 406 AA.
 DE Human factor VII polypeptide mutant F374Y/ V158T/ M298Q/ L305V/ K337A.
 PN W02004000366-A1.
 PD 31-DEC-2003.
 PA (NOVO) NOVO NORDISK AS.
 Query Match 7.1%; Score 280.5; DB 8; Length 406;
 Best Local Similarity 22.5%; Pred. No. 2.1e-07;
 RESULT 1245
 ID ADJ55887 standard; protein; 406 AA.
 DE Human factor VII polypeptide mutant V158D/ M298Q/ L305V/ K337A.
 PN W02004000366-A1.
 PD 31-DEC-2003.
 PA (NOVO) NOVO NORDISK AS.
 Query Match 7.1%; Score 280.5; DB 8; Length 406;
 Best Local Similarity 22.5%; Pred. No. 2.1e-07;
 RESULT 1246
 ID ADJ55914 standard; protein; 406 AA.
 DE Human factor VII polypeptide mutant M298Q/ L305V/ S314E.
 PN W02004000366-A1.
 PD 31-DEC-2003.
 PA (NOVO) NOVO NORDISK AS.
 Query Match 7.1%; Score 280.5; DB 8; Length 406;
 Best Local Similarity 22.5%; Pred. No. 2.1e-07;
 RESULT 1247
 ID ADJ56004 standard; protein; 406 AA.
 DE Human factor VII polypeptide mutant F374Y/ L305V/ K337A/ M298Q.
 PN W02004000366-A1.
 PD 31-DEC-2003.
 PA (NOVO) NOVO NORDISK AS.
 Query Match 7.1%; Score 280.5; DB 8; Length 406;
 Best Local Similarity 22.5%; Pred. No. 2.1e-07;
 RESULT 1248
 ID ADJ010616 standard; protein; 406 AA.
 DE Human factor VII/VIIa protein mutant #52.
 PN W02004029091-A2.
 PD 08-APR-2004.
 PA (MAXY-) MAXYGEN APS.
 Query Match 7.1%; Score 280.5; DB 8; Length 406;
 Best Local Similarity 22.5%; Pred. No. 2.1e-07;
 RESULT 1249
 ID ADJ010607 standard; protein; 406 AA.
 DE Human factor VII/VIIa protein mutant #43.
 PN W02004029091-A2.
 PD 08-APR-2004.
 PA (MAXY-) MAXYGEN APS.
 Query Match 7.1%; Score 280.5; DB 8; Length 406;
 Best Local Similarity 22.5%; Pred. No. 2.1e-07;
 RESULT 1250
 ID AAR09221 standard; protein; 526 AA.
 DE c-PA deletion variant d297.
 PN W03002798-A.
 PD 22-MAR-1990.
 PA (GEHTH) GENENTECH INC.
 Query Match 7.1%; Score 280.5; DB 2; Length 526;
 Best Local Similarity 23.1%; Pred. No. 2.7e-07;
 RESULT 1251
 ID AAV70020 standard; protein; 561 AA.
 DE Sequence of tissue plasminogen activator (tPA).
 PN EP242836-A.
 PD 28-OCT-1987.
 PA (BOE) BOEHRINGER MANNHEIM GMBH.
 Query Match 7.1%; Score 280.5; DB 1; Length 561;
 Best Local Similarity 21.7%; Pred. No. 2.9e-07;
 RESULT 1252
 ID ABR62449 standard; protein; 583 AA.

DE Bovine recombinant prothrombin, expressed in Escherichia coli.
FN WO2003052059-A2.
PD 26-JUN-2003.
PA (ELIL) LILLY & CO ELI.
Query Match 7.1%; Score 280.5; DB 7; Length 583;
Best Local Similarity 21.9%; Pred. No. 3e-07;
RESULT 1253
ID ABR62451 standard; protein; 635 AA.
DE Bovine recombinant prothrombin, expressed in CHO cells.
FN WO2003052059-A2.
PD 26-JUN-2003.
PA (ELIL) LILLY & CO ELI.
Query Match 7.1%; Score 280.5; DB 7; Length 635;
Best Local Similarity 21.9%; Pred. No. 3.2e-07;
RESULT 1254
ID AAR37402 standard; protein; 448 AA.
DE Factor X.
FN WO9309803-A1.
PD 27-MAY-1993.
PA (SCHAF) SCHAFER S C.
PA (SCRI) SCRIPPS RES INST.
Query Match 7.1%; Score 280; DB 2; Length 448;
Best Local Similarity 24.0%; Pred. No. 2.5e-07;
RESULT 1255
ID AAW66092 standard; peptide; 448 AA.
DE Human factor X variant.
FN WO9839456-A1.
PD 11-SEP-1998.
PA (UNIV) UNIV WASHINGTON.
Query Match 7.1%; Score 280; DB 2; Length 448;
Best Local Similarity 24.0%; Pred. No. 2.5e-07;
RESULT 1256
ID AAR09245 standard; protein; 525 AA.
DE t-PA deletion variant d297, d305.
FN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 280; DB 2; Length 525;
Best Local Similarity 23.1%; Pred. No. 2.9e-07;
RESULT 1257
ID AAR05488 standard; protein; 527 AA.
DE tPA024 precursor protein.
FN EP973896-A.
PD 20-JUN-1990.
PA (YAMA) YAMANOUCHI PHARM CO LTD.
PA (YAMA) NIPPON STEEL CORP.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 2.9e-07;
RESULT 1258
ID AAR09267 standard; protein; 527 AA.
DE t-PA variant D283A, H287A.
FN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 2.9e-07;
RESULT 1259
ID AAR09282 standard; protein; 527 AA.
DE t-PA variant D460A, R462A.
FN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 2.9e-07;
RESULT 1260
ID AAR13911 standard; protein; 527 AA.
DE t-PA deriv. (II).
FN EP445464-A.
PD 11-SEP-1991.
PA (KANF) KANEGAFUCHI KAGAKU KOGYO KK.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 2.9e-07;
RESULT 1261

ID AAR13914 standard; protein; 527 AA.
DE t-PA deriv. (V).
FN EP445464-A.
PD 11-SEP-1991.
PA (KANF) KANEGAFUCHI KAGAKU KOGYO KK.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 2.9e-07;
RESULT 1262
ID AAR13912 standard; protein; 527 AA.
DE t-PA deriv. (III).
FN EP445464-A.
PD 11-SEP-1991.
PA (KANF) KANEGAFUCHI KAGAKU KOGYO KK.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 2.9e-07;
RESULT 1263
ID AAR13910 standard; protein; 527 AA.
DE t-PA deriv. (I).
FN EP445464-A.
PD 11-SEP-1991.
PA (KANF) KANEGAFUCHI KAGAKU KOGYO KK.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 2.9e-07;
RESULT 1264
ID AAR21594 standard; protein; 527 AA.
DE tPA variant - D95A.
FN WO9202612-A.
PD 20-FEB-1992.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 2.9e-07;
RESULT 1265
ID AAR21593 standard; protein; 527 AA.
DE tPA variant - E94A.
FN WO9202612-A.
PD 20-FEB-1992.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.4%; Pred. No. 2.9e-07;
RESULT 1266
ID AAR20221 standard; protein; 527 AA.
DE t-PA analogue expressed by pCDM6-013.
FN JP03285680-A.
PD 16-DEC-1991.
PA (SUMU) SUMITOMO SEIYAKU KK.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 2.9e-07;
RESULT 1267
ID AAR20215 standard; protein; 527 AA.
DE R462S t-PA analogue.
FN JP03285680-A.
PD 16-DEC-1991.
PA (SUMU) SUMITOMO SEIYAKU KK.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 2.9e-07;
RESULT 1268
ID AAR20216 standard; protein; 527 AA.
DE R462G t-PA analogue.
FN JP03285680-A.
PD 16-DEC-1991.
PA (SUMU) SUMITOMO SEIYAKU KK.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 2.9e-07;
RESULT 1269
ID AAR20222 standard; protein; 527 AA.
DE t-PA analogue expressed by pCDM6-014.
FN JP03285680-A.
PD 16-DEC-1991.
PA (SUMU) SUMITOMO SEIYAKU KK.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 2.9e-07;
RESULT 1270
ID AAR20223 standard; protein; 527 AA.

DE t-PA analogue expressed by pCDM8-018.
PN JP03285680-A.
PD 16-DEC-1991.
PA (SUMU) SUMITOMO SEIYAKU KK.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 2.9e-07;
RESULT 1271
ID AAR44811 standard; protein; 527 AA.
DE Human tPA variant N67.
PN US5270198-A.
PD 14-DEC-1993.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 2.9e-07;
RESULT 1272
ID AAR70865 standard; protein; 527 AA.
DE Human t-PA variant (N67,A410).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 22.9%; Pred. No. 2.9e-07;
RESULT 1273
ID AAW57778 standard; protein; 527 AA.
DE R275E,H417D human tissue-type plasminogen activator protein mutant.
PN WO9821320-A2.
PD 22-MAY-1998.
PA (SCRI) SCRIPPS RES INST.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 2.9e-07;
RESULT 1274
ID AAW45907 standard; peptide; 527 AA.
DE Single chain form of the intact t-PA molecule.
PN WO9802454-A2.
PD 22-JAN-1998.
PA (ADPR-) ADPROTECH PLC.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 2.9e-07;
RESULT 1275
ID AAE24190 standard; protein; 527 AA.
DE Human tissue plasminogen activator (tPA) protein.
PN WO200240656-A2.
PD 23-MAY-2002.
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
Query Match 7.1%; Score 280; DB 5; Length 527;
Best Local Similarity 23.0%; Pred. No. 2.9e-07;
RESULT 1276
ID AAG79362 standard; protein; 527 AA.
DE Human tissue plasminogen activator.
PN WO200243747-A2.
PD 06-JUN-2002.
PA (ISIS-) ISIS INNOVATION LTD.
Query Match 7.1%; Score 280; DB 5; Length 527;
Best Local Similarity 23.0%; Pred. No. 2.9e-07;
RESULT 1277
ID AAE25044 standard; protein; 527 AA.
DE Human tissue plasminogen activator (tPA) protein.
PN WO200240650-A2.
PD 23-MAY-2002.
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
Query Match 7.1%; Score 280; DB 5; Length 527;
Best Local Similarity 23.0%; Pred. No. 2.9e-07;
RESULT 1278
ID ADL92126 standard; protein; 527 AA.
DE Alteplase protein sequence.
PN WO200309862-A1.
PD 04-DEC-2003.
PA (NANO-) APPLIED NANOSYSTEMS BV.
Query Match 7.1%; Score 280; DB 8; Length 527;
Best Local Similarity 23.0%; Pred. No. 2.9e-07;
RESULT 1279
ID AAM82630 standard; protein; 534 AA.
DE Human diagnostic and therapeutic protein SEQ ID NO.2879.

PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 7.1%; Score 280; DB 8; Length 534;
Best Local Similarity 22.7%; Pred. No. 2.9e-07;
RESULT 1280
ID AAM82821 standard; protein; 534 AA.
DE Human diagnostic and therapeutic protein SEQ ID NO.3070.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 7.1%; Score 280; DB 8; Length 534;
Best Local Similarity 22.7%; Pred. No. 2.9e-07;
RESULT 1281
ID AAR13020 standard; protein; 557 AA.
DE T-PA variant contg. fibronectin for thrombosis lysis (4).
PN JP03061482-A.
PD 18-MAR-1991.
PA (FUJI) FUJISAWA PHARM CO LTD.
Query Match 7.1%; Score 280; DB 2; Length 557;
Best Local Similarity 23.0%; Pred. No. 3e-07;
RESULT 1282
ID AAR13149 standard; protein; 557 AA.
DE T-PA variant contg. fibronectin for thrombosis lysis (4).
PN JP03061482-A.
PD 18-MAR-1991.
PA (FUJI) FUJISAWA PHARM CO LTD.
Query Match 7.1%; Score 280; DB 2; Length 557;
Best Local Similarity 23.0%; Pred. No. 3e-07;
RESULT 1283
ID AAP50219 standard; protein; 561 AA.
DE Tissue plasminogen activator encoded by cDNA clone.
PN EP143081-A.
PD 29-MAY-1985.
PA (CIBA) CIBA GEIGY AG.
Query Match 7.1%; Score 280; DB 1; Length 561;
Best Local Similarity 23.0%; Pred. No. 3.1e-07;
RESULT 1284
ID AAP60790 standard; protein; 562 AA.
DE Sequence of human pre-tissue plasminogen activator (pre-t-PA).
PN GB2173804-A.
PD 22-OCT-1986.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 280; DB 1; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.1e-07;
RESULT 1285
ID AAP60810 standard; protein; 562 AA.
DE Sequence of modified human tissue plasminogen activator (t-PA).
PN FR2581652-A.
PD 14-NOV-1986.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 280; DB 1; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.1e-07;
RESULT 1286
ID AAP60214 standard; protein; 562 AA.
DE Sequence of active human uterine tissue plasminogen activator (UTPA).
PN EP178105-A.
PD 16-APR-1986.
PA (INTE-) INTEG GENETICS INC.
Query Match 7.1%; Score 280; DB 1; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.1e-07;
RESULT 1287
ID AAP81913 standard; protein; 562 AA.
DE Tissue plasminogen activator encoded by pEM1-tPA.
PN WO8800242-A.
PD 14-JAN-1988.
PA (DAMO-) DAMON BIOTECH INC.
Query Match 7.1%; Score 280; DB 1; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.1e-07;
RESULT 1288
ID AAP80655 standard; protein; 562 AA.
DE Tissue plasminogen activator analogue.
PN EP293934-A.

PD 07-DEC-1988.
PA (ZYMO) ZYMOGENETICS INC.
PA (NOVO) NOVO IND AS.
PA (EISA) EISA CO LTD.
Query Match
Best Local Similarity 7.1%; Score 280; DB 1; Length 562;
RESULT 1289
ID AAP94406 standard; protein; 562 AA.
DE Sequence encoded by native cPA of plasmid pST112.
PN EP302456-A.
PD 08-FEB-1989.
PA (FUJII) FUJISAWA PHARM CO LTD.
Query Match
Best Local Similarity 7.1%; Score 280; DB 1; Length 562;
RESULT 1290
ID AAP93716 standard; protein; 562 AA.
DE Human melanoma c-PA encoded by plasmid pKG12.
PN EP297066-A.
PD 28-DEC-1988.
PA (KABI) KABIGEN AB.
Query Match
Best Local Similarity 7.1%; Score 280; DB 1; Length 562;
RESULT 1291
ID AAP90916 standard; protein; 562 AA.
DE Human tissue plasminogen activator.
PN JP01174388-A.
PD 10-JUL-1989.
PA (FUJII) FUJISAWA PHARM CO LTD.
Query Match
Best Local Similarity 7.1%; Score 280; DB 1; Length 562;
RESULT 1292
ID AAR09288 standard; protein; 562 AA.
DE Sequence of tissue plasminogen activator analogue BBNT11 (Ser 67, Leu 68).
PN WO8912681-A.
PD 28-DEC-1989.
PA (BBBI-) BRIT BIO-TECHN LTD.
Query Match
Best Local Similarity 7.1%; Score 280; DB 2; Length 562;
RESULT 1293
ID AAR06237 standard; protein; 562 AA.
DE Novel tissue plasminogen activator (tPA) encoded by plasmid pST112.
PN EP379890-A.
PD 01-AUG-1990.
PA (FUJII) FUJISAWA PHARM CO LTD.
Query Match
Best Local Similarity 7.1%; Score 280; DB 2; Length 562;
RESULT 1294
ID AAR04700 standard; protein; 562 AA.
DE Sequence of tissue plasminogen activator (t-PA) analogue t-PA C87S, H420S with altered residues 419 and 420.
PN EP351246-A.
PD 17-JAN-1990.
PA (NOVO) NOVO-NORDISK AS.
PA (NOVO) NOVO-NORDISK AS.
Query Match
Best Local Similarity 7.1%; Score 280; DB 2; Length 562;
RESULT 1295
ID AAR04701 standard; protein; 562 AA.
DE Sequence of tissue plasminogen activator (t-PA) analogue t-PA K419S with altered residue 419.
PN EP351246-A.
PD 17-JAN-1990.
PA (NOVO) NOVO-NORDISK AS.
PA (NOVO) NOVO-NORDISK AS.
Query Match
Best Local Similarity 7.1%; Score 280; DB 2; Length 562;
RESULT 1296
ID AAR04699 standard; protein; 562 AA.
DE Native tissue plasminogen activator (t-PA).
PN EP351246-A.
PD 17-JAN-1990.
PA (NOVO) NOVO-NORDISK AS.

PA (NOVO) NOVO-NORDISK AS.
Query Match
Best Local Similarity 7.1%; Score 280; DB 2; Length 562;
RESULT 1297
ID AAR13727 standard; protein; 562 AA.
DE T-PA67+ mutant with supernumerary N-linked oligosaccharide side chain.
PN US5041376-A.
PD 20-AUG-1991.
PA (TEXA) UNIV TEXAS SYSTEM.
PA (COLD-) COLD SPRING HARBOR LAB.
Query Match
Best Local Similarity 7.1%; Score 280; DB 2; Length 562;
RESULT 1298
ID AAR12847 standard; protein; 562 AA.
DE T-PA Kringle 1 domain substitution mutant.
PN JP03127987-A.
PD 31-MAY-1991.
PA (KANF) KANEGAFUCHI CHEM KK.
Query Match
Best Local Similarity 7.1%; Score 280; DB 2; Length 562;
RESULT 1299
ID AAR23811 standard; protein; 562 AA.
DE t-PA (Glu 296, Glu 298, Glu 299) triple mutant.
PN WO9206203-A.
PD 16-APR-1992.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match
Best Local Similarity 7.1%; Score 280; DB 2; Length 562;
RESULT 1300
ID AAR23806 standard; protein; 562 AA.
DE t-PA (Glu 296) mutant.
PN WO9206203-A.
PD 16-APR-1992.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match
Best Local Similarity 7.1%; Score 280; DB 2; Length 562;
RESULT 1301
ID AAR23804 standard; protein; 562 AA.
DE t-PA (Glu 304) mutant.
PN WO9206203-A.
PD 16-APR-1992.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match
Best Local Similarity 7.1%; Score 280; DB 2; Length 562;
RESULT 1302
ID AAR34426 standard; protein; 562 AA.
DE Sequence of human pre-pro tissue plasminogen activator (t-PA).
PN US5200340-A.
PD 06-APR-1993.
PA (ZYMO) ZYMOGENETICS INC.
Query Match
Best Local Similarity 7.1%; Score 280; DB 2; Length 562;
RESULT 1303
ID AAR96220 standard; protein; 562 AA.
DE Full-length tissue plasminogen activator.
PN US5504001-A.
PD 02-APR-1996.
PA (ZYMO) ZYMOGENETICS INC.
Query Match
Best Local Similarity 7.1%; Score 280; DB 2; Length 562;
RESULT 1304
ID AAY50868 standard; protein; 562 AA.
DE Human tissue plasminogen activator protein fragment.
PN WO9957251-A2.
PD 11-NOV-1999.
PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.
Query Match
Best Local Similarity 7.1%; Score 280; DB 3; Length 562;
RESULT 1305
ID AAY43397 standard; protein; 562 AA.
DE Human tissue plasminogen activator protein sequence.
PN US5985607-A.
PD 16-NOV-1999.

PA (CANG-) CANGENE CORP.
 Query Match 7.1%; Score 280; DB 3; Length 562;
 Best Local Similarity 23.0%; Pred. No. 3.1e-07;
 RESULT 1306
 ID AAY959590 standard; protein; 562 AA.
 DE Human tissue-type plasminogen activator t-PA.
 PN W0200032759-A1.
 PD 08-JUN-2000.
 PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.
 Query Match 7.1%; Score 280; DB 3; Length 562;
 Best Local Similarity 23.0%; Pred. No. 3.1e-07;
 RESULT 1307
 ID AAU97700 standard; protein; 562 AA.
 DE Human tissue plasminogen activator (t-PA) protein sequence.
 PN W0200232446-A2.
 PD 25-APR-2002.
 PA (PFIZ) PFIZER LTD.
 Query Match 7.1%; Score 280; DB 5; Length 562;
 Best Local Similarity 23.0%; Pred. No. 3.1e-07;
 RESULT 1308
 ID AAB37130 standard; protein; 562 AA.
 DE Human tissue-type plasminogen activator (tPA) protein.
 PN W02003033009-A2.
 PD 24-APR-2003.
 PA (OMNI-) OMNIO AB.
 Query Match 7.1%; Score 280; DB 6; Length 562;
 Best Local Similarity 23.0%; Pred. No. 3.1e-07;
 RESULT 1309
 ID AAR55851 standard; protein; 562 AA.
 DE Human tissue-type plasminogen activator (TPA) .
 PN W02003031464-A2.
 PD 17-APR-2003.
 PA (NEOS-) NEOSE TECHNOLOGIES INC.
 Query Match 7.1%; Score 280; DB 6; Length 562;
 Best Local Similarity 23.0%; Pred. No. 3.1e-07;
 RESULT 1310
 ID ABUS7646 standard; protein; 562 AA.
 DE Differentially expressed breast cancer associated protein #33.
 PN US2002156263-A1.
 PD 24-OCT-2002.
 PA (CHEN/) CHEN H.
 Query Match 7.1%; Score 280; DB 6; Length 562;
 Best Local Similarity 23.0%; Pred. No. 3.1e-07;
 RESULT 1311
 ID ADN95624 standard; protein; 562 AA.
 DE Human BEC/Lec-related protein sequence SeqID547.
 PN W02003080640-A1.
 PD 02-OCT-2003.
 PA (LUDW-) LUDWIG INST CANCER RES.
 Query Match 7.1%; Score 280; DB 7; Length 562;
 Best Local Similarity 23.0%; Pred. No. 3.1e-07;
 RESULT 1312
 ID ADN49698 standard; protein; 562 AA.
 DE Human tissue type plasminogen activator TPA protein SeqID 26.
 PN W02004033651-A2.
 PD 22-APR-2004.
 PA (NEOS-) NEOSE TECHNOLOGIES INC.
 Query Match 7.1%; Score 280; DB 8; Length 562;
 Best Local Similarity 23.0%; Pred. No. 3.1e-07;
 RESULT 1313
 ID ADO28679 standard; protein; 562 AA.
 DE Human tPA protein SEQ ID NO:108.
 PN W02004044178-A2.
 PD 27-MAY-2004.
 PA (GETH) GENENTECH INC.
 Query Match 7.1%; Score 280; DB 8; Length 562;
 Best Local Similarity 23.0%; Pred. No. 3.1e-07;
 RESULT 1314
 ID AAM80983 standard; protein; 562 AA.
 DE Tumour-associated antigenic target (TAR) polypeptide PRO4, SEQ:2535.
 PN W02004030615-A2.

PD 15-APR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 7.1%; Score 280; DB 8; Length 562;
 Best Local Similarity 23.0%; Pred. No. 3.1e-07;
 RESULT 1315
 ID ADQ39248 standard; protein; 562 AA.
 DE Human myocardial infarction-associated gene derived protein, SEQ ID 911.
 PN W02004058052-A2.
 PD 15-JUL-2004.
 PA (APPL-) APPLERA CORP.
 Query Match 7.1%; Score 280; DB 8; Length 562;
 Best Local Similarity 23.0%; Pred. No. 3.1e-07;
 RESULT 1316
 ID AAO30591 standard; protein; 406 AA.
 DE Human coagulation factor VII variant (K316H/L305V/V158T/M298Q) .
 PN W02003037932-A2.
 PD 08-MAY-2003.
 PA (NOVO) NOVO NORDISK AS.
 Query Match 7.1%; Score 279.5; DB 6; Length 406;
 Best Local Similarity 22.5%; Pred. No. 2.4e-07;
 RESULT 1317
 ID AAO30599 standard; protein; 406 AA.
 DE Human coagulation factor VII variant (K316H/L305V/V158T/M298Q) .
 PN W02003037932-A2.
 PD 08-MAY-2003.
 PA (NOVO) NOVO NORDISK AS.
 Query Match 7.1%; Score 279.5; DB 6; Length 406;
 Best Local Similarity 22.5%; Pred. No. 2.4e-07;
 RESULT 1318
 ID AAO30597 standard; protein; 406 AA.
 DE Human coagulation factor VII variant (K316H/L305V/V158D/M298Q) .
 PN W02003037932-A2.
 PD 08-MAY-2003.
 PA (NOVO) NOVO NORDISK AS.
 Query Match 7.1%; Score 279.5; DB 6; Length 406;
 Best Local Similarity 22.5%; Pred. No. 2.4e-07;
 RESULT 1319
 ID ADJ55873 standard; protein; 406 AA.
 DE Human factor VII polypeptide mutant M298Q/L305V.
 PN W02004000366-A1.
 PD 31-DEC-2003.
 PA (NOVO) NOVO NORDISK AS.
 Query Match 7.1%; Score 279.5; DB 8; Length 406;
 Best Local Similarity 22.5%; Pred. No. 2.4e-07;
 RESULT 1320
 ID ADJ55985 standard; protein; 406 AA.
 DE Human factor VII polypeptide mutant F374Y/L305V/M298Q.
 PN W02004000366-A1.
 PD 31-DEC-2003.
 PA (NOVO) NOVO NORDISK AS.
 Query Match 7.1%; Score 279.5; DB 8; Length 406;
 Best Local Similarity 22.5%; Pred. No. 2.4e-07;
 RESULT 1321
 ID ADJ55941 standard; protein; 406 AA.
 DE Human factor VII polypeptide mutant V158D/M298Q/L305V/K316H.
 PN W02004000366-A1.
 PD 31-DEC-2003.
 PA (NOVO) NOVO NORDISK AS.
 Query Match 7.1%; Score 279.5; DB 8; Length 406;
 Best Local Similarity 22.5%; Pred. No. 2.4e-07;
 RESULT 1322
 ID ADJ55943 standard; protein; 406 AA.
 DE Human factor VII polypeptide mutant V158T/M298Q/L305V/K316H.
 PN W02004000366-A1.
 PD 31-DEC-2003.
 PA (NOVO) NOVO NORDISK AS.
 Query Match 7.1%; Score 279.5; DB 8; Length 406;
 Best Local Similarity 22.5%; Pred. No. 2.4e-07;
 RESULT 1323
 ID ADJ56009 standard; protein; 406 AA.
 DE Human factor VII polypeptide mutant F374Y/L305V/V158D/M298Q.
 PN W02004000366-A1.
 PD 31-DEC-2003.

PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 279.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1324
ID A055879 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158D/ M298Q/ L305V.
PN W02004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 279.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1325
ID A055604 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant F374Y/ L305V/ V158T/ M298Q.
PN W02004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 279.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1326
ID A055881 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158T/ M298Q/ L305V.
PN W02004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 279.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1327
ID A055936 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant M298Q/ L305V/ K316H.
PN W02004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 279.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1328
ID A010619 standard; protein; 406 AA.
DE Human factor VII/VIII protein mutant #55.
PN W02004029091-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN APS.
Query Match 7.1%; Score 279.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.4e-07;
RESULT 1329
ID A010619 standard; protein; 406 AA.
DE Human factor VII/VIII protein mutant #55.
PN W02004029091-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.1%; Score 279.5; DB 8; Length 406;
Best Local Similarity 22.6%; Pred. No. 2.4e-07;
RESULT 1329
ID A074689 standard; protein; 520 AA.
DE t-PA mutein (N117Q, N184Q, delta 296-302, 44-50 replaced by QRLASQA).
PN CNI082111-A.
PD 16-FEB-1994.
PA (BIOE-) BIOENGINEERING INST ACAD MILITARY.
Query Match 7.1%; Score 279.5; DB 2; Length 520;
Best Local Similarity 23.3%; Pred. No. 3e-07;
RESULT 1330
ID AAR09229 standard; protein; 526 AA.
DE t-PA deletion variant d305.
PN W09002798-A.
PD 22-MAR-1990.
PA (GENTECH) GENENTECH INC.
Query Match 7.1%; Score 279.5; DB 2; Length 526;
Best Local Similarity 23.0%; Pred. No. 3.1e-07;
RESULT 1331
ID AAR09228 standard; protein; 526 AA.
DE t-PA deletion variant d304.
PN W09002798-A.
PD 22-MAR-1990.
PA (GENTECH) GENENTECH INC.
Query Match 7.1%; Score 279.5; DB 2; Length 526;
Best Local Similarity 23.0%; Pred. No. 3.1e-07;
RESULT 1332
ID AAR09218 standard; protein; 528 AA.
DE t-PA insertion variant 1305 H, T, N, K, R, Q.
PN W09002798-A.
PD 22-MAR-1990.

PA (GENTECH) GENENTECH INC.
Query Match 7.1%; Score 279.5; DB 2; Length 528;
Best Local Similarity 23.0%; Pred. No. 3.1e-07;
RESULT 1333
ID A056427 standard; protein; 782 AA.
DE Human ovarian cancer marker OV82.
PN W0200271928-A2.
PD 19-SEP-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 7.1%; Score 279.5; DB 5; Length 782;
Best Local Similarity 20.8%; Pred. No. 4.4e-07;
RESULT 1334
ID AAB84871 standard; protein; 401 AA.
DE Mutant blood coagulant factor VII (FVII-39).
PN JP2001061479-A.
PD 13-MAR-2001.
PA (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
Query Match 7.1%; Score 279; DB 4; Length 401;
Best Local Similarity 22.8%; Pred. No. 2.5e-07;
RESULT 1335
ID AAR09250 standard; protein; 483 AA.
DE t-PA variant d1-44, V213K, F305H.
PN W09002798-A.
PD 22-MAR-1990.
PA (GENTECH) GENENTECH INC.
Query Match 7.1%; Score 279; DB 2; Length 483;
Best Local Similarity 23.0%; Pred. No. 3e-07;
RESULT 1336
ID AAR09248 standard; protein; 483 AA.
DE t-PA variant d1-44, I210R, G211A, K212R, V213R, F305H.
PN W09002798-A.
PD 22-MAR-1990.
PA (GENTECH) GENENTECH INC.
Query Match 7.1%; Score 279; DB 2; Length 483;
Best Local Similarity 22.8%; Pred. No. 3e-07;
RESULT 1337
ID AAR09247 standard; protein; 483 AA.
DE t-PA variant d1-44, F305H.
PN W09002798-A.
PD 22-MAR-1990.
PA (GENTECH) GENENTECH INC.
Query Match 7.1%; Score 279; DB 2; Length 483;
Best Local Similarity 23.0%; Pred. No. 3e-07;
RESULT 1338
ID AAR09251 standard; protein; 483 AA.
DE t-PA variant d1-44, T252R, F305H.
PN W09002798-A.
PD 22-MAR-1990.
PA (GENTECH) GENENTECH INC.
Query Match 7.1%; Score 279; DB 2; Length 483;
Best Local Similarity 23.0%; Pred. No. 3e-07;
RESULT 1339
ID AAR09263 standard; protein; 483 AA.
DE t-PA variant Y67N, F305H.
PN W09002798-A.
PD 22-MAR-1990.
PA (GENTECH) GENENTECH INC.
Query Match 7.1%; Score 279; DB 2; Length 483;
Best Local Similarity 23.0%; Pred. No. 3e-07;
RESULT 1340
ID AAR09252 standard; protein; 483 AA.
DE t-PA variant d1-44, V213K, T252R, F305H.
PN W09002798-A.
PD 22-MAR-1990.
PA (GENTECH) GENENTECH INC.
Query Match 7.1%; Score 279; DB 2; Length 483;
Best Local Similarity 23.0%; Pred. No. 3e-07;
RESULT 1341
ID AAR09253 standard; protein; 483 AA.
DE t-PA variant d1-44, I210K, F305H.
PN W09002798-A.
PD 22-MAR-1990.
PA (GENTECH) GENENTECH INC.

Query Match 7.1%; Score 279; DB 2; Length 483;
Best Local Similarity 23.0%; Pred. No. 3e-07;
RESULT 1342
ID AAR09243 standard; protein; 525 AA.
DE t-PA deletion variant d304-305.
PN W09002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 279; DB 2; Length 525;
Best Local Similarity 23.0%; Pred. No. 3.2e-07;
RESULT 1343
ID AAR04186 standard; protein; 527 AA.
DE Plasmidogen activator.
PN EP365468-A.
PD 25-APR-1990.
PA (CIBA) CIBA GEIGY AG.
PA (UCPG-) UCP GEN-PHARMA AG.
Query Match 7.1%; Score 279; DB 2; Length 527;
Best Local Similarity 23.4%; Pred. No. 3.3e-07;
RESULT 1344
ID AAR06236 standard; protein; 527 AA.
DE Novel tissue plasminogen activator (tPA) encoding plasmid PTPA102.
PN EP379890-A.
PD 01-AUG-1990.
PA (FUJI) FUJISAWA PHARM CO LTD.
Query Match 7.1%; Score 279; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 3.3e-07;
RESULT 1345
ID AAR09256 standard; protein; 527 AA.
DE t-PA variant 1210R, G211A, K212R, V213R, F305H.
PN W09002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 279; DB 2; Length 527;
Best Local Similarity 22.8%; Pred. No. 3.3e-07;
RESULT 1346
ID AAR09275 standard; protein; 527 AA.
DE t-PA variant E410A.
PN W09002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 279; DB 2; Length 527;
Best Local Similarity 22.8%; Pred. No. 3.3e-07;
RESULT 1347
ID AAR09215 standard; protein; 527 AA.
DE t-PA variant F305 H, T, N, K, R, Q.
PN W09002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 279; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.3e-07;
RESULT 1348
ID AAR09262 standard; protein; 527 AA.
DE t-PA variant Y67N, F305H.
PN W09002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 279; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.3e-07;
RESULT 1349
ID AAR21596 standard; protein; 527 AA.
DE tPA variant - E94A, D95A, N117Q.
PN W09202612-A.
PD 20-FEB-1992.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 279; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.3e-07;
RESULT 1350
ID AAR21595 standard; protein; 527 AA.
DE tPA variant - D95G.
PN W09202612-A.
PD 20-FEB-1992.
PA (GETH) GENENTECH INC.

Query Match 7.1%; Score 279; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.3e-07;
RESULT 1351
ID AAR21597 standard; protein; 527 AA.
DE tPA variant - E94A, D95A, D236A, D238A, K240A.
PN W09202612-A.
PD 20-FEB-1992.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 279; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 3.3e-07;
RESULT 1352
ID AAR44813 standard; protein; 527 AA.
DE Human tPA variant (N105, S107).
PN US5270198-A.
PD 14-DEC-1993.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 279; DB 2; Length 527;
Best Local Similarity 23.4%; Pred. No. 3.3e-07;
RESULT 1353
ID AAR70905 standard; protein; 527 AA.
DE Human t-PA variant (N103, A445, A449).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 279; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.3e-07;
RESULT 1354
ID AAM57779 standard; protein; 527 AA.
DE R275E, H417E human tissue-type plasminogen activator protein mutant.
PN W09821320-A2.
PD 22-MAY-1998.
PA (SCRI) SCRIPPS RES INST.
Query Match 7.1%; Score 279; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.3e-07;
RESULT 1355
ID AAR25435 standard; protein; 528 AA.
DE t-PA variant R299D.
PN W09211377-A1.
PD 09-JUL-1992.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 279; DB 2; Length 528;
Best Local Similarity 23.5%; Pred. No. 3.3e-07;
RESULT 1356
ID AAR09219 standard; protein; 529 AA.
DE t-PA insertion variant 1305 HH.
PN W09002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 279; DB 2; Length 529;
Best Local Similarity 23.0%; Pred. No. 3.3e-07;
RESULT 1357
ID AAP70882 standard; protein; 530 AA.
DE Thrombolytic protein 1-13-1-21 having t-PA activity, deleted or replaced
DE R275 is and containing a modified N-linked glycosylation site.
PN W08704722-A.
PD 13-AUG-1987.
PA (GEMV) GENETICS INST INC.
PA (LARS/) LARSEN G R.
Query Match 7.1%; Score 279; DB 1; Length 530;
Best Local Similarity 23.0%; Pred. No. 3.3e-07;
RESULT 1358
ID AAP71659 standard; protein; 530 AA.
DE Thrombolytic protein with t-PA activity where R275 is deleted or replaced
DE and containing a modified N-linked glycosylation site.
PN W08704722-A.
PD 13-AUG-1987.
PA (GEMV) GENETICS INST INC.
PA (LARS/) LARSEN G R.
Query Match 7.1%; Score 279; DB 1; Length 530;
Best Local Similarity 23.0%; Pred. No. 3.3e-07;
RESULT 1359
ID AAP70879 standard; protein; 530 AA.
DE Thrombolytic proteins 1-1-1-7 having t-PA activity, where R275 is deleted

DE or replaced.
PN W08704722-A.
PD 13-AUG-1987.
PA (GEMV) GENETICS INST INC.
PA (LARS/) LARSEN G R.
Query Match 7.1%; Score 279; DB 1; Length 530;
Best Local Similarity 23.0%; Pred. No. 3.3e-07;
RESULT 1360
ID AAP92377 standard; protein; 530 AA.
DE Sequence of modified tPA-type thrombolytic proteins.
PN W08810119-A.
PD 29-DEC-1988.
PA (GEMV) GENETICS INST INC.
Query Match 7.1%; Score 279; DB 1; Length 530;
Best Local Similarity 23.0%; Pred. No. 3.3e-07;
RESULT 1361
ID AAP30001 standard; protein; 562 AA.
DE Sequence of full length tissue plasminogen activator (t-PA).
PN EP93619-A.
PD 09-NOV-1983.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 279; DB 1; Length 562;
Best Local Similarity 22.9%; Pred. No. 3.5e-07;
RESULT 1362
ID AAP94238 standard; protein; 562 AA.
DE Human tissue plasminogen activator (t-PA) gene.
PN W08900197-A.
PD 12-JAN-1989.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 279; DB 1; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.5e-07;
RESULT 1363
ID AAR23803 standard; protein; 562 AA.
DE t-PA (Ser 304) mutant.
PN W09206203-A.
PD 16-APR-1992.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match 7.1%; Score 279; DB 2; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.5e-07;
RESULT 1364
ID AAR23801 standard; protein; 562 AA.
DE Zymogen-like t-PA (His 305).
PN W09206203-A.
PD 16-APR-1992.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match 7.1%; Score 279; DB 2; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.5e-07;
RESULT 1365
ID AAW47536 standard; protein; 562 AA.
DE Tissue plasminogen activator variant R275E.
PN US5714372-A.
PD 03-FEB-1998.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 279; DB 2; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.5e-07;
RESULT 1366
ID AAW47537 standard; protein; 562 AA.
DE Tissue plasminogen activator variant I276P.
PN US5714372-A.
PD 03-FEB-1998.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 279; DB 2; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.5e-07;
RESULT 1367
ID AAW47535 standard; protein; 562 AA.
DE Tissue plasminogen activator variant R275G.
PN US5714372-A.
PD 03-FEB-1998.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 279; DB 2; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.5e-07;
RESULT 1368
ID AAW48426 standard; protein; 562 AA.

DE Tissue type plasminogen activator, tPA.
PN KRI41262-B1.
PD 15-JUN-1998.
PA (GLDS) LG CHEM LTD.
Query Match 7.1%; Score 279; DB 3; Length 562;
Best Local Similarity 22.9%; Pred. No. 3.5e-07;
RESULT 1369
ID ADR43718 standard; protein; 932 AA.
DE Human protease PRS-6, SEQ ID 6.
PN W0200220736-A2.
PD 14-MAR-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 7.1%; Score 279; DB 5; Length 932;
Best Local Similarity 23.4%; Pred. No. 5.5e-07;
RESULT 1370
ID AAU82743 standard; protein; 970 AA.
DE Amino acid sequence of novel human protease #42.
PN W0200200860-A2.
PD 03-JAN-2002.
PA (SUGEN-) SUGEN INC.
Query Match 7.1%; Score 279; DB 5; Length 970;
Best Local Similarity 23.4%; Pred. No. 5.8e-07;
RESULT 1371
ID ABR39439 standard; protein; 264 AA.
DE Human GENSET polypeptide clone name vCTRL-1.
PN W02003014151-A2.
PD 20-FEB-2003.
PA (GEST) GENSET SA.
Query Match 7.1%; Score 278.5; DB 6; Length 264;
Best Local Similarity 27.2%; Pred. No. 1.8e-07;
RESULT 1372
ID AAB84867 standard; protein; 406 AA.
DE Mutant blood coagulant factor VII (FVII-5).
PN JP2001061479-A.
PD 13-MAR-2001.
PA (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
Query Match 7.1%; Score 278.5; DB 4; Length 406;
Best Local Similarity 23.0%; Pred. No. 2.7e-07;
RESULT 1373
ID AAM52183 standard; protein; 406 AA.
DE Human FVII mutant V253N.
PN W0200158935-A2.
PD 16-AUG-2001.
PA (MAXY-) MAXYGEN APS.
Query Match 7.1%; Score 278.5; DB 4; Length 406;
Best Local Similarity 22.6%; Pred. No. 2.7e-07;
RESULT 1374
ID AAO30631 standard; protein; 406 AA.
DE Human factor VII variant (K316Q/L305V/V158T/E296V/M298Q/K337A).
PN W02003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 278.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.7e-07;
RESULT 1375
ID AAO30610 standard; protein; 406 AA.
DE Human coagulation factor VII variant (K316Q/L305V/K337A).
PN W02003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 278.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.7e-07;
RESULT 1376
ID AAO30615 standard; protein; 406 AA.
DE Human coagulation factor VII variant (K316Q/L305V/V158T).
PN W02003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 278.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.7e-07;
RESULT 1377
ID AAO30587 standard; protein; 406 AA.
DE Human factor VII variant (S314E/L305V/V158T/E296V/M298Q/K337A).

PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 278.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.7e-07;
RESULT 1378
ID AAO30571 standard; protein; 406 AA.
DE Human coagulation factor VII variant (S314E/L305V/K337A/V158T).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 278.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.7e-07;
RESULT 1379
ID AAO30630 standard; protein; 406 AA.
DE Human factor VII variant (K316Q/L305V/V158D/E296V/M298Q/K337A).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 278.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.7e-07;
RESULT 1380
ID AAO30574 standard; protein; 406 AA.
DE Human coagulation factor VII variant (S314E/L305V/K337A/V158D).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 278.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.7e-07;
RESULT 1381
ID AAO30618 standard; protein; 406 AA.
DE Human coagulation factor VII variant (K316Q/L305V/K337A/V158D).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 278.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.7e-07;
RESULT 1382
ID AAO30586 standard; protein; 406 AA.
DE Human factor VII variant (S314E/L305V/V158D/E296V/M298Q/K337A).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 278.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.7e-07;
RESULT 1383
ID AAO30566 standard; protein; 406 AA.
DE Human coagulation factor VII variant (S314E/L305V/K337A).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 278.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.7e-07;
RESULT 1384
ID ADJ5562 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158D/ L305V/ K316Q/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 278.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.7e-07;
RESULT 1385
ID ADJ55651 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant F374Y/ V158T/ L305V/ S314E/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 278.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.7e-07;
RESULT 1386
ID ADJ55818 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158D/ L305V/ S314E/ K337A.
PN WO2004000366-A1.

PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 278.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.7e-07;
RESULT 1387
ID ADJ56069 standard; protein; 406 AA.
DE Human factor VII mutant F374Y/ V158T/ E296V/ M298Q/ L305V/ S314E/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 278.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.7e-07;
RESULT 1388
ID ADJ55917 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158T/ L305V/ S314E/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 278.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.7e-07;
RESULT 1389
ID ADJ55931 standard; protein; 406 AA.
DE Human factor VII protein mutant V158T/ E296V/ M298Q/ L305V/ S314E/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 278.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.7e-07;
RESULT 1390
ID ADJ55972 standard; protein; 406 AA.
DE Human factor VII protein mutant V158D/ E296V/ M298Q/ L305V/ K316Q/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 278.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.7e-07;
RESULT 1391
ID ADJ56005 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant F374Y/ L305V/ K337A/ S314E.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 278.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.7e-07;
RESULT 1392
ID ADJ56039 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant F374Y/ S314E/ M298Q/ V158DK337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 278.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.7e-07;
RESULT 1393
ID ADJ56041 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant F374Y/ V158D/ L305V/ S314E/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 278.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.7e-07;
RESULT 1394
ID ADJ55928 standard; protein; 406 AA.
DE Human factor VII protein mutant V158D/ E296V/ M298Q/ L305V/ S314E/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 278.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.7e-07;
RESULT 1395
ID ADJ56064 standard; protein; 406 AA.
DE Human factor VII mutant F374Y/ V158D/ E296V/ M298Q/ L305V/ S314E/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.

PA (NOVO) NOVO NORDISK AS.
 Query Match 7.1%; Score 278.5; DB 8; Length 406;
 Best Local Similarity 22.5%; Pred. No. 2.7e-07;
 RESULT 1396
 ID ADJ56074 standard; protein; 406 AA.
 DE Human factor VII polypeptide mutant V253N.
 PN WO2004000366-A1.
 PD 31-DEC-2003.
 PA (NOVO) NOVO NORDISK AS.
 Query Match 7.1%; Score 278.5; DB 8; Length 406;
 Best Local Similarity 22.6%; Pred. No. 2.7e-07;
 RESULT 1397
 ID ADJ55961 standard; protein; 406 AA.
 DE Human factor VII polypeptide mutant V158T/ L305V/ K316Q/ K337A.
 PN WO2004000366-A1.
 PD 31-DEC-2003.
 PA (NOVO) NOVO NORDISK AS.
 Query Match 7.1%; Score 278.5; DB 8; Length 406;
 Best Local Similarity 22.5%; Pred. No. 2.7e-07;
 RESULT 1398
 ID ADJ56017 standard; protein; 406 AA.
 DE Human factor VII polypeptide mutant F374Y/ K337A/ S314E/ M298Q.
 PN WO2004000366-A1.
 PD 31-DEC-2003.
 PA (NOVO) NOVO NORDISK AS.
 Query Match 7.1%; Score 278.5; DB 8; Length 406;
 Best Local Similarity 22.3%; Pred. No. 2.7e-07;
 RESULT 1399
 ID ADJ55954 standard; protein; 406 AA.
 DE Human factor VII polypeptide mutant L305V/ K316Q/ K337A.
 PN WO2004000366-A1.
 PD 31-DEC-2003.
 PA (NOVO) NOVO NORDISK AS.
 Query Match 7.1%; Score 278.5; DB 8; Length 406;
 Best Local Similarity 22.5%; Pred. No. 2.7e-07;
 RESULT 1400
 ID ADJ55910 standard; protein; 406 AA.
 DE Human factor VII polypeptide mutant L305V/ S314E/ K337A.
 PN WO2004000366-A1.
 PD 31-DEC-2003.
 PA (NOVO) NOVO NORDISK AS.
 Query Match 7.1%; Score 278.5; DB 8; Length 406;
 Best Local Similarity 22.5%; Pred. No. 2.7e-07;
 RESULT 1401
 ID ADJ55975 standard; protein; 406 AA.
 DE Human factor VII protein mutant V158T/ E296V/ M298Q/ L305V/ K316Q/ K337A.
 PN WO2004000366-A1.
 PD 31-DEC-2003.
 PA (NOVO) NOVO NORDISK AS.
 Query Match 7.1%; Score 278.5; DB 8; Length 406;
 Best Local Similarity 22.5%; Pred. No. 2.7e-07;
 RESULT 1402
 ID ADJ56050 standard; protein; 406 AA.
 DE Human factor VII polypeptide mutant F374Y/ V158T/ M298Q/ S314E/ K337A.
 PN WO2004000366-A1.
 PD 31-DEC-2003.
 PA (NOVO) NOVO NORDISK AS.
 Query Match 7.1%; Score 278.5; DB 8; Length 406;
 Best Local Similarity 22.3%; Pred. No. 2.7e-07;
 RESULT 1403
 ID ADJ010592 standard; protein; 406 AA.
 DE Human factor VII/VIIa protein mutant #28.
 PN WO2004029091-A2.
 PD 08-APR-2004.
 PA (MAXY-) MAXYGEN APS.
 Query Match 7.1%; Score 278.5; DB 8; Length 406;
 Best Local Similarity 22.6%; Pred. No. 2.7e-07;
 RESULT 1404
 ID ADJ010602 standard; protein; 406 AA.
 DE Human factor VII/VIIa protein mutant #38.
 PN WO2004029091-A2.
 PD 08-APR-2004.

PA (MAXY-) MAXYGEN HOLDINGS LTD.
 Query Match 7.1%; Score 278.5; DB 8; Length 406;
 Best Local Similarity 22.6%; Pred. No. 2.7e-07;
 RESULT 1405
 ID AAP60056 standard; protein; 466 AA.
 DE Factor VII peptide encoded by cDNA clone lambda VII2463.
 PN EP200421-A.
 PD 10-DEC-1986.
 PA (ZYMO) ZYMOGENETICS INC.
 Query Match 7.1%; Score 278.5; DB 1; Length 466;
 Best Local Similarity 22.0%; Pred. No. 3.1e-07;
 RESULT 1406
 ID AAR52562 standard; protein; 466 AA.
 DE Factor VIII.
 PN WO9323074-A1.
 PD 25-NOV-1993.
 PA (OKLA-) OKLAHOMA MED RES FOUND.
 Query Match 7.1%; Score 278.5; DB 2; Length 466;
 Best Local Similarity 22.0%; Pred. No. 3.1e-07;
 RESULT 1407
 ID AAW69606 standard; protein; 466 AA.
 DE Human Factor VIIa.
 PN WO9831394-A2.
 PD 23-JUL-1998.
 PA (TEXA-) UNIV TEXAS SYSTEM.
 Query Match 7.1%; Score 278.5; DB 2; Length 466;
 Best Local Similarity 22.0%; Pred. No. 3.1e-07;
 RESULT 1408
 ID APB36327 standard; protein; 466 AA.
 DE Human factor VII (F7) protein reference sequence.
 PN US2003087244-A1.
 PD 08-MAY-2003.
 PA (VITI-) VITIVITY INC.
 Query Match 7.1%; Score 278.5; DB 7; Length 466;
 Best Local Similarity 22.0%; Pred. No. 3.1e-07;
 RESULT 1409
 ID AAR74682 standard; protein; 521 AA.
 DE t-PA mutein (N117Q, N184Q, delta 296-302, 44-50 replaced by ERHSTVQT) .
 PN CN1082111-A.
 PD 16-FEB-1994.
 PA (BIOE-) BIOENGINEERING INST ACAD MILITARY.
 Query Match 7.1%; Score 278.5; DB 2; Length 521;
 Best Local Similarity 22.9%; Pred. No. 3.4e-07;
 RESULT 1410
 ID AAR09222 standard; protein; 526 AA.
 DE t-PA deletion variant d298.
 PN WO9002798-A.
 PD 22-MAR-1990.
 PA (GETH) GENENTECH INC.
 Query Match 7.1%; Score 278.5; DB 2; Length 526;
 Best Local Similarity 23.3%; Pred. No. 3.5e-07;
 RESULT 1411
 ID AAR09224 standard; protein; 526 AA.
 DE t-PA deletion variant d300.
 PN WO9002798-A.
 PD 22-MAR-1990.
 PA (GETH) GENENTECH INC.
 Query Match 7.1%; Score 278.5; DB 2; Length 526;
 Best Local Similarity 23.3%; Pred. No. 3.5e-07;
 RESULT 1412
 ID AAR09223 standard; protein; 526 AA.
 DE t-PA deletion variant d299.
 PN WO9002798-A.
 PD 22-MAR-1990.
 PA (GETH) GENENTECH INC.
 Query Match 7.1%; Score 278.5; DB 2; Length 526;
 Best Local Similarity 23.3%; Pred. No. 3.5e-07;
 RESULT 1413
 ID AAR09225 standard; protein; 526 AA.
 DE t-PA deletion variant d301.
 PN WO9002798-A.
 PD 22-MAR-1990.

PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 278.5; DB 2; Length 526;
Best Local Similarity 23.1%; Pred. No. 3.5e-07;
RESULT 1414
ID AAR09227 standard; protein: 526 AA.
DE t-PA deletion variant d303.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 278.5; DB 2; Length 526;
Best Local Similarity 23.0%; Pred. No. 3.5e-07;
RESULT 1415
ID AAR12343 standard; protein: 562 AA.
DE t-PA with -ve charged finger and/or kringle domain (2).
PN JP03061483-A.
PD 18-MAR-1991.
PA (FUJI) FUJISAWA PHARM CO LTD.
Query Match 7.1%; Score 278.5; DB 2; Length 562;
Best Local Similarity 21.9%; Pred. No. 3.7e-07;
RESULT 1416
ID AAR12423 standard; protein: 562 AA.
DE T-PA variant having Lys416 substitution (1).
PN JP03061484-A.
PD 18-MAR-1991.
PA (FUJI) FUJISAWA PHARM CO LTD.
Query Match 7.1%; Score 278.5; DB 2; Length 562;
Best Local Similarity 21.9%; Pred. No. 3.7e-07;
RESULT 1417
ID AAR12424 standard; protein: 562 AA.
DE T-PA variant having Lys416 substitution (3).
PN JP03061484-A.
PD 18-MAR-1991.
PA (FUJI) FUJISAWA PHARM CO LTD.
Query Match 7.1%; Score 278.5; DB 2; Length 562;
Best Local Similarity 21.9%; Pred. No. 3.7e-07;
RESULT 1418
ID ADU57511 standard; protein: 701 AA.
DE Human FVII-19G1 Fc domain fusion protein.
PN WO2004006962-A2.
PD 22-JAN-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 278.5; DB 8; Length 701;
Best Local Similarity 22.0%; Pred. No. 4.5e-07;
RESULT 1419
ID ABB71752 standard; protein: 408 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 42048.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (BEKE) BE CORP NY.
Query Match 7.0%; Score 278; DB 4; Length 408;
Best Local Similarity 25.2%; Pred. No. 2.9e-07;
RESULT 1420
ID AAR35762 standard; protein: 448 AA.
DE Factor X (X).
PN WO9309804-A1.
PD 27-MAY-1993.
PA (SCRI) SCRIPPS RES INST.
Query Match 7.0%; Score 278; DB 2; Length 448;
Best Local Similarity 24.0%; Pred. No. 3.2e-07;
RESULT 1421
ID AAR22511 standard; protein: 488 AA.
DE Human Factor Xa1.
PN WO9204378-A.
PD 19-MAR-1992.
PA (CORT-) COR THERAPEUTICS IN.
Query Match 7.0%; Score 278; DB 2; Length 488;
Best Local Similarity 24.0%; Pred. No. 3.4e-07;
RESULT 1422
ID ADO17444 standard; protein: 488 AA.
DE Human bofe tissue sercoma-upregulated protein - SEQ ID 261.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.

Query Match 7.0%; Score 278; DB 8; Length 488;
Best Local Similarity 24.0%; Pred. No. 3.4e-07;
RESULT 1423
ID AAR09232 standard; protein: 523 AA.
DE t-PA deletion variant d297-300.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 278; DB 2; Length 523;
Best Local Similarity 23.2%; Pred. No. 3.7e-07;
RESULT 1424
ID AAR09244 standard; protein: 525 AA.
DE t-PA deletion variant d297, d300.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 278; DB 2; Length 525;
Best Local Similarity 23.2%; Pred. No. 3.7e-07;
RESULT 1425
ID AAR05806 standard; protein: 527 AA.
DE Thrombolytic protein with secondary structure of human tissue plasminogen
DE activator.
PN JP02145184-A.
PD 04-JUN-1990.
PA (YAMA) YAMANOUCHI PHARM CO LTD.
Query Match 7.0%; Score 278; DB 2; Length 527;
Best Local Similarity 22.9%; Pred. No. 3.7e-07;
RESULT 1426
ID AAR22621 standard; protein: 527 AA.
DE Mutated recombinant tPA.
PN JP04094684-A.
PD 26-MAR-1992.
PA (KANF) KANEKA CORP.
Query Match 7.0%; Score 278; DB 2; Length 527;
Best Local Similarity 23.1%; Pred. No. 3.7e-07;
RESULT 1427
ID AAR70896 standard; protein: 527 AA.
DE Human t-PA variant (N103,A339,A342).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 278; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 3.7e-07;
RESULT 1428
ID AAR70858 standard; protein: 527 AA.
DE Human t-PA variant (N67,A296,A297,A298,A299).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 278; DB 2; Length 527;
Best Local Similarity 23.3%; Pred. No. 3.7e-07;
RESULT 1429
ID AAR70897 standard; protein: 527 AA.
DE Human t-PA variant (N103,A347,A348,A349,A351).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 278; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 3.7e-07;
RESULT 1430
ID AAR70856 standard; protein: 527 AA.
DE Human t-PA variant (N67,A267).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 278; DB 2; Length 527;
Best Local Similarity 23.5%; Pred. No. 3.7e-07;
RESULT 1431
ID AAR70873 standard; protein: 527 AA.
DE Human t-PA variant (N67,A477).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.

Query Match 7.0%; Score 278; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 3.7e-07;
RESULT 1432
ID AAF71450 standard; protein; 528 AA.
DE Modified human tissue plasminogen activator.
PN EP238304-A.
PD 23-SEP-1987.
PA (GENTECH) GENENTECH INC.
Query Match 7.0%; Score 278; DB 1; Length 528;
Best Local Similarity 22.9%; Pred. No. 3.7e-07;
RESULT 1433
ID AAR07033 standard; protein; 528 AA.
DE Thrombolytic protein with secondary structure of human tissue plasminogen activator.
PN JP02145184-A.
PD 04-JUN-1990.
PA (YAMA) YAMANOUCHI PHARM CO LTD.
Query Match 7.0%; Score 278; DB 2; Length 528;
Best Local Similarity 22.9%; Pred. No. 3.7e-07;
RESULT 1434
ID AAF70881 standard; protein; 530 AA.
DE Thrombolytic protein 1-12-18 having t-PA activity, deleted or replaced DE R275 is and containing a modified N-linked glycosylation site.
PN W08704722-A.
PD 13-AUG-1987.
PA (GENY) GENETICS INST INC.
PA (LARS) LARSEN G R.
Query Match 7.0%; Score 278; DB 1; Length 530;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1435
ID AAR07034 standard; protein; 531 AA.
DE Thrombolytic protein with secondary structure of human tissue plasminogen activator.
PN JP02145184-A.
PD 04-JUN-1990.
PA (YAMA) YAMANOUCHI PHARM CO LTD.
Query Match 7.0%; Score 278; DB 2; Length 531;
Best Local Similarity 22.9%; Pred. No. 3.7e-07;
RESULT 1436
ID AAR13153 standard; protein; 558 AA.
DE T-PA with -ve charged finger and/or kringle domain (8).
PN JP03061483-A.
PD 18-MAR-1991.
PA (FUJI) FUJISAWA PHARM CO LTD.
Query Match 7.0%; Score 278; DB 2; Length 558;
Best Local Similarity 23.0%; Pred. No. 3.9e-07;
RESULT 1437
ID AAR13151 standard; protein; 559 AA.
DE T-PA with -ve charged finger and/or kringle domain (4).
PN JP03061483-A.
PD 18-MAR-1991.
PA (FUJI) FUJISAWA PHARM CO LTD.
Query Match 7.0%; Score 278; DB 2; Length 559;
Best Local Similarity 23.0%; Pred. No. 3.9e-07;
RESULT 1438
ID AAR13155 standard; protein; 559 AA.
DE T-PA variant having Lys416 substitution (4).
PN JP03061484-A.
PD 18-MAR-1991.
PA (FUJI) FUJISAWA PHARM CO LTD.
Query Match 7.0%; Score 278; DB 2; Length 559;
Best Local Similarity 23.0%; Pred. No. 3.9e-07;
RESULT 1439
ID AAR13154 standard; protein; 559 AA.
DE T-PA variant having Lys416 substitution (2).
PN JP03061484-A.
PD 18-MAR-1991.
PA (FUJI) FUJISAWA PHARM CO LTD.
Query Match 7.0%; Score 278; DB 2; Length 559;
Best Local Similarity 23.0%; Pred. No. 3.9e-07;
RESULT 1440
ID AAF81359 standard; protein; 562 AA.
DE Pre-pro tissue plasminogen activator.
PN EP293934-A.
PD 07-DEC-1988.
PA (ZYMO) ZYMOGENETICS INC.
PA (NOVO) NOVO IND AS.
PA (EISA) EISA CO LTD.
Query Match 7.0%; Score 278; DB 1; Length 562;
Best Local Similarity 23.2%; Pred. No. 3.9e-07;
RESULT 1441
ID AAR07079 standard; protein; 562 AA.
DE Thrombolytic protein with secondary structure of human tissue plasminogen activator.
PN JP02145184-A.
PD 04-JUN-1990.
PA (YAMA) YAMANOUCHI PHARM CO LTD.
Query Match 7.0%; Score 278; DB 2; Length 562;
Best Local Similarity 22.9%; Pred. No. 3.9e-07;
RESULT 1442
ID AAR04702 standard; protein; 562 AA.
DE Sequence of tissue plasminogen activator (t-PA) analogue t-PA C878; K4195 DE with altered residues 87 and 419.
PN EP351246-A.
PD 17-JAN-1990.
PA (NOVO) NOVO-NORDISK AS.
PA (NOVO) NOVO-NORDISK AS.
Query Match 7.0%; Score 278; DB 2; Length 562;
Best Local Similarity 22.7%; Pred. No. 3.9e-07;
RESULT 1443
ID AAR23809 standard; protein; 562 AA.
DE t-PA (Glu 299) mutant.
PN W09206203-A.
PD 16-APR-1992.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match 7.0%; Score 278; DB 2; Length 562;
Best Local Similarity 23.5%; Pred. No. 3.9e-07;
RESULT 1444
ID ADI27177 standard; protein; 1113 AA.
DE Mouse LRP binding family protein #17.
PN W0200310657-A2.
PD 24-DEC-2003.
PA (STOW) STOWERS INST MEDICAL RES.
Query Match 7.0%; Score 278; DB 8; Length 1113;
Best Local Similarity 20.7%; Pred. No. 7.4e-07;
RESULT 1445
ID ADR29372 standard; protein; 1113 AA.
DE Murine Lrp4 dopaminergic neuronal marker SEQ ID NO:3.
PN W0200406559-A1.
PD 05-AUG-2004.
PA (EISA) EISA CO LTD.
Query Match 7.0%; Score 278; DB 8; Length 1113;
Best Local Similarity 20.7%; Pred. No. 7.4e-07;
RESULT 1446
ID AAO30596 standard; protein; 406 AA.
DE Human coagulation factor VII variant (K316H/L305V/K337A/V158D).
PN W02003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 3.1e-07;
RESULT 1447
ID AAO30549 standard; protein; 406 AA.
DE Human coagulation factor VII variant (S314E/K337A).
PN W02003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 6; Length 406;
Best Local Similarity 22.6%; Pred. No. 3.1e-07;
RESULT 1448
ID AAO30561 standard; protein; 406 AA.
DE Human coagulation factor VII variant (K316Q/K337A).
PN W02003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 6; Length 406;
Best Local Similarity 22.6%; Pred. No. 3.1e-07;
RESULT 1449
ID AAO30561 standard; protein; 406 AA.
DE Human coagulation factor VII variant (K316Q/K337A).
PN W02003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 6; Length 406;

Best Local Similarity 22.6%; Pred. No. 3.1e-07;
RESULT 1449
ID AAO30570 standard; protein; 406 AA.
DE Human coagulation factor VII variant (S314E/L305V/V158T).
PN W02003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 3.1e-07;
RESULT 1450
ID AAO30588 standard; protein; 406 AA.
DE Human coagulation factor VII variant (K316H/L305V/K337A).
PN W02003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 3.1e-07;
RESULT 1451
ID AAO30623 standard; protein; 406 AA.
DE Human coagulation factor VII variant (K316Q/L305V/E296V/M298Q).
PN W02003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 3.1e-07;
RESULT 1452
ID AAO30611 standard; protein; 406 AA.
DE Human coagulation factor VII variant (K316Q/L305V/V158D).
PN W02003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 3.1e-07;
RESULT 1453
ID AAO30567 standard; protein; 406 AA.
DE Human coagulation factor VII variant (S314E/L305V/V158D).
PN W02003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 3.1e-07;
RESULT 1454
ID AAO30529 standard; protein; 406 AA.
DE Human coagulation factor VII variant (S314E/K316Q).
PN W02003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 6; Length 406;
Best Local Similarity 22.6%; Pred. No. 3.1e-07;
RESULT 1455
ID AAO30548 standard; protein; 406 AA.
DE Human coagulation factor VII variant (S314E/L305V).
PN W02003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 3.1e-07;
RESULT 1456
ID AAO30564 standard; protein; 406 AA.
DE Human coagulation factor VII variant (K316Q/M298Q).
PN W02003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 6; Length 406;
Best Local Similarity 22.3%; Pred. No. 3.1e-07;
RESULT 1457
ID AAO30609 standard; protein; 406 AA.
DE Human factor VII variant (K316H/L305V/V158T/E296V/M298Q/K337A).
PN W02003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 3.1e-07;

RESULT 1458
ID AAO30579 standard; protein; 406 AA.
DE Human coagulation factor VII variant (S314E/L305V/E296V/M298Q).
PN W02003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 3.1e-07;
RESULT 1459
ID AAO30581 standard; protein; 406 AA.
DE Human coagulation factor VII variant (S314E/L305V/V158T/E296V/M298Q).
PN W02003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 3.1e-07;
RESULT 1460
ID AAO30593 standard; protein; 406 AA.
DE Human coagulation factor VII variant (K316H/L305V/K337A/V158T).
PN W02003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 3.1e-07;
RESULT 1461
ID AAO30624 standard; protein; 406 AA.
DE Human coagulation factor VII variant (K316Q/L305V/V158D/E296V/M298Q).
PN W02003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 3.1e-07;
RESULT 1462
ID AAO30632 standard; protein; 406 AA.
DE Human factor VII variant (L305V/K337A).
PN W02003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 3.1e-07;
RESULT 1463
ID AAO30552 standard; protein; 406 AA.
DE Human coagulation factor VII variant (S314E/M298Q).
PN W02003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 6; Length 406;
Best Local Similarity 22.3%; Pred. No. 3.1e-07;
RESULT 1464
ID AAO30580 standard; protein; 406 AA.
DE Human coagulation factor VII variant (S314E/L305V/V158T/E296V/M298Q).
PN W02003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 3.1e-07;
RESULT 1465
ID AAO30614 standard; protein; 406 AA.
DE Human coagulation factor VII variant (K316Q/L305V/V158T).
PN W02003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 3.1e-07;
RESULT 1466
ID AAO30608 standard; protein; 406 AA.
DE Human factor VII variant (K316H/L305V/V158D/E296V/M298Q/K337A).
PN W02003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 3.1e-07;
RESULT 1467

ID AA030625 standard; protein; 406 AA.
DE Human coagulation factor VII variant (K316Q/L305V/V158T/E296V/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 3.1e-07;
RESULT 1468
ID AA030560 standard; protein; 406 AA.
DE Human coagulation factor VII variant (K316Q/L305V).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 3.1e-07;
RESULT 1469
ID ADJ55906 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant L305V/ K316Q.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 3.1e-07;
RESULT 1470
ID ADJ55601 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant F374Y/ M298Q/ S314E.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 8; Length 406;
Best Local Similarity 22.3%; Pred. No. 3.1e-07;
RESULT 1471
ID ADJ56022 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant F374Y/ K337A/ M298Q/ V158D.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 8; Length 406;
Best Local Similarity 22.3%; Pred. No. 3.1e-07;
RESULT 1472
ID ADJ56024 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant F374Y/ K337A/ M298Q/ V158T.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 8; Length 406;
Best Local Similarity 22.3%; Pred. No. 3.1e-07;
RESULT 1473
ID ADJ55878 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158D/ L305V/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 8; Length 406;
Best Local Similarity 22.3%; Pred. No. 3.1e-07;
RESULT 1474
ID ADJ55983 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant F374Y/ L305V/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 3.1e-07;
RESULT 1475
ID ADJ56019 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant F374Y/ K337A/ S314E/ V158T.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 8; Length 406;
Best Local Similarity 22.6%; Pred. No. 3.1e-07;
RESULT 1476
ID ADJ56037 standard; protein; 406 AA.

DE Human factor VII polypeptide mutant F374Y/ S314E/ E296V/ M298Q/ L305V.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 3.1e-07;
RESULT 1477
ID ADJ55909 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant K316Q/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 8; Length 406;
Best Local Similarity 22.6%; Pred. No. 3.1e-07;
RESULT 1478
ID ADJ55953 standard; protein; 406 AA.
DE Human factor VII protein mutant V158T/ E296V/ M298Q/ L305V/ K316H/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 3.1e-07;
RESULT 1479
ID ADJ55955 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158D/ L305V/ K316Q.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 3.1e-07;
RESULT 1480
ID ADJ55893 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant S314E/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 8; Length 406;
Best Local Similarity 22.6%; Pred. No. 3.1e-07;
RESULT 1481
ID ADJ55932 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant L305V/ K316H/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 3.1e-07;
RESULT 1482
ID ADJ55897 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant M298Q/ S314E.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 8; Length 406;
Best Local Similarity 22.3%; Pred. No. 3.1e-07;
RESULT 1483
ID ADJ55956 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158T/ L305V/ K316Q.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 3.1e-07;
RESULT 1484
ID ADJ56036 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant F374Y/ E296V/ M298Q/ L305V/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 3.1e-07;
RESULT 1485
ID ADJ55875 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158T/ L305V/ K337A.

PN W02004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 3.1e-07;
RESULT 1486
ID ADJ55912 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158T/ L305V/ S314E.
PN W02004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 3.1e-07;
RESULT 1487
ID ADJ55940 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158D/ L305V/ K316H/ K337A.
PN W02004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 3.1e-07;
RESULT 1488
ID ADJ56029 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant F374Y/ S314E/ M298QV158T.
PN W02004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 8; Length 406;
Best Local Similarity 22.3%; Pred. No. 3.1e-07;
RESULT 1489
ID ADJ55609 standard; protein; 406 AA.
DE Human factor VII protein mutant F374Y/ V158D/ E296V/ M298Q/ S314E/ K337A.
PN W02004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 8; Length 406;
Best Local Similarity 22.1%; Pred. No. 3.1e-07;
RESULT 1490
ID ADJ55891 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant S314E/ K316Q.
PN W02004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 8; Length 406;
Best Local Similarity 22.6%; Pred. No. 3.1e-07;
RESULT 1491
ID ADJ55923 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant E296V/ M298Q/ L305V/ S314E.
PN W02004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 3.1e-07;
RESULT 1492
ID ADJ55925 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158T/ E296V/ M298Q/ L305V/ S314E.
PN W02004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 3.1e-07;
RESULT 1493
ID ADJ55939 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158T/ L305V/ K316H/ K337A.
PN W02004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 3.1e-07;
RESULT 1494
ID ADJ55968 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158D/ E296V/ M298Q/ L305V/ K316Q.
PN W02004000366-A1.

PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 3.1e-07;
RESULT 1495
ID ADJ55969 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158T/ E296V/ M298Q/ L305V/ K316Q.
PN W02004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 3.1e-07;
RESULT 1496
ID ADJ56010 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant F374Y/ L305V/ V158D/ S314E.
PN W02004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 3.1e-07;
RESULT 1497
ID ADJ56026 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant F374Y/ S314E/ M298Q/ V158D.
PN W02004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 8; Length 406;
Best Local Similarity 22.3%; Pred. No. 3.1e-07;
RESULT 1498
ID ADJ55861 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant L305V/ K337A.
PN W02004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 3.1e-07;
RESULT 1499
ID ADJ55950 standard; protein; 406 AA.
DE Human factor VII protein mutant V158D/ E296V/ M298Q/ L305V/ K316H/ K337A.
PN W02004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 3.1e-07;
RESULT 1500
ID ADJ56020 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant F374Y/ K337A/ S314E/ V158D.
PN W02004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.0%; Score 277.5; DB 8; Length 406;
Best Local Similarity 22.6%; Pred. No. 3.1e-07;

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OM protein - protein search, using sw model

Run on: July 12, 2005, 17:08:11 ; Search time 43 Seconds
(without alignments)
1611.071 Million cell updates/sec

Title: US-10-063-546-38

Perfect score: 3945
Sequence: 1 MEIGCWTLQGLTFLLQULLIS.....LSTAFKVLPRFKDWIRNNK 720

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :
1: p1r1:.*
2: p1r2:.*
3: p1r3:.*
4: p1r4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	949	24.1	181	2	T08805	hypothetical prote
2	672	17.0	1039	2	A38783	coagulation factor
3	482	12.2	699	1	I54763	Ra-reactive factor
4	403.5	10.2	705	1	C1HURB	complement subcomp
5	400.5	10.2	686	1	A59271	Ra-reactive factor
6	378.5	9.6	695	1	S05008	complement subcomp
7	354	9.0	1524	2	T30337	polyprotein - Afri
8	340.5	8.6	694	2	JC6554	complement subcomp
9	334	8.5	688	1	C1HUS	complement subcomp
10	331.5	8.4	1019	1	A56318	enteropeptidase (E
11	330.5	8.4	1034	1	A53663	enteropeptidase (E
12	320	8.1	461	1	JX0210	protein C (activat
13	317.5	8.0	1035	1	A43090	enteropeptidase (E
14	314.5	8.0	475	1	EXCH	coagulation factor
15	313	7.9	855	2	JC7731	membrane-bound arg
16	310.5	7.9	461	1	KCHU	protein C (activat
17	299.5	7.6	443	2	I46932	coagulation factor
18	293.5	7.4	407	1	KFB07	coagulation factor
19	292	7.4	461	1	A18994	protein C (activat
20	285.5	7.2	452	1	A30351	coagulation factor
21	283.5	7.2	482	1	EXRT	coagulation factor
22	282	7.1	456	1	KXBO	protein C (activat
23	281.5	7.1	558	2	JCS878	plasma hyaluronan-
24	281	7.1	492	2	EXBO	coagulation factor
25	280.5	7.1	264	2	I38136	chymotrypsin-like
26	280	7.1	562	1	UKHUT	t-plasminogen acti
27	278.5	7.1	466	1	KFHU7	coagulation factor
28	278	7.0	488	1	EXHU	coagulation factor
29	278	7.0	1113	2	JE0315	low-density lipopr

30	277	7.0	559	1	A29941	t-plasminogen acti
31	277	7.0	559	1	A35029	t-plasminogen acti
32	276.5	7.0	559	1	A46888	hepatocyte growth
33	274.5	7.0	625	1	TBBO	thrombin (EC 3.4.2
34	273	6.9	560	1	JC4795	plasma hyaluronan-
35	270	6.8	477	2	JS0597	t-plasminogen acti
36	264.5	6.7	431	2	JS0599	t-plasminogen acti
37	264.5	6.7	431	2	A35827	thrombin (EC 3.4.2
38	262.5	6.7	461	1	KFHU	coagulation factor
39	262	6.6	477	2	JS0598	t-plasminogen acti
40	261.5	6.6	442	1	UKPG	u-plasminogen acti
41	261	6.6	431	1	UKHU	u-plasminogen acti
42	261	6.6	433	1	UN0560	u-plasminogen acti
43	260	6.6	477	1	A34369	t-plasminogen acti
44	259	6.6	244	2	S72219	chymotrypsin B - A
45	259	6.6	416	1	KFB0	coagulation factor
46	258.5	6.6	786	1	A47547	serine proteinase
47	258	6.5	251	2	PC1235	29K serine protein
48	258	6.5	433	1	UKBAY	u-plasminogen acti
49	257.5	6.5	1004	2	T30338	oviductin (EC 3.4.
50	255.5	6.5	763	2	I50807	complement factor
51	254	6.4	617	2	S10511	thrombin (EC 3.4.2
52	253	6.4	1070	2	T31069	colloid-BMP-1 like
53	249.5	6.3	400	1	A48050	coagulation factor
54	249.5	6.3	986	1	B58788	procollagen C-endo
55	248.5	6.3	459	2	JQ0419	coagulation factor
56	248	6.3	263	2	A31299	chymotrypsin (EC 3
57	248	6.3	638	1	KOHNP	plasma kallikrein
58	247.5	6.3	991	2	I49540	procollagen C-endo
59	247	6.3	275	2	A32410	trypsin (EC 3.4.2
60	247	6.3	764	1	BBHU	complement factor
61	246.5	6.2	347	2	G00006	haptoglobin - blac
62	246.5	6.2	622	1	TBHU	thrombin (EC 3.4.2
63	246	6.2	236	2	C42696	thrombin (EC 3.4.2
64	246	6.2	812	1	PLBO	plasma (EC 3.4.21
65	245	6.2	234	2	F42896	thrombin (EC 3.4.2
66	244	6.2	638	1	KOMSP	plasma kallikrein
67	242.5	6.1	730	1	BMHU1	procollagen C-endo
68	241.5	6.1	823	1	A58788	procollagen C-endo
69	240	6.1	406	2	S49489	trypsin (EC 3.4.21
70	239.5	6.1	242	2	HPHU2	haptoglobin precu
71	239	6.1	245	1	KYBOA	chymotrypsin (EC 3
72	238	6.0	237	1	TRCY1	trypsin (EC 3.4.21
73	238	6.0	263	2	A21195	chymotrypsin (EC 3
74	238	6.0	347	1	HPHU1	haptoglobin precu
75	238	6.0	375	1	A23689	limulus clotting e
76	237.5	6.0	810	2	I46260	plasma (EC 3.4.21
77	237	6.0	263	1	KYRTB	chymotrypsin (EC 3
78	236.5	6.0	274	2	JC4171	trypsin (EC 3.4.2
79	236.5	6.0	707	2	JC2218	procollagen C-endo
80	235	6.0	270	2	S56160	mast cell trypsin
81	235	6.0	345	2	I36941	haptoglobin precu
82	235	6.0	1420	2	A32869	apolipoprotein(a)
83	233.5	5.9	263	2	S47537	chymotrypsin (EC 3
84	232	5.9	416	1	S33777	hepsin (EC 3.4.21
85	232	5.9	638	1	KORPPL	plasma kallikrein
86	229.5	5.8	329	1	HPDG	haptoglobin precu
87	228.5	5.8	225	2	E42696	thrombin (EC 3.4.2
88	228.5	5.8	347	1	HPMS	haptoglobin precu
89	228.5	5.8	861	2	A48825	Notch homolog Motc
90	228.5	5.8	2531	2	A46019	notch-1 protein -
91	228	5.8	812	1	PLMS	plasma (EC 3.4.21
92	227.5	5.8	242	2	S11775	trypsin (EC 3.4.21
93	227.5	5.8	349	2	I36944	haptoglobin - chim
94	227	5.8	242	2	S31776	trypsin (EC 3.4.21
95	227	5.8	1464	2	S58984	development protei
96	226.5	5.7	238	2	S31779	trypsin (EC 3.4.21
97	226.5	5.7	761	2	JC5759	brain-specific ser
98	226	5.7	394	2	JS0600	t-plasminogen acti
99	226	5.7	625	1	KFHU1	coagulation factor
100	225	5.7	615	1	KFHU12	coagulation factor
101	224.5	5.7	271	1	ELRT2-	pancreatic elasta
102	224	5.7	245	1	KYBOB	chymotrypsin (EC 3

103	223.5	5.7	274	2	S35339	trypsin (EC 3.4.21	176	199.5	5.1	2555	2	A40043	notch protein homo
104	223.5	5.7	348	1	HPHUR	haptogloblin-relate	177	198.5	5.0	229	1	TRBOTR	trypsin (EC 3.4.21
105	222.5	5.6	417	1	S00845	hepsin (EC 3.4.21.	178	198.5	5.0	222	1	KQBP	tissue kallikrein
106	222.5	5.6	434	1	A35005	u-plasminogen acti	179	198.5	5.0	237	2	S55378	serine proteinase
107	222.5	5.6	790	1	PLPG	plasmin (EC 3.4.21	180	198	5.0	259	2	S68424	allergen Der f III
108	222	5.6	269	2	A26823	pancreatic elastas	181	198	5.0	270	2	B29934	pancreatic elastas
109	222	5.6	275	2	B35863	trypsin (EC 3.4.2	182	198	5.0	760	2	C2MS	classical-comple
110	221.5	5.6	2531	2	B31868	notch protein homo	183	197.5	5.0	250	1	T01779	trypsin (EC 3.4.21
111	221	5.6	231	2	S31778	trypsin (EC 3.4.21	184	197.5	5.0	258	2	I36947	haptogloblin Hpp -
112	220.5	5.6	274	2	A45754	trypsin (EC 3.4.2	185	196.5	5.0	269	2	C26623	pancreatic elastas
113	220.5	5.6	1057	1	A39288	dorsal-ventral pat	186	196.5	5.0	570	2	A48836	fibropellin C prec
114	220	5.6	275	2	A35863	trypsin (EC 3.4.2	187	196.5	5.0	767	2	T30018	hypothetical prote
115	219.5	5.6	235	2	H42666	trypsin (EC 3.4.2	188	196.5	5.0	2524	2	A35844	Notch protein - Af
116	219.5	5.6	271	2	A25528	pancreatic elastas	189	196	5.0	3623	2	T08618	intrinsic factor-B
117	219.5	5.6	761	1	BBMS	complement factor	190	195.5	5.0	271	2	I46580	factor IX - pig (f
118	219	5.6	343	1	A57018	prostatein (EC 3.4.	191	195	4.9	432	1	S18932	trypsin (EC 3.4.21
119	218	5.5	271	1	S41308	serine proteinase (192	194.5	4.9	246	1	TRRT1	tissue kallikrein
120	217.5	5.5	243	2	A56338	venom proteinase (193	194	4.9	261	2	A25606	tissue kallikrein
121	217	5.5	239	2	A27207	tissue kallikrein	194	194	4.9	267	2	S40006	trypsin (EC 3.4.21
122	217	5.5	268	2	S68825	pancreatic elastas	195	193.5	4.9	249	2	A55634	granzyme M (EC 3.4
123	217	5.5	273	2	A47246	trypsin (EC 3.4.2	196	193.5	4.9	347	1	HPRT	haptogloblin precu
124	217	5.5	603	2	S28941	coagulation factor	197	193.5	4.9	2471	2	A49128	cell-fate determin
125	217	5.5	2703	1	A24430	notch protein - fr	198	193	4.9	240	1	CPBOA3	procaboxypeptidas
126	216.5	5.5	236	2	I42696	thrombin (EC 3.4.2	199	193	4.9	246	1	DBHT	complement factor
127	216.5	5.5	346	2	I36942	haptogloblin - chlm	200	191.5	4.9	247	1	A25852	trypsin (EC 3.4.21
128	216.5	5.5	2616	2	A57096	mdel protein prec	201	191.5	4.9	281	2	T13596	trypsin homolog -
129	216	5.5	810	1	PLHU	plasmin (EC 3.4.21	202	191.5	4.9	830	2	A30359	P-selectin precurs
130	215.5	5.5	247	1	TRDG	trypsin (EC 3.4.21	203	190.5	4.8	579	2	UC7629	membrane-type fritz
131	215.5	5.5	248	1	S55066	trypsin (EC 3.4.21	204	190.5	4.8	768	2	A42755	P-selectin precurs
132	215	5.4	241	2	S39048	trypsin (EC 3.4.21	205	190.5	4.8	1064	2	A40136	fibropellin Ia - 8
133	215	5.4	268	2	S68826	pancreatic elastas	206	189.5	4.8	266	2	S54146	trypsin (EC 3.4.21
134	214.5	5.4	247	2	S13813	trypsin (EC 3.4.21	207	189.5	4.8	1737	2	T00209	MEGF8 protein - hu
135	214.5	5.4	366	2	JB0105	teuticular serine	208	189	4.8	246	2	UQ1472	trypsin (EC 3.4.21
136	214.5	5.4	593	2	S45281	coagulation factor	209	189	4.8	247	2	S05494	trypsin (EC 3.4.21
137	214	5.4	275	2	C35863	trypsin (EC 3.4.2	210	189	4.8	253	2	A53968	serine proteinase
138	213.5	5.4	235	2	D12696	thrombin (EC 3.4.2	211	189	4.8	258	4	S70439	pancreatic elastas
139	213.5	5.4	2352	2	T30201	Notch homolog prot	212	189	4.8	267	4	A56615	probable pancreati
140	212	5.4	260	2	I56559	neutropain - mouse	213	189	4.8	646	2	UN0473	P-selectin precurs
141	212	5.4	455	2	A61545	plasmin (EC 3.4.21	214	188.5	4.8	282	2	I84621	coagulation factor
142	211	5.3	237	2	S68702	trypsin (EC 3.4.2	215	188	4.8	263	2	S15686	tissue kallikrein
143	211	5.3	276	2	A38654	mat cell proteina	216	187.5	4.8	250	2	S55493	serine proteinase
144	210.5	5.3	1220	2	A56136	jagged protein pre	217	187.5	4.8	259	2	I38363	trypsin (EC 3.4.21
145	210	5.3	2437	1	S42612	transmembrane prot	218	187.5	4.8	304	2	S33496	trypsin (EC 3.4.21
146	209	5.3	433	1	UKMS	u-plasminogen acti	219	187	4.7	246	2	UQ1471	trypsin (EC 3.4.21
147	208.5	5.3	258	2	I36945	thrombin (EC 3.4.2	220	187	4.7	261	2	S45303	tissue kallikrein
148	207.5	5.3	239	2	G42696	haptogloblin Hp - c	221	187	4.7	271	2	S29239	chymotrypsin (EC 3
149	207.5	5.3	269	2	B26823	pancreatic elastas	222	186	4.7	1594	2	T30549	hensin - rabbit
150	207	5.2	238	1	TRW5T	trypsin-like prote	223	185.5	4.7	927	1	U00948	macrophage-actinula
151	206.5	5.2	246	1	TRRT2	trypsin (EC 3.4.21	224	185.5	4.7	256	1	NGMSA	AS antigen precurs
152	206.5	5.2	256	2	T10109	trypsin (EC 3.4.21	225	185	4.7	272	2	S45303	7S nerve growth fa
153	206	5.2	430	1	A24702	serine proteinase	226	183.5	4.7	1372	2	T25933	hypothetical prote
154	206	5.2	4548	1	S00657	apoptein(a) (EC	227	183	4.6	392	1	KORTP	tissue kallikrein
155	205.5	5.2	269	2	B32410	matocytoma protei	228	183	4.6	482	2	JCS092	serine proteinase
156	205.5	5.2	460	2	B61545	plasmin (EC 3.4.21	229	182.5	4.6	722	2	JCS092	E-selectin - pig
157	204.5	5.2	367	1	JE0104	teuticular serine	230	182.5	4.6	2531	2	I48324	notch homolog - se
158	204.5	5.2	752	1	C2HU	complement C2 prec	231	182.5	4.6	261	1	TRMSM5	tissue kallikrein
159	204.5	5.2	1203	1	A49175	Morch B protein -	232	182	4.6	247	1	PRMSCL	granzyme B (EC 3.4
160	203.5	5.2	247	1	B25852	trypsin (EC 3.4.21	233	181.5	4.6	247	2	S12764	trypsin (EC 3.4.21
161	203.5	5.2	263	1	I55608	complement factor	234	181.5	4.6	256	2	A45161	serine proteinase
162	203.5	5.2	285	2	I48144	coagulation factor	235	181.5	4.6	437	2	S18407	acrosin (EC 3.4.21
163	203.5	5.2	309	2	B49878	intrinsic factor-B	236	181.5	4.6	261	1	NGMSG	7S nerve growth fa
164	203.5	5.2	3623	2	T09456	probable trypsin V	237	181	4.6	418	2	A37344	acrosin (EC 3.4.21
165	203	5.1	403	2	C82228	trypsin (EC 3.4.21	238	181	4.6	424	2	S37344	hypothetical prote
166	202	5.1	240	2	S39047	trypsin (EC 3.4.21	239	181	4.6	1291	2	T21694	trypsin (EC 3.4.21
167	202	5.1	2321	2	S78549	notch3 protein - h	240	180.5	4.6	248	2	S55067	factor IX - rabbit
168	201.5	5.1	246	2	B25528	trypsin (EC 3.4.21	241	180.5	4.6	275	2	I46712	acrosin (EC 3.4.21
169	200.5	5.1	226	1	KCPU	brechhyurin (EC 3.4	242	180.5	4.6	436	2	UX0172	trypsin-like prote
170	200.5	5.1	231	1	TRPGTR	trypsin (EC 3.4.21	243	180	4.6	254	2	S49329	tissue kallikrein
171	200.5	5.1	810	2	B30848	plasmin (EC 3.4.21	244	180	4.6	261	2	S01971	trypsin (EC 3.4.21
172	199.5	5.1	247	2	A27547	trypsin (EC 3.4.21	245	180	4.6	275	2	S40005	trypsin (EC 3.4.21
173	199.5	5.1	257	2	S33772	tissue kallikrein	246	179.5	4.6	243	1	A35871	trypsin (EC 3.4.21
174	199.5	5.1	258	2	G02959	haptogloblin - rhes	247	179.5	4.6	259	2	WMMS28	complement factor
175	199.5	5.1	275	2	S40007	trypsin (EC 3.4.21	248	179.5	4.6	274	2	I47078	coagulation factor

249	179.5	4.6	728	2	150719	C-Delta-1 - chick	322	161.5	4.1	250	2	S31384	trypsin (EC 3.4.21
250	179.5	4.6	1047	2	A55617	maequeride precurs	323	161.5	4.1	261	2	S40162	cathepsin G (EC 3.
251	179	4.5	266	1	ELPG	pancreatic elastase	324	161.5	4.1	265	2	T115451	hypothetical prote
252	179	4.5	612	2	B42755	E-selectin precurs	325	161.5	4.1	832	2	A31246	neurogenic protein
253	178.5	4.5	402	2	JH0403	procollagen I C-pr	326	161.5	4.1	880	2	S00670	neurogenic repetit
254	177.5	4.5	248	2	A43520	natural killer cel	327	161.5	4.1	1025	1	A43526	complement C3d/Eps
255	177.5	4.5	420	2	A55283	acrosin (EC 3.4.21	328	161	4.1	187	2	T34288	hypothetical prote
256	177.5	4.5	1964	2	T09059	notch4 - mouse	329	160.5	4.1	661	1	KFH013	coagulation factor
257	177	4.5	268	2	JQ1473	pancreatic elastase	330	160	4.1	262	1	A31372	granzyme A (EC 3.4
258	177	4.5	473	2	A56175	adhesive plaque pr	331	160	4.1	3002	2	A47221	fibrillin 1 precu
259	177	4.5	747	2	IS1579	complement factor	332	159.5	4.0	1722	2	E89753	protein P11C7.4 (l
260	176.5	4.5	1091	1	PL0009	complement C3d/Eps	333	159	4.0	244	2	A44284	tissue kallikrein
261	176	4.5	261	2	A29745	tissue kallikrein	334	159	4.0	261	2	A48062	gamma-tenin (EC 3.
262	176	4.5	261	2	A31136	tissue kallikrein	335	159	4.0	2907	2	A57278	fibrillin-2 precu
263	176	4.5	264	2	S32794	trypsin-like prote	336	158.5	4.0	247	2	S59135	mast cell proteina
264	176	4.5	2318	2	S45306	notch 3 protein -	337	158.5	4.0	385	2	S53718	homeotic protein d
265	175.5	4.4	274	2	S40004	trypsin-related pr	338	158.5	4.0	833	2	S19087	gene Delta protein
266	175	4.4	270	2	A29934	pancreatic elastase	339	158	4.0	610	2	T16761	hypothetical prote
267	175	4.4	421	1	S11674	acrosin (EC 3.4.21	340	158	4.0	2918	2	A54105	fibrillin-2 precu
268	174.5	4.4	232	2	S32398	serine proteinase	341	157.5	4.0	579	2	A56740	apern-egg recognit
269	174.5	4.4	246	1	TRDGC	trypsin (EC 3.4.21	342	157.5	4.0	907	2	T27317	hypothetical prote
270	174	4.4	259	2	A29746	tissue kallikrein	343	157	4.0	261	2	JE0236	tissue kallikrein
271	174	4.4	261	1	KQMS1	tissue kallikrein	344	157	4.0	610	2	A35046	E-selectin precurs
272	174	4.4	1295	2	A32901	gip1 protein precu	345	156.5	4.0	232	2	A36172	procytotoxic T-lym
273	173.5	4.4	548	2	D82175	probable trypsin V	346	156.5	4.0	275	2	UC6506	tumor necrosis fac
274	173	4.4	229	1	TRDFS	trypsin (EC 3.4.21	347	156.5	4.0	1429	2	S06434	homeotic protein 1
275	173	4.4	768	2	IS3821	P-selectin - rat	348	156.5	4.0	3635	2	T110053	laminin alpha 5 ch
276	172.5	4.4	248	1	PRM5C2	granzyme C (EC 3.4	349	156	4.0	259	1	KQRTTN	tonin (EC 3.4.21.-
277	172.5	4.4	277	2	S35340	trypsin (EC 3.4.21	350	156	4.0	261	2	A29586	tissue kallikrein
278	172.5	4.4	431	2	S47538	acrosin (EC 3.4.21	351	156	4.0	702	2	T16832	hypothetical prote
279	172.5	4.4	449	2	A55362	procollagen I C-pr	352	155.5	3.9	213	2	S17537	fibrinolytic prote
280	172	4.4	254	2	S65465	trypsin-like prote	353	155.5	3.9	485	2	S36772	E-selectin - bovin
281	172	4.4	261	2	A24378	tissue kallikrein	354	155.5	3.9	533	2	UC7985	brain-specific CUB
282	172	4.4	435	1	A34170	acrosin (EC 3.4.21	355	155	3.9	250	2	S15685	kallikrein, glandu
283	171.5	4.3	230	2	A27802	hyaluronin C (EC 3	356	155	3.9	2489	2	I73012	complement C3b/C4b
284	171.5	4.3	262	1	KQHU	tissue kallikrein	357	154.5	3.9	252	2	A34877	Cab-binding protei
285	171.5	4.3	2403	2	A59386	saako - human	358	154	3.9	699	2	S65551	Factor H - bovine
286	171	4.3	257	2	B45061	granzyme A (EC 3.4	359	153.5	3.9	251	2	JC2125	chymase (EC 3.4.21
287	171	4.3	260	2	A45061	granzyme A (EC 3.4	360	153.5	3.9	387	2	B49125	Motch A protein -
288	171	4.3	266	1	ELRT1	pancreatic elastase	361	153.5	3.9	551	2	I46709	endothelial leukoc
289	171	4.3	273	2	S40003	trypsin-related pr	362	153.5	3.9	1786	1	MMMSB1	laminin beta-1 cha
290	171	4.3	2139	2	A35672	crumbs protein - f	363	153	3.9	152	2	A53274	complement factor
291	170	4.3	248	2	S33756	granzyme-like prote	364	153	3.9	254	1	TRWV3Y	trypsin-like prote
292	170	4.3	266	2	JC4850	trypsin-like prote	365	153	3.9	2871	2	A55567	fibrillin 1 - bovi
293	169.5	4.3	251	2	T10262	mast cell serine p	366	152.5	3.9	248	1	S01007	granzyme F (EC 3.4
294	169.5	4.3	261	1	S35711	semenogelase (EC 3	367	152.5	3.9	264	2	S65563	granzyme 3 (EC 3.4
295	169.5	4.3	421	2	S29599	acrosin (EC 3.4.21	368	152.5	3.9	385	2	A54785	preadipocyte facto
296	169.5	4.3	560	2	T16833	hypothetical prote	369	152.5	3.9	422	1	KXHU2	plasma protein Z p
297	169	4.3	214	2	S17680	fibrinolytic prote	370	152	3.9	281	3	A61021	granzyme B (EC 3.4
298	169	4.3	246	2	S64707	chymase (EC 3.4.21	371	151.5	3.9	686	2	JC7569	Delta-4 protein -
299	169	4.3	259	2	B31136	tissue kallikrein	372	151.5	3.8	716	1	A40332	cisue kallikrein
300	169	4.3	504	2	S56745	mucin (clone pGM31	373	151.5	3.8	716	1	A40332	macrophage-stimula
301	168.5	4.3	597	2	S37355	granzyme-like prote	374	151.5	3.8	977	2	A52657	seizure-related pr
302	168	4.3	248	2	S71352	metalloproteinase	375	151	3.8	249	1	A35842	chymase (EC 3.4.21
303	168	4.3	2014	1	I36936	complement recepto	376	151	3.8	1620	2	T27283	tissue kallikrein
304	167.5	4.2	261	1	A32297	semenogelase (EC 3	377	151	3.8	1620	2	T27283	hypothetical prote
305	167.5	4.2	383	2	S53716	delta-like homeoti	378	150.5	3.8	248	2	S43259	granzyme-like prote
306	167	4.2	247	2	S45113	granzyme-like prote	379	150.5	3.8	277	2	A41735	hyaluronate-bindin
307	167	4.2	260	2	A37938	tissue kallikrein	380	150.5	3.8	285	2	T35195	prolabe serine pr
308	166	4.2	265	2	T10495	chymotrypsin (EC 3	381	150.5	3.8	685	2	JC7570	Delta-4 protein -
309	165	4.2	2043	2	T18524	scavenger receptor	382	150.5	3.8	1053	2	S46199	complement
310	164.5	4.2	449	1	NBHUS	complement factor	383	150	3.8	263	1	MMVZSP	apolipoprotein H h
311	164.5	4.2	1231	1	NBHUS	complement factor	384	150	3.8	267	1	ELHTL	leukocyte elastase
312	164	4.2	230	2	I48685	mast cell proteina	385	150	3.8	601	2	B36346	fibrulin 1 precu
313	164	4.2	613	2	S15468	complement C3b/C4b	386	150	3.8	770	2	T00203	LDL receptor-relat
314	164	4.2	2871	2	A55624	fibrillin-1 precu	387	150	3.8	3712	2	S18253	laminin alpha-1 ch
315	163	4.1	868	2	T20239	hypothetical prote	388	149.5	3.8	236	1	A32121	snake venom factor
316	162.5	4.1	276	2	A47290	TSG-6 homolog PS4	389	149.5	3.8	259	1	TRSMG	trypsin (EC 3.4.21
317	162.5	4.1	1290	2	A57190	ebnetin precursor	390	149.5	3.8	13288	2	T03099	mucin, submaxillar
318	162.5	4.1	2083	2	T42721	CRP-ductin-alpha p	391	149	3.8	216	1	KTVH20	chymotrypsin (EC 3
319	162	4.1	261	1	EGMSB	tissue kallikrein	392	149	3.8	683	2	C36346	fibrulin 1 precu
320	161.5	4.1	226	2	S69370	duodenase - bovine	393	149	3.8	770	2	T00204	LDL receptor relat
321	161.5	4.1	248	2	S01006	cytotoxic T-lympho	394	149	3.8	1408	2	S16148	gene serrate prote

395	148	3.8	218	1	KTVH2C	chymotrypsin (EC 3	468	134	3.4	3034	2	T14119	seven-pass transme
396	148	3.8	668	2	A46013	coagulation factor	469	133.5	3.4	154	2	S35207	protease 7 - buf
397	148	3.8	1469	2	B36655	slit protein 2 pre	470	133.5	3.4	1687	2	T30176	EGF repeat transme
398	148	3.8	1480	2	A36655	slit protein 1 pre	471	133.5	3.4	3507	2	T34513	hypothetical prote
399	147.5	3.7	244	2	A46721	chymase (EC 3.4.21	472	133	3.4	810	2	T10756	Nel-homolog protei
400	147.5	3.7	244	2	A34910	mast cell proteina	473	132.5	3.4	331	2	T27906	hypothetical prote
401	147.5	3.7	597	1	S53711	CABP alpha chain p	474	132	3.3	246	2	A36678	mast cell proteina
402	147.5	3.7	1786	1	MMHUB1	laminin beta-1 cha	475	132	3.3	372	2	UCS377	L-selectin precurs
403	147.5	3.7	4391	2	A38096	perlecan precursor	476	132	3.3	558	2	S57953	CABP protein alpha
404	147	3.7	236	2	A28566	T-cell suppressor	477	132	3.3	2109	1	150421	aggreccan precursor
405	147	3.7	259	2	D33863	tiasee kallikrein	478	132	3.3	3871	2	T22812	hypothetical prote
406	147	3.7	262	1	UC4803	venomobin A (EC 3.4	479	131.5	3.3	302	1	MMBS1E	secretory compleme
407	147	3.7	716	1	UCS061	macrophage-stimula	480	131.5	3.3	1268	2	S52781	neurocan - mouse
408	147	3.7	1557	2	T28811	hypothetical prote	481	130.5	3.3	1257	2	S28764	neurocan precursor
409	147	3.7	3084	1	MMMSA	laminin alpha-1 ch	482	130.5	3.3	3672	2	T23433	hypothetical prote
410	146.5	3.7	236	1	B32121	snake venom factor	483	130.5	3.3	3704	2	T37316	probable laminin a
411	146.5	3.7	3707	2	S18252	heparan sulfate pr	484	129.5	3.3	233	1	UG0169	venomobin A (EC 3.4
412	146	3.7	263	2	T28450	hypothetical prote	485	129.5	3.3	376	2	UC4892	L-selectin precurs
413	145	3.7	256	1	TRPF	trypsin-like prote	486	129.5	3.3	381	1	B26359	decay-accelerating
414	145	3.7	263	1	C36838	complement control	487	129.5	3.3	440	2	A26359	decay-accelerating
415	145	3.7	782	1	A32375	L-selectin precurs	488	129	3.3	235	1	S65621	venomobin AB (EC 3.
416	145	3.7	382	2	A61625	tenascin-like prote	489	128.5	3.3	255	2	A27122	cathepsin G (EC 3.
417	144.5	3.7	245	2	B38678	mast cell proteina	490	128.5	3.3	321	2	T33161	hypothetical prote
418	144.5	3.7	303	2	T13598	trypsin homolog -	491	128	3.2	219	1	TRPGXZ	azurocidin - pig
419	144.5	3.7	360	2	T12921	complement control	492	128	3.2	5147	1	UCPFTM	cadherin-related c
420	144	3.7	685	2	B72152	B1BL protein - var	493	127.5	3.2	1531	2	T42218	lysozyme 2 - rat
421	144	3.7	263	2	B78040	fibulin, eplice fo	494	127	3.2	258	2	156220	laminin gamma-1 ch
422	143.5	3.6	247	2	S23504	chymase (EC 3.4.21	495	127	3.2	1609	1	MMHUB2	laminin gamma-2 ch
423	143	3.6	3075	2	S14458	laminin alpha-1 ch	496	127	3.2	1751	1	MMHUB1	laminin alpha-2 ch
424	142.5	3.6	260	2	S26043	chymase (EC 3.4.21	497	127	3.2	3106	1	S53868	laminin alpha-2 ch
425	142	3.6	272	2	UC4170	trypsin-like prote	498	126.5	3.2	1025	2	T42626	secreted leucine-r
426	141.5	3.6	310	2	S41055	metalloproteinase	499	126	3.2	265	2	A38894	serine proteinase
427	141.5	3.6	385	1	A34015	L-selectin precurs	500	126	3.2	285	2	US0260	serine proteinase
428	141	3.6	225	2	S45356	probable serine pr	501	126	3.2	330	2	156100	complement factor
429	141	3.6	246	2	A32692	cytotoxic T-lympho	502	126	3.2	642	2	S53433	plasma protein S p
430	140.5	3.6	246	1	A46504	chymase (EC 3.4.21	503	125.5	3.2	254	2	S35585	chymotrypsin-like
431	140.5	3.6	1234	1	NMWSH	complement factor	504	125.5	3.2	265	2	I48679	neutrophil elastas
432	140.5	3.6	2406	2	A54148	odt protein - fruit	505	125.5	3.2	597	1	NBHUC4	Ccb-binding proteol
433	140.5	3.6	2515	2	S47008	tenascin-like prot	506	125	3.2	152	2	S35209	serine proteinase
434	140	3.5	396	1	KXBOZ	plasma protein 2 -	507	125	3.2	507	1	MMFPI1	L-selectin precurs
435	139.5	3.5	258	1	S44184	chymotrypsin (EC 3	508	125	3.2	1790	1	MMFPI2	laminin beta-1 cha
436	139.5	3.5	288	2	T33224	hypothetical prote	509	124.5	3.2	548	2	A33412	cytotoxic T-lympho
437	139.5	3.5	319	2	151569	UVS.2 protein - Af	510	124.5	3.2	548	2	T16642	hypothetical prote
438	139	3.5	1820	2	A55494	latent transformin	511	124	3.1	330	2	T46256	brevican - human (
439	138.5	3.5	244	2	S26042	chymase (EC 3.4.21	512	124	3.1	710	1	S49126	heparocyte growth
440	138.5	3.5	247	1	KYHUCM	chymase (EC 3.4.21	513	124	3.1	883	2	S49126	brevican precursor
441	138.5	3.5	705	2	S34968	fibulin, eplice fo	514	124	3.1	1221	2	A49457	fibulin-2 precurs
442	138.5	3.5	1111	2	T26972	hypothetical prote	515	124	3.1	1523	2	T13953	MEGFS protein - ra
443	138.5	3.5	191	2	S54115	complement factor	516	124	3.1	1584	2	T22674	hypothetical prote
444	137.5	3.5	808	2	D35069	complement factor	517	124	3.1	2180	2	T29764	hypothetical prote
445	137	3.5	258	2	S57960	CABP protein beta	518	123.5	3.1	151	2	S35205	proteinase 5 - buf
446	137	3.5	283	2	S23936	L-selectin precurs	519	123.5	3.1	259	1	S49129	chymotrypsin (EC 3
447	137	3.5	283	2	P87908	protein T22A3.8 [i	520	123.5	3.1	370	2	S22124	L-selectin precurs
448	137	3.5	2823	2	T23064	hypothetical prote	521	123.5	3.1	699	2	T33375	hypothetical prote
449	137	3.5	3102	2	T43291	laminin alpha chai	522	123.5	3.1	1184	2	A55184	fibulin-2 precurs
450	136.5	3.5	247	1	PRRTG	mast cell proteina	523	123	3.1	248	2	S49333	chymotrypsin (EC 3
451	136.5	3.5	1274	1	T42017	cyteine rich prot	524	123	3.1	308	2	UC7125	epidermal growth f
452	136	3.4	360	1	MMBE2E	membrane-bound com	525	123	3.1	340	2	156234	decay-accelerating
453	136	3.4	676	2	A45900	complement C3b rec	526	123	3.1	798	2	T22793	hypothetical prote
454	136	3.4	1574	2	T13954	MEGF6 protein - ra	527	123	3.1	2844	2	S28291	hypothetical prote
455	136	3.4	1607	1	MMMSB2	laminin gamma-1 ch	528	122.5	3.1	1081	2	T31329	receptor tyrosine
456	135.5	3.4	226	2	UC0151	myonase (EC 3.4.-	529	122	3.1	152	2	S35206	serine proteinase
457	135.5	3.4	372	2	T29359	hypothetical prote	530	122	3.1	198	2	146002	CABP beta chain -
458	135.5	3.4	452	2	A35068	complement factor	531	122	3.1	676	1	KXHUS	plasma protein S p
459	135.5	3.4	469	1	NMMSCA	Cab-binding protei	532	122	3.1	1810	1	A32230	tenascin precursor
460	135	3.4	159	2	I84615	coagulation factor	533	122	3.1	1955	1	AGCH	agrin precursor -
461	135	3.4	343	1	NMHWU	apolipoprotein H-r	534	121.5	3.1	245	2	A48598	kallikrein-like se
462	135	3.4	345	1	NBHU	apolipoprotein H p	535	121.5	3.1	416	2	T20448	hypothetical prote
463	135	3.4	3051	2	S42373	hypothetical prote	536	121.5	3.1	610	1	146001	Cab-binding protei
464	134.5	3.4	601	2	T23025	hypothetical prote	537	121.5	3.1	5376	2	T42215	tenascin - easlern
465	134.5	3.4	601	2	D89711	protein F40B10.4 [538	121	3.1	647	2	A43902	pregnancy-associa
466	134	3.4	232	1	A54361	venomobin A (EC 3.4	539	121	3.1	1627	2	S65464	versican precursor
467	134	3.4	2824	2	T22759	hypothetical prote	540	121	3.1	2409	1	A60979	

541	120.5	3.1	247	2	S64708	614	112	2.8	228	1	S35689	venombin A (EC 3.4
542	120.5	3.1	252	2	T46247	918	112	2.8	918	2	UC4361	scavenger receptor
543	120.5	3.1	345	1	JN0465	616	112	2.8	1155	1	S57846	protein-tyrosine k
544	120.5	3.1	497	2	JC2054	1353	112	2.8	1353	1	JH0675	restictin precurs
545	120.5	3.1	646	2	S38819	618	112	2.8	1639	1	MMFPB2	laminin gamma-1 ch
546	120.5	3.1	689	2	T42760	619	112	2.8	3562	2	A47171	chondroitin sulfat
547	120.5	3.1	712	2	T42950	620	112	2.8	4507	2	T20721	hypothetical prote
548	120.5	3.1	728	1	A60185	621	112	2.8	159	2	S35202	proteinase 2 - buf
549	120.5	3.1	1394	2	A35626	622	111.5	2.8	370	2	JC7592	spinal cord-derive
550	120.5	3.1	1801	1	MMRTS	623	111.5	2.8	651	2	T19477	hypothetical prote
551	120	3.0	257	1	JC2479	624	111.5	2.8	1338	2	T43060	agrin - electric r
552	120	3.0	363	2	B45900	625	111.5	2.8	1797	2	A55677	laminin beta-2 cha
553	120	3.0	493	2	JC5621	626	111.5	2.8	2019	1	UQ1322	tenascin precursor
554	120	3.0	589	2	T43210	627	111.5	2.8	2531	2	T16743	hypothetical prote
555	120	3.0	912	2	A54423	628	111.5	2.8	4351	2	T00252	MEGF1 protein - ra
556	120	3.0	1548	2	S34583	629	111	2.8	231	2	A60468	venombin A (EC 3.4
557	120	3.0	1643	2	T14274	630	111	2.8	915	2	T21773	hypothetical prote
558	120	3.0	2397	1	A55535	631	110.5	2.8	234	1	S20407	venombin A (EC 3.4
559	120	3.0	3381	2	T42389	632	110.5	2.8	297	1	NBRT	apolipoprotein H p
560	119.5	3.0	161	2	I48158	633	110.5	2.8	408	2	T22801	hypothetical prote
561	119.5	3.0	482	2	A43924	634	110.5	2.8	583	2	A29154	complement factor
562	119.5	3.0	675	1	KXBOS	635	110.5	2.8	678	2	B48089	growth arrest-spec
563	119.5	3.0	835	1	JP0076	636	110.5	2.8	692	2	T32980	hypothetical prote
564	119.5	3.0	1247	1	MMHUND	637	110.5	2.8	961	1	TSHPD4	thrombospondin 4 p
565	119.5	3.0	1506	2	T30886	638	110.5	2.8	1217	1	EGMSMG	epidermal growth f
566	119.5	3.0	258	2	A57290	639	110.5	2.8	1894	2	JC4980	plexin 1 precursor
567	119	3.0	513	2	D88991	640	110	2.8	266	2	T19292	hypothetical prote
568	118.5	3.0	674	2	I55476	641	110	2.8	1134	1	I58388	protein-tyrosine k
569	118.5	3.0	728	1	A35644	642	110	2.8	1905	2	I51553	plexin - Affrican c
570	118.5	3.0	728	1	UH0579	643	109.5	2.8	198	2	S06176	cytotoxic T-lympho
571	118	3.0	133	2	S21114	644	109.5	2.8	2215	2	T00348	IKK1 protein - mou
572	118	3.0	196	2	T08808	645	109	2.8	661	2	T42754	hypothetical prote
573	118	3.0	293	2	B26637	646	109	2.8	1808	2	T15099	hypothetical prote
574	118	3.0	838	2	T20125	647	109	2.8	2610	2	T20968	hypothetical prote
575	118	3.0	883	2	S57653	648	108.5	2.8	236	1	A41456	venombin A (EC 3.4
576	117.5	3.0	188	2	B32340	649	108.5	2.8	2825	1	T14271	Doc4 protein, bre
577	117.5	3.0	259	2	T21011	650	108	2.7	251	1	TRH0A2	azurocidin precurs
578	117.5	3.0	642	2	S53434	651	108	2.7	1450	2	T30273	hypothetical prote
579	117.5	3.0	996	2	JE0237	652	108	2.7	1700	2	S08167	Balblani ring 3 pr
580	117.5	3.0	1160	2	P88369	653	108	2.7	2476	2	T34022	zonadhesin - pig
581	117.5	3.0	2295	2	C88369	654	107.5	2.7	640	2	T19346	hypothetical prote
582	117.5	3.0	3375	2	T19821	655	107.5	2.7	670	2	I65967	disintegrin-like m
583	116.5	3.0	256	1	PRH03	656	107.5	2.7	3566	1	A40701	tenascin-X precurs
584	116.5	3.0	377	2	I54479	657	107.5	2.7	4544	1	S02392	alpha-2-macroglobu
585	116.5	3.0	378	2	B59180	658	107	2.7	280	2	G02741	skeletal muscle li
586	116.5	3.0	384	2	S01896	659	107	2.7	497	2	T27827	hypothetical prote
587	116.5	3.0	1170	2	A53612	660	106.5	2.7	192	2	E70414	hypothetical prote
588	116	2.9	1376	2	G00043	661	106.5	2.7	362	2	JC5194	membrane cofactor
589	115.5	2.9	440	2	A43519	662	106.5	2.7	369	2	JC5138	hypothetical prote
590	115.5	2.9	1474	2	D88550	663	106.5	2.7	616	2	T29234	cartilage oligomer
591	115.5	2.9	1680	2	A43434	664	106.5	2.7	755	2	A44315	hypothetical prote
592	115	2.9	279	2	JG0164	665	106	2.7	417	2	T33376	hypothetical prote
593	115	2.9	1207	1	EGHU	666	106	2.7	657	2	T00859	hypothetical prote
594	114.5	2.9	270	2	I37278	667	106	2.7	927	2	T21772	epidermal growth f
595	114.5	2.9	349	2	G02913	668	106	2.7	1133	1	EGRT	hypothetical prote
596	114.5	2.9	369	2	I57988	669	106	2.7	1142	2	T30272	hypothetical prote
597	114.5	2.9	1798	2	S53869	670	106	2.7	1522	2	H88380	proteinin T22F7 3 [i
598	114	2.9	255	1	A28169	671	106	2.7	1805	2	T21888	hypothetical prote
599	114	2.9	741	2	T46488	672	106	2.7	2195	2	T34264	hypothetical prote
600	114	2.9	846	2	A30889	673	105.5	2.7	346	2	T46914	variant-specific s
601	114	2.9	1069	2	T42681	674	105.5	2.7	596	2	A45664	growth arrest-spec
602	113.5	2.9	502	2	T22919	675	105.5	2.7	673	2	A48089	IDL receptor precu
603	113.5	2.9	502	2	T20130	676	105	2.7	860	1	ORHND	hypothetical prote
604	113.5	2.9	558	2	T17324	677	105	2.7	1107	2	T15884	hypothetical prote
605	113.5	2.9	574	2	B88465	678	105	2.7	1746	1	S19694	tenascin precursor
606	113.5	2.9	879	1	ORRTLD	679	105	2.7	2201	1	A32160	tenascin-C - human
607	113.5	2.9	1712	2	A38261	680	104.5	2.6	345	1	NBMS	apolipoprotein H p
608	112.5	2.9	161	2	I62744	681	104.5	2.6	1360	2	T33922	hypothetical prote
609	112.5	2.9	264	2	A28942	682	104	2.6	345	1	NBBO	apolipoprotein H p
610	112.5	2.9	370	2	UC7591	683	104	2.6	360	1	A55198	transcription fact
611	112.5	2.9	677	2	C42125	684	104	2.6	379	2	A59180	Wnt inhibitory fac
612	112.5	2.9	1228	2	A57384	685	104	2.6	473	2	T32326	hypothetical prote
613	112.5	2.9	1797	2	T21889	686	104	2.6	2101	2	S57245	insulin receptor (

687	104	2.6	4135	2	T42629	tenascin-X - bovin
688	103.5	2.6	383	2	T21946	hypothetical prote
689	103	2.6	331	2	A45222	complement factor
690	103	2.6	412	2	S72579	hypothetical prote
691	103	2.6	1296	2	T16859	hypothetical prote
692	103	2.6	2148	1	A56081	insulin receptor -
693	102.5	2.6	153	2	S35204	proteinase 4 - buf
694	102.5	2.6	473	2	I49283	ADAM 4 protein pre
695	102.5	2.6	565	2	T16408	hypothetical prote
696	102.5	2.6	873	1	QRRVD	VDL receptor prec
697	102	2.6	149	2	S35208	serine proteinase
698	102	2.6	280	2	G01884	LIM protein FHL-1,
699	102	2.6	380	2	G01639	transmembrane proc
700	102	2.6	411	2	D88087	protein B0454.7 [i
701	102	2.6	718	2	T29448	hypothetical prote
702	102	2.6	863	1	S51789	VDL receptor prec
703	102	2.6	1168	2	I56985	kelinin B1 - mouse
704	102	2.6	1713	2	A55347	adhesive ligand ep
705	102	2.6	4006	2	T09070	probable tenascin
706	101.5	2.6	379	2	T16213	APX-1 protein homo
707	101.5	2.6	1106	2	T18739	hypothetical prote
708	101.5	2.6	1959	1	AGRT	agrin - rat
709	101.5	2.6	2415	1	A39086	aggreacan precursor
710	101	2.6	377	2	C68710	protein C4362.5 [i
711	101	2.6	463	2	T26655	hypothetical prote
712	101	2.6	557	2	A48434	variant-specific a
713	101	2.6	1371	2	A38337	insulin-like growt
714	101	2.6	1378	1	I48751	protein-tyrosine k
715	101	2.6	1875	2	A36429	integrin beta-4 ch
716	100.5	2.5	417	2	T20199	hypothetical prote
717	100.5	2.5	670	2	S77463	transketolase [EC
718	100.5	2.5	802	2	T24293	hypothetical prote
719	100.5	2.5	949	2	T24294	hypothetical prote
720	100.5	2.5	956	1	A46016	thrombospondin 3 -
721	100.5	2.5	1252	2	S36016	occyar wall protei
722	100.5	2.5	1356	2	A45445	janusin precursor,
723	100	2.5	152	2	S35203	serine proteinase
724	100	2.5	421	2	T25383	hypothetical prote
725	100	2.5	667	2	A48579	trophozoite surfac
726	100	2.5	873	1	A49729	VDL receptor prec
727	100	2.5	1122	2	I54237	protein-tyrosine k
728	100	2.5	1123	1	UJ0712	protein-tyrosine k
729	100	2.5	1125	1	UJ0771	protein-tyrosine k
730	100	2.5	1151	2	I38004	M130 antigen precu
731	100	2.5	1156	2	I38005	M130 antigen precu
732	100	2.5	1251	2	A57293	latent transformin
733	100	2.5	1299	2	T43251	furin (EC 3.4.21.7
734	99.5	2.5	330	2	I55975	X/Y protein - mus
735	99.5	2.5	640	1	A30452	uromodulin precus
736	99.5	2.5	686	2	S43562	KOBE5.3 protein -
737	99.5	2.5	914	1	S07047	iodide peroxidase
738	99.5	2.5	1280	2	A39117	170K lectin precu
739	99.5	2.5	1350	2	S00647	finger protein - A
740	99.5	2.5	1766	2	A42125	trophozoite cystei
741	99.5	2.5	1847	2	T18308	probable vitelloge
742	99.5	2.5	1984	2	T13171	probable vitelloge
743	99	2.5	589	2	B38128	epithelin/granulin
744	99	2.5	591	2	I48141	acroganin - guine
745	99	2.5	675	1	KXMS	plasma protein S p
746	99	2.5	675	1	KXRTS	plasma protein S p
747	99	2.5	805	2	S68441	leptin receptor, b
748	99	2.5	892	2	S68439	leptin receptor, b
749	99	2.5	894	2	S68437	leptin receptor, b
750	99	2.5	900	2	S68440	leptin receptor, b
751	99	2.5	1162	2	S68438	leptin receptor, b
752	99	2.5	1558	2	AB2457	two-component hydr
753	99	2.5	2809	2	T30213	G-gadherin - sea u
754	98.5	2.5	317	2	T28605	hypothetical prote
755	98.5	2.5	317	2	F72172	H7R protein - vari
756	98.5	2.5	317	2	G36855	B7R protein - vari
757	98.5	2.5	427	2	S74211	PAS-6/7 protein pr
758	98.5	2.5	1178	1	A39804	thrombospondin pre
759	98	2.5	82	2	T46510	hypothetical prote
760	98	2.5	102	2	B55885	chondroitin sulfat
761	98	2.5	357	2	S23403	sperm surface prot
762	98	2.5	909	1	QRXUL1	LDL receptor 1 pre
763	98	2.5	937	2	I53282	gene PAC64 protein
764	98	2.5	1087	2	T31100	probable potassium
765	98	2.5	1748	1	UJ0786	integrin beta-4 ch
766	98	2.5	2588	2	T14342	NSD1 protein - mou
767	98	2.5	4660	2	T42737	gp330 protein prec
768	97.5	2.5	577	2	A60501	thrombospondin pre
769	97.5	2.5	837	1	A29512	LDL receptor precu
770	97.5	2.5	878	2	B71460	probable outer mem
771	97.5	2.5	884	2	T18649	hypothetical prote
772	97.5	2.5	1162	2	T21557	hypothetical prote
773	97.5	2.5	2946	2	T15840	hypothetical prote
774	97	2.5	126	2	A23473	chymotrypsin-like
775	97	2.5	379	2	T27350	hypothetical prote
776	97	2.5	429	2	T27113	hypothetical prote
777	97	2.5	626	2	T27319	hypothetical prote
778	97	2.5	799	1	IUMSFB	fibronectin recept
779	97	2.5	808	2	T23129	hypothetical prote
780	97	2.5	862	2	S43922	versican - pig-tal
781	97	2.5	915	1	A48225	subtilisin-like pr
782	97	2.5	1138	1	S24066	protein-tyrosine k
783	97	2.5	1193	2	A44018	laminin B2t chain
784	97	2.5	1292	2	T09229	galactose binding
785	96.5	2.4	149	1	KQMSN	lysine kallikrein
786	96.5	2.4	317	2	D42526	BSR protein - vacc
787	96.5	2.4	613	2	A69535	aldehyde ferredoxi
788	96.5	2.4	956	2	A57121	thrombospondin 3 p
789	96.5	2.4	1149	2	I38006	M130 antigen precu
790	96.5	2.4	1193	2	T21133	hypothetical prote
791	96.5	2.4	1297	2	T30274	proteolipaisin - be
792	96.5	2.4	1313	2	S52093	hemocytin - silkw
793	96	2.4	116	2	S17567	ADON-3 protein - pi
794	96	2.4	116	2	S39434	epemadhesin ADON-3
795	96	2.4	256	2	A56593	cyprin-related pr
796	96	2.4	392	2	T25213	hypothetical prote
797	96	2.4	788	2	A28193	integrin beta-1 ch
798	96	2.4	798	2	B28193	integrin beta-1* c
799	96	2.4	886	2	A57172	probable hormone r
800	96	2.4	4753	1	A47437	LDL-receptor-relat
801	95.5	2.4	177	2	S23505	chymase (EC 3.4.21
802	95.5	2.4	218	2	H70770	probable regulator
803	95.5	2.4	330	2	B82415	probable serine pr
804	95.5	2.4	427	2	JC4915	aga protein precu
805	95.5	2.4	561	2	T27318	hypothetical prote
806	95.5	2.4	1042	2	A57534	mucin 5AC (clone l
807	95.5	2.4	1135	1	J01928	G2-G1 polyprotein
808	95.5	2.4	1270	2	T22615	hypothetical prote
809	95.5	2.4	3191	2	T22945	hypothetical prote
810	95	2.4	463	2	T39621	peptidyl prollyl ci
811	95	2.4	850	2	S56015	gastric mucin MUC5
812	95	2.4	869	1	JC4858	VDL receptor prec
813	95	2.4	989	2	T01519	hypothetical prote
814	95	2.4	1245	1	MMMSUD	nidogen precursor
815	95	2.4	1321	2	JB0352	mucin MUC5B, trach
816	94.5	2.4	111	2	S21211	epemadhesin ADON-1
817	94.5	2.4	643	2	T25473	hypothetical prote
818	94.5	2.4	736	2	S47645	LMDC I protein - c
819	94.5	2.4	862	2	ORMSUD	LDL receptor precu
820	94.5	2.4	1216	2	T26104	hypothetical prote
821	94.5	2.4	1416	2	E88550	protein ZC84.1 [im
822	94.5	2.4	1717	1	A45558	epidermal growth f
823	94	2.4	258	1	B37252	insulin-like growt
824	94	2.4	370	2	JC7998	platelet-derived g
825	94	2.4	634	2	T02594	hypothetical prote
826	94	2.4	713	2	T44447	neuregulin-3 [limo
827	94	2.4	736	2	T06757	hypothetical prote
828	94	2.4	899	2	G02428	subtilisin-like pr
829	94	2.4	915	2	JC6148	subtilisin-like pr
830	94	2.4	932	2	I52527	PAC64A - mouse (fr
831	94	2.4	1381	2	T31083	paranodin - rat
832	94	2.4	1381	2	T14158	neurexin IV - mou

833	94	2.4	3097	2	T00021	DN-cadherin - fru	906	89.5	2.3	854	1	QRHYLD	LDL receptor precu
834	93.5	2.4	258	2	A45403	insulin-like growt	907	89.5	2.3	1164	2	T01871	RNA-directed DNA p
835	93.5	2.4	317	2	J01799	BSR protein precu	908	89.5	2.3	1258	2	A12155	WD-repeat protein
836	93.5	2.4	449	2	T35048	probable ATP /GTP	909	89.5	2.3	1364	2	T00250	MEGF2 protein - hu
837	93.5	2.4	456	2	T31483	hypothetical prote	910	89	2.3	319	2	A53502	foliistatin - Afri
838	93.5	2.4	486	2	S49820	PH1 protein - Ara	911	89	2.3	354	2	T22274	hypothetical prote
839	93.5	2.4	612	2	JH0799	laminin-related pr	912	89	2.3	359	2	F81178	histone deacetylase
840	93.5	2.4	739	2	B88553	protein K04H4.2b l	913	89	2.3	390	2	C90208	hypothetical prote
841	93.5	2.4	1115	2	S40241	G protein-coupled	914	89	2.3	469	1	NM1V27	exo-alpha-sialidas
842	93.5	2.4	1136	1	S57845	protein-tyrosine k	915	89	2.3	525	2	T21357	hypothetical prote
843	93	2.4	104	2	T19868	hypothetical prote	916	89	2.3	907	2	I50404	p50b/p97 (lyt-10)
844	93	2.4	329	2	A48805	insulin-like growt	917	89	2.3	1110	1	B42544	G2-G1 polypotein
845	93	2.4	873	1	I48952	VLDL receptor prec	918	89	2.3	1170	1	A40558	Chromospondin 1 p
846	93	2.4	995	2	A56599	embryo kinase 5 -	919	88.5	2.2	317	2	T37442	EBV gp42,ps/hr pro
847	93	2.4	2767	1	UIHU	thyroglobulin prec	920	88.5	2.2	356	2	T20656	hypothetical prote
848	93	2.4	4545	1	S25111	alpha-2-macroglobu	921	88.5	2.2	438	2	T40509	lim domain protein
849	92.5	2.3	211	2	A46458	human CR1 homolog	922	88.5	2.2	633	2	I37570	zinc finger protei
850	92.5	2.3	736	2	T19366	hypothetical prote	923	88.5	2.2	754	2	T47886	transketolase-like
851	92.5	2.3	756	2	S47656	LMDC II protein -	924	88.5	2.2	905	2	S55059	feritin alpha-I -
852	92.5	2.3	803	1	IUCH3	Integrin, band 3 p	925	88.5	2.2	1077	2	T41146	probable cysteine-
853	92.5	2.3	955	2	A45441	thrombospondin 4 -	926	88.5	2.2	1096	2	T16875	hypothetical prote
854	92.5	2.3	1367	1	TGHU1	insulin-like growt	927	88.5	2.2	1170	1	TSHP1	thrombospondin 1 p
855	92	2.3	334	2	T23027	hypothetical prote	928	88.5	2.2	1978	2	T07081	acetyl-CoA carboxy
856	92	2.3	650	2	A34498	glycoprotein antiq	929	88	2.2	621	2	I38467	low density lipopr
857	92	2.3	719	2	T00266	hypothetical prote	930	88	2.2	656	2	JC2005	integrin beta-5 ch
858	92	2.3	915	2	B48225	probable proprotei	931	88	2.2	798	2	B27079	fibronectin recept
859	92	2.3	964	2	JC5545	Integrin beta-4 pr	932	88	2.2	799	2	A38308	integrin beta-5 ch
860	92	2.3	1097	2	S68685	adenylate cyclase	933	88	2.2	962	2	JC5571	ubiquitin-like pr
861	92	2.3	1444	2	T18856	angiogenesis inhib	934	88	2.2	1085	2	C96797	unknown protein [i
862	92	2.3	1895	2	T15861	hypothetical prote	935	88	2.2	1175	2	S52417	E-selectin ligand-
863	92	2.3	2533	2	T28675	alpha-5ID ImmoBili	936	88	2.2	1192	2	S69000	laminin gamma 2 ch
864	92	2.3	3869	2	A48205	All-1 protein +GTE	937	87.5	2.2	554	2	A45818	cytolysin precu
865	91.5	2.3	237	2	I47031	insulin-like growt	938	87.5	2.2	580	2	A37107	spermatogenesis pr
866	91.5	2.3	250	2	T30124	hypothetical prote	939	87.5	2.2	584	1	C8HUA	complement C8 alph
867	91.5	2.3	303	2	H35068	apolipoprotein H-r	940	87.5	2.2	667	2	T01999	hypothetical prote
868	91.5	2.3	511	2	T17298	hypothetical prote	941	87.5	2.2	914	1	JN0550	iodide peroxidase
869	91.5	2.3	588	2	T33815	hypothetical prote	942	87.5	2.2	1807	2	JC6319	integrin beta-4 ch
870	91.5	2.3	640	2	S49932	MET30 protein - ye	943	87.5	2.2	1816	2	S68960	laminin alpha-4 ch
871	91.5	2.3	1101	2	T16840	hypothetical prote	944	87	2.2	387	2	I38449	extracellular prot
872	91.5	2.3	1161	2	D83076	type 4 fimbrial bl	945	87	2.2	706	2	S74610	hypothetical prote
873	91.5	2.3	2144	2	S71490	aah1 protein - fru	946	87	2.2	743	2	T40521	hypothetical prote
874	91.5	2.3	2672	2	A48126	translational activa	947	87	2.2	860	2	T16892	hypothetical prote
875	91.5	2.3	2910	2	T42214	ocogelin - mouse	948	87	2.2	970	2	I78842	receptor protein-c
876	91	2.3	94	2	PC2013	tissue kallikrein	949	87	2.2	975	2	JC5570	subtilisin-like pr
877	91	2.3	293	1	T09065	hypothetical prote	950	87	2.2	1042	2	T26644	hypothetical prote
878	91	2.3	319	1	I50370	transcription fact	951	87	2.2	1056	2	A53767	mucin MUC5B, trach
879	91	2.3	398	2	E71539	hypothetical prote	952	87	2.2	1134	1	JN0711	protein-tyrosine k
880	91	2.3	435	2	I54182	tumor necrosis fac	953	87	2.2	1945	2	T13937	plexin A - fruit f
881	91	2.3	478	2	S47040	gene Tt52 protein	954	87	2.2	2481	2	A43908	fibronectin - Afri
882	91	2.3	909	1	ORXL2	IDL receptor 2 pre	955	87	2.2	3968	2	A44265	criothorax homolo
883	91	2.3	2543	2	T31687	surface antigen - p	956	86.5	2.2	222	2	S72795	hypothetical prote
884	91	2.3	4543	1	A53102	alpha-2-macroglobu	957	86.5	2.2	264	2	T16471	hypothetical prote
885	90.5	2.3	53	2	S17294	epidermal growth f	958	86.5	2.2	336	2	D69074	polyferredoxin 4x2
886	90.5	2.3	330	1	JN0561	urokinase-type pla	959	86.5	2.2	391	2	T34284	hypothetical prote
887	90.5	2.3	642	1	JP0079	lim protein kinase	960	86.5	2.2	471	2	I79528	alkaline phosphata
888	90.5	2.3	746	1	HYHUMA	meprin A (EC 3.4.2	961	86.5	2.2	585	2	I46686	complement compo
889	90.5	2.3	776	2	S28258	androgen-regulated	962	86.5	2.2	632	2	T22288	hypothetical prote
890	90.5	2.3	960	2	JB0356	gamma-aminobutyric	963	86.5	2.2	632	2	T21602	hypothetical prote
891	90.5	2.3	1104	2	I38869	transcription fact	964	86.5	2.2	638	2	AF3463	flagellar protein
892	90.5	2.3	1148	1	GNVUNE	M polypotein prec	965	86.5	2.2	641	2	F71810	type III DNA modif
893	90.5	2.3	1357	2	T16860	hypothetical prote	966	86.5	2.2	651	2	T05869	hypothetical prote
894	90.5	2.3	1436	2	A46496	antigen MCL1 prec	967	86.5	2.2	700	2	A32392	protein kinase C (
895	90.5	2.3	2813	1	VMHU	von Willebrand fac	968	86.5	2.2	734	2	C81399	isocitrate dehydro
896	90	2.3	156	2	B23863	tissue kallikrein	969	86.5	2.2	1172	2	A42887	thrombospondin 2 p
897	90	2.3	340	2	T34423	hypothetical prote	970	86.5	2.2	1376	1	J01534	E2 glycoprotei
898	90	2.3	409	2	T11743	pf47 protein - pig	971	86.5	2.2	1418	2	D75281	ribonucleoside-dip
899	90	2.3	417	2	T29864	hypothetical prote	972	86.5	2.2	1473	2	A20872	ovostatin precu
900	90	2.3	522	2	T29767	hypothetical prote	973	86.5	2.2	3712	1	YGCEVC	alpha-antioadipyl-
901	90	2.3	577	2	B37057	integrin beta-6 ch	974	86	2.2	445	2	B82525	conserved hypotet
902	90	2.3	814	1	I39627	nicotine denydroge	975	86	2.2	713	2	A35502	major surface-labe
903	90	2.3	2533	1	T28674	alpha-5ID-ImmoBili	976	86	2.2	738	2	S40992	hypothetical prote
904	89.5	2.3	417	2	T39939	DNA binding protei	977	86	2.2	905	2	T23229	hypothetical prote
905	89.5	2.3	748	2	S24134	endopeptidase 2 (E	978	86	2.2	906	2	A71438	probable resistanc

979	86	2.2	933	1	OPHUT	1052	83.5	2.1	311	2	JC7873	l-rhamnose-binding
980	86	2.2	969	1	A39490	1053	83.5	2.1	344	2	A32141	follietatin 1 prec
981	86	2.2	1487	2	S48719	1054	83.5	2.1	348	2	T28623	hypothetical prote
982	86	2.2	1572	2	T00027	1055	83.5	2.1	354	2	G64475	GTP-binding protei
983	86	2.2	1650	2	S53457	1056	83.5	2.1	358	1	A55973	transcription fact
984	86	2.2	2233	2	T28669	1057	83.5	2.1	366	2	I53035	crithorax homolog
985	86	2.2	317	2	A38493	1058	83.5	2.1	491	2	H83770	hypothetical prote
986	85.5	2.2	340	1	B55973	1059	83.5	2.1	579	2	B84192	pyruvate kinase [i
987	85.5	2.2	344	1	A27701	1060	83.5	2.1	589	2	C38128	epithelin/granulin
988	85.5	2.2	358	2	B64427	1061	83.5	2.1	697	2	H86457	protein C05D11.8 f
989	85.5	2.2	463	1	A36479	1062	83.5	2.1	873	2	D88482	gene shuttle craft
990	85.5	2.2	515	2	T05863	1063	83.5	2.1	1106	2	T13938	alpha tectorin - c
991	85.5	2.2	638	2	S22491	1064	83.5	2.1	210	2	S09118	G surface protein
992	85.5	2.2	663	2	T01010	1065	83.5	2.1	270	2	A59143	polyestic kidney
993	85.5	2.2	798	2	S01659	1066	83.5	2.1	4302	2	A38971	hypothetical prote
994	85.5	2.2	1162	2	PC4184	1067	83.5	2.1	13055	2	T16580	probable transcrip
995	85.5	2.2	1229	2	H84465	1068	83.5	2.1	304	2	A83513	NOV protein - chic
996	85.5	2.2	2452	1	RWZ021	1069	83	2.1	351	2	S20078	probable phospho-2
997	85.5	2.2	2457	2	T18492	1070	83	2.1	372	2	T39244	denosylmethionine-
998	85	2.2	200	2	T42678	1071	83	2.1	451	2	F83747	anthranilate synth
999	85	2.2	291	2	I38098	1072	83	2.1	492	2	D35114	granulin precursor
1000	85	2.2	318	2	H86342	1073	83	2.1	593	1	GYHU	leukocyte adhesion
1001	85	2.2	343	2	S55369	1074	83	2.1	770	2	S04847	protein P57C12.1 f
1002	85	2.2	359	1	T51734	1075	83	2.1	770	2	D89447	leukocyte adhesion
1003	85	2.2	413	2	T23098	1076	83	2.1	771	2	A45839	leukocyte adhesion
1004	85	2.2	542	2	A84554	1077	83	2.1	800	2	S54623	probable microchond
1005	85	2.2	552	2	F83417	1078	83	2.1	816	2	C69493	hypothetical prote
1006	85	2.2	606	2	S43118	1079	83	2.1	1046	2	F71432	hypothetical prote
1007	85	2.2	638	2	S22490	1080	83	2.1	1066	2	B95037	hyaluronidase [imp
1008	85	2.2	653	2	G96675	1081	83	2.1	1111	2	T00324	hypothetical prote
1009	85	2.2	671	1	UTPV15	1082	83	2.1	1137	2	JE0095	gastric mucin MUC5
1010	85	2.2	752	2	T26508	1083	83	2.1	1116	1	ZLVNSY	genome polypeptin
1011	85	2.2	794	2	F88508	1084	83	2.1	3020	2	A43932	mucin 2 precursor,
1012	85	2.2	895	2	S74225	1085	82.5	2.1	328	2	F83599	hypothetical prote
1013	85	2.2	1021	2	S26985	1086	82.5	2.1	429	2	A42972	coagulation factor
1014	85	2.2	1078	2	P97907	1087	82.5	2.1	466	2	S29302	allin lyase (EC 4
1015	85	2.2	1148	1	UQ1604	1088	82.5	2.1	591	1	C6HUB	complement C8 beta
1016	85	2.2	1533	2	T00344	1089	82.5	2.1	753	2	T19338	hypothetical prote
1017	85	2.2	1538	2	S73296	1090	82.5	2.1	761	2	B82223	ribonucleoside-dip
1018	85	2.2	2150	2	T32497	1091	82.5	2.1	781	2	S43534	integrin betas3 - c
1019	85	2.2	271	2	S12783	1092	82.5	2.1	984	2	T00326	hypothetical prote
1020	84.5	2.1	337	2	I47079	1093	82.5	2.1	1175	2	I57549	adenosine deaminas
1021	84.5	2.1	344	2	I45894	1094	82.5	2.1	1372	2	A34157	insulin receptor p
1022	84.5	2.1	429	2	T16656	1095	82	2.1	188	2	A39787	teratocarcinoma de
1023	84.5	2.1	494	2	A99683	1096	82	2.1	235	2	AB0114	deoxyribonuclease
1024	84.5	2.1	494	2	B85533	1097	82	2.1	318	2	S65019	chitinase (EC 3.2.
1025	84.5	2.1	505	2	A46570	1098	82	2.1	343	2	S45321	follietatin - mous
1026	84.5	2.1	615	2	S06546	1099	82	2.1	349	2	D72175	G2R protein - vari
1027	84.5	2.1	654	2	T30136	1100	82	2.1	432	2	D83904	carbon storage regu
1028	84.5	2.1	696	2	A12849	1101	82	2.1	528	2	B42560	4-chloroendazole-C
1029	84.5	2.1	696	2	G97626	1102	82	2.1	583	2	T34121	steroid/thyroid/re
1030	84.5	2.1	744	2	A43253	1103	82	2.1	599	2	B82439	formate-tetrahydro
1031	84.5	2.1	746	2	F87243	1104	82	2.1	711	2	T27358	hypothetical prote
1032	84.5	2.1	760	2	A40195	1105	82	2.1	868	2	T02635	D2 protein homolog
1033	84.5	2.1	788	2	A26547	1106	82	2.1	1530	2	I45944	neurexin I -alpha -
1034	84.5	2.1	789	2	S28259	1107	82	2.1	1609	2	S44821	PAE2.4 protein -
1035	84.5	2.1	864	2	T49574	1108	82	2.1	1661	2	T31330	head-activator bin
1036	84.5	2.1	917	2	I48950	1109	82	2.1	2214	2	T16305	hypothetical prote
1037	84.5	2.1	950	2	T28793	1110	82	2.1	4861	2	S71752	giant protein p619
1038	84	2.1	278	2	T21718	1111	82	2.1	209	2	T02394	hypothetical prote
1039	84	2.1	335	2	T32657	1112	81.5	2.1	251	2	A55035	cysteine-rich prot
1040	84	2.1	349	2	D36858	1113	81.5	2.1	349	2	S57453	polyteredoxin 4x2
1041	84	2.1	413	2	T34123	1114	81.5	2.1	383	2	D88633	protein f5683.2 [i
1042	84	2.1	471	2	A84741	1115	81.5	2.1	429	2	S01919	klirp protein - f
1043	84	2.1	520	2	G88846	1116	81.5	2.1	432	2	A25483	env polyprotein, r
1044	84	2.1	567	2	T49942	1117	81.5	2.1	443	2	T29147	hypothetical prote
1045	84	2.1	572	2	A30363	1118	81.5	2.1	460	2	S67174	hypothetical prote
1046	84	2.1	1034	2	JC5598	1119	81.5	2.1	482	2	A83655	lysine decarboxyla
1047	84	2.1	1047	2	T34946	1120	81.5	2.1	496	2	T08674	probable finger pr
1048	84	2.1	1599	2	T16210	1121	81.5	2.1	519	2	S54300	transketolase (EC
1049	84	2.1	2153	2	T14893	1122	81.5	2.1	604	1	HMNZCD	hemagglutinin - ca
1050	83.5	2.1	202	1	A44247	1123	81.5	2.1	625	2	S37622	hematopoietic grow
1051	83.5	2.1	278	2	AH0282	1124	81.5	2.1	626	2		proto-oncogene - m

1125	81.5	2.1	724	2	A48569	antigen Em100 - E1	1198	80	2.0	644	2	I84634	Tamm-Horsfall proc
1126	81.5	2.1	977	2	S49004	tyrosine kinase Mp	1199	80	2.0	656	1	S59631	endo-1,4-beta-xyla
1127	81.5	2.1	1187	2	T18355	hypothetical prote	1200	80	2.0	680	1	PN0510	integrin beta-3 ch
1128	81.5	2.1	1210	2	D88013	protein K10B4.1 [1	1201	80	2.0	713	2	GC6012	glutamine-fructose
1129	81.5	2.1	1507	2	A40238	neurexin I -alpha p	1202	80	2.0	741	2	GC4888	probable transket
1130	81	2.1	180	2	AE1010	conserved hypochet	1203	80	2.0	746	2	GC4505	hypothetical prote
1131	81	2.1	296	2	C81906	hypothetical prote	1204	80	2.0	753	2	UC7386	retinovin - chicke
1132	81	2.1	348	2	A56247	natural killer cel	1205	80	2.0	817	2	T24063	hypothetical prote
1133	81	2.1	428	2	T04472	probable porphobil	1206	80	2.0	902	2	T01127	curly leaf protein
1134	81	2.1	494	2	T40455	penicillin binding	1207	80	2.0	1138	2	T36406	hypothetical prote
1135	81	2.1	501	2	JC7181	maternal transcrip	1208	80	2.0	1184	2	A96638	hypothetical prote
1136	81	2.1	554	2	A31300	perforin precursor	1209	80	2.0	1342	2	A36223	kinase-related tra
1137	81	2.1	560	2	S25092	jasmomate-induced	1210	80	2.0	1385	2	H88569	protein K03H1.5 [1
1138	81	2.1	732	2	T52588	wall-associated se	1211	80	2.0	1409	2	S41028	hypothetical prote
1139	81	2.1	735	2	G02937	fertilin beta - cr	1212	80	2.0	2219	2	T27684	hypothetical prote
1140	81	2.1	735	2	T48101	ADAM 6 protein pre	1213	80	2.0	2229	2	T16199	hypothetical prote
1141	81	2.1	769	2	JC1121	leukocyte adhesion	1214	80	2.0	2643	2	T29149	hypothetical prote
1142	81	2.1	787	2	T49614	related to col pro	1215	80	2.0	3140	2	S47508	genome polyprotein
1143	81	2.1	799	2	JC4126	integrin beta olig	1216	80	2.0	71	2	A59412	KGD-bearing platel
1144	81	2.1	821	1	A39667	brain-derived neur	1217	79.5	2.0	217	2	D90033	conserved hypochet
1145	81	2.1	1166	1	S06142	protein-tyrosine k	1218	79.5	2.0	254	2	I48599	insulin-like growt
1146	81	2.1	1344	2	H84557	hypothetical prote	1219	79.5	2.0	254	2	JC1464	insulin-like growt
1147	81	2.1	1365	2	T00833	RNA-directed DNA p	1220	79.5	2.0	317	2	D64167	transaldolase (EC
1148	81	2.1	1438	2	A48216	neurexin III -alpha	1221	79.5	2.0	318	2	S43317	chitinase (EC 3.2.
1149	81	2.1	1471	2	B48218	neurexin III -alpha	1222	79.5	2.0	324	2	S20581	chitinase (EC 3.2.
1150	81	2.1	1578	2	T48216	neurexin III -alpha	1223	79.5	2.0	336	2	A25918	chromomodulin - b
1151	81	2.1	1895	2	T06609	disease resistance	1224	79.5	2.0	391	2	S49300	AW1236 protein -
1152	81	2.1	3898	2	S57437	genome polyprotein	1225	79.5	2.0	457	2	C86464	hypothetical prote
1153	80.5	2.0	371	2	B72461	hypothetical prote	1226	79.5	2.0	474	2	A57480	hypothetical prote
1154	80.5	2.0	390	2	T27256	hypothetical prote	1227	79.5	2.0	614	2	T40652	tubulointerstitial
1155	80.5	2.0	409	2	B87661	conserved hypochet	1228	79.5	2.0	661	2	C85758	hypothetical prote
1156	80.5	2.0	416	2	A37877	hemorrhagic protei	1229	79.5	2.0	661	2	B90861	hypothetical prote
1157	80.5	2.0	431	2	S49821	PL2 protein - Ara	1230	79.5	2.0	694	2	S58083	transketolase (EC
1158	80.5	2.0	454	2	T26654	hypothetical prote	1231	79.5	2.0	700	2	HYHMB	meprin A (EC 3.4.2
1159	80.5	2.0	471	1	PAECA	alkaline phosphata	1232	79.5	2.0	713	2	I65253	disintegrin-like t
1160	80.5	2.0	479	2	D86182	protein F13W7.11 [1233	79.5	2.0	741	2	T09015	transketolase (EC
1161	80.5	2.0	502	2	T16716	hypothetical prote	1234	79.5	2.0	868	2	G84674	probable selenium-
1162	80.5	2.0	509	2	T22238	hypothetical prote	1235	79.5	2.0	952	2	T28792	diacylglycerol kin
1163	80.5	2.0	516	2	S53007	citrate synthase -	1236	79.5	2.0	1161	1	S31213	nitrogen precursor
1164	80.5	2.0	555	2	T21028	hypothetical prote	1237	79.5	2.0	1178	2	S08405	hypothetical prote
1165	80.5	2.0	570	2	T46261	hypothetical prote	1238	79.5	2.0	1260	2	A86323	protein F14D16.3 [
1166	80.5	2.0	604	2	T15796	hypothetical prote	1239	79.5	2.0	1350	2	S51364	sperm tail-specific
1167	80.5	2.0	627	2	T00603	hypothetical prote	1240	79.5	2.0	1402	2	T24664	hypothetical prote
1168	80.5	2.0	656	2	B49423	semaphorin I - fru	1241	79.5	2.0	2261	2	T07084	acetyl-CoA carboxy
1169	80.5	2.0	658	2	A86878	transketolase (EC	1242	79.5	2.0	2499	1	A30788	mannose 6-phosphat
1170	80.5	2.0	673	2	A49878	coagulation factor	1243	79.5	2.0	171	2	S57894	lamatin - Hydra vu
1171	80.5	2.0	704	2	A48040	meprin A (EC 3.4.2	1244	79.5	2.0	188	2	A30362	teratocarcinoma-de
1172	80.5	2.0	741	2	B81143	leocitrate dehydro	1245	79.5	2.0	192	1	B57143	chitosulfate-dithio
1173	80.5	2.0	742	2	I37225	leucocyte antigen	1246	79.5	2.0	192	2	AC0763	chitosulfate reduct
1174	80.5	2.0	773	2	T46059	beta-1 integrin su	1247	79.5	2.0	206	2	D97285	ribosomal protein
1175	80.5	2.0	1055	2	T05653	hypothetical prote	1248	79.5	2.0	206	2	S32695	Mnt-2 protein - Ca
1176	80.5	2.0	1119	2	A88481	protein C16A3.6 [1	1249	79.5	2.0	364	2	T24153	hypothetical prote
1177	80.5	2.0	1245	1	VHMV82	structural polypro	1250	79.5	2.0	332	2	T33444	hypothetical prote
1178	80.5	2.0	1376	1	VG1HJ2	E2 glycoprotein pr	1251	79.5	2.0	333	2	A64036	hypothetical prote
1179	80.5	2.0	1382	1	INHUR	insulin receptor p	1252	79.5	2.0	415	2	D87020	probable membrane
1180	80.5	2.0	1526	2	T19473	hypothetical prote	1253	79.5	2.0	417	2	T08724	hypothetical prote
1181	80.5	2.0	1558	2	C89114	protein C37C3.6a [1254	79.5	2.0	587	2	C85044	hypothetical prote
1182	80.5	2.0	1611	2	G84493	probable retroelem	1255	79.5	2.0	602	2	B81420	GTP-binding protei
1183	80.5	2.0	2167	2	T34395	hypothetical prote	1256	79.5	2.0	606	2	T22105	hypothetical prote
1184	80.5	2.0	2262	2	T30890	calcium channel al	1257	79.5	2.0	630	2	T48369	hypothetical prote
1185	80.5	2.0	211	1	CYRTB3	beta-crystallin B3	1258	79.5	2.0	660	2	S71949	metalloproteinase
1186	80	2.0	243	2	T27036	hypothetical prote	1259	79.5	2.0	687	2	T16352	hypothetical prote
1187	80	2.0	284	2	T25938	hypothetical prote	1260	79.5	2.0	729	2	A45716	leukemia virus cel
1188	80	2.0	290	2	T46470	hypothetical prote	1261	79.5	2.0	738	2	T41730	hypothetical prote
1189	80	2.0	335	2	A39743	u-plasminogen acti	1262	79.5	2.0	753	2	B36268	platelet glycoproc
1190	80	2.0	395	2	S64299	probable membrane	1263	79.5	2.0	773	2	JE0387	exo-alpha-sialidas
1191	80	2.0	398	1	S24802	polyferidoxin 6x2	1264	79.5	2.0	788	2	A60798	platelet glycoproc
1192	80	2.0	437	2	S05478	properdin - mouse	1265	79.5	2.0	788	2	I77349	phenylalanine-tRNA
1193	80	2.0	464	2	H82928	ATP synthase beta	1266	79.5	2.0	790	2	D61568	monocyte surface a
1194	80	2.0	500	2	A36388	RNA-directed RNA p	1267	79.5	2.0	826	2	T04867	hypothetical prote
1195	80	2.0	589	2	I38598	zinc finger protei	1268	79.5	2.0	871	2	T04867	disintegrin and me
1196	80	2.0	642	2	C89124	protein K07C11.9 [1269	79.5	2.0	952	2	T18900	
1197	80	2.0	644	1	A40212	uromodulin precurs	1270	79.5	2.0	1023	2	T30257	IgG Fc binding pro

1271	79	2.0	1289	1	RMXRR3	mRNA guanylyltrans	1344	78	2.0	4085	2	S28600	hypothetical prote
1272	79	2.0	1391	2	T20406	hypothetical prote	1345	77.5	2.0	46	2	UT0747	epiregulin - rat
1273	79	2.0	1513	2	A54895	mucin 2, intestina	1346	77.5	2.0	162	2	S68401	epiregulin precurs
1274	79	2.0	1522	2	T00028	brain-specific ang	1347	77.5	2.0	244	2	AB2505	histidine kinase-1
1275	79	2.0	1642	2	T19130	hypothetical prote	1348	77.5	2.0	255	2	H96776	hypothetical prote
1276	79	2.0	1777	2	T00490	nonstructural prote	1349	77.5	2.0	295	2	JC5559	lectin-B - Virgin
1277	79	2.0	1777	2	AC2088	sealine/threonine k	1350	77.5	2.0	296	2	G81111	conserved hypobet
1278	79	2.0	1777	2	AC2088	spermadhesin PSP-1	1351	77.5	2.0	400	2	A55647	phyllipod - fruit
1279	78.5	2.0	116	2	S65875	fructokinase (EC 2	1352	77.5	2.0	402	2	S02099	phosphotribulokinas
1280	78.5	2.0	307	1	S18523	urokinase-type pla	1353	77.5	2.0	407	2	C82428	glucose-1-phosphat
1281	78.5	2.0	341	2	I61725	natural killer ass	1354	77.5	2.0	413	4	FOHJBE	retrovirus-related
1282	78.5	2.0	344	2	I57698	folliclatin - rat	1355	77.5	2.0	457	2	B85749	ATP-dependent RNA
1283	78.5	2.0	355	2	C70457	hypothetical prote	1356	77.5	2.0	457	2	G90869	ATP-dependent RNA
1284	78.5	2.0	363	1	C55973	transcription fact	1357	77.5	2.0	457	2	B64884	ATP-dependent RNA
1285	78.5	2.0	376	2	E70361	chaperone DnaJ - A	1358	77.5	2.0	459	2	T36362	probable DNA repai
1286	78.5	2.0	389	2	D75180	hypothetical prote	1359	77.5	2.0	488	2	T21701	hypothetical prote
1287	78.5	2.0	401	2	S65138	glycoprotein antig	1360	77.5	2.0	546	2	B75375	probable amidase -
1288	78.5	2.0	436	2	S06884	viad2 protein - Ag	1361	77.5	2.0	548	2	S38864	Ig epsilon chain C
1289	78.5	2.0	474	2	B38634	tumor necrosis fac	1362	77.5	2.0	569	2	B85076	probable transposo
1290	78.5	2.0	495	2	A57053	germ cell nuclear	1363	77.5	2.0	645	2	S20138	probable protein k
1291	78.5	2.0	507	2	T64552	probable legumin A	1364	77.5	2.0	717	2	B32838	DNA-directed RNA p
1292	78.5	2.0	517	1	FMPMLA	legumin A precursor	1365	77.5	2.0	729	2	A39707	erythrocyte membra
1293	78.5	2.0	552	2	C45710	R transactivator h	1366	77.5	2.0	759	2	A69202	conserved hypobet
1294	78.5	2.0	600	2	I49281	fertilin alpha pre	1367	77.5	2.0	767	2	B85079	hypothetical prote
1295	78.5	2.0	638	2	D86477	protein F1504.27 l	1368	77.5	2.0	809	2	A57283	integrin beta chai
1296	78.5	2.0	658	2	F85024	probable GHP-rich	1369	77.5	2.0	845	2	G82773	phage-related proc
1297	78.5	2.0	662	2	I37892	IL12 receptor comp	1370	77.5	2.0	848	2	AF0020	nitrite reductase
1298	78.5	2.0	717	2	T25431	hypothetical prote	1371	77.5	2.0	933	2	A31930	cytoactin - chick
1299	78.5	2.0	748	2	T00732	hypothetical prote	1372	77.5	2.0	1017	2	D75028	h+-transporting AT
1300	78.5	2.0	757	2	T05688	hypothetical prote	1373	77.5	2.0	1079	1	TVFVMI	gag-RmlI-env polyp
1301	78.5	2.0	763	2	T49089	hypothetical prote	1374	77.5	2.0	1142	2	A45031	cysteine-rich fibr
1302	78.5	2.0	842	2	T04555	hypothetical prote	1375	77.5	2.0	1322	2	E88257	protein let-23 lim
1303	78.5	2.0	819	2	T16720	probable membrane	1376	77.5	2.0	1374	2	S70712	protein-tyrosine k
1304	78.5	2.0	1121	2	S57058	hypothetical prote	1377	77.5	2.0	2895	2	T08437	hypesplastic discs
1305	78.5	2.0	1131	2	T30951	hypothetical prote	1378	77.5	2.0	3085	2	T00327	polyprotein - infe
1306	78.5	2.0	1137	2	T18625	hypothetical prote	1379	77.5	2.0	194	2	S70663	lectin heavy chain
1307	78.5	2.0	1188	2	UC4889	hypothetical prote	1380	77.5	2.0	230	2	T31722	hypothetical prote
1308	78.5	2.0	3473	1	A46112	phosphatidylinosit	1381	77.5	2.0	230	2	A44074	probable EGF-like
1309	78.5	2.0	3473	1	A46112	genome polyprotein	1382	77.5	2.0	279	2	T16201	hypothetical prote
1310	78.5	2.0	3864	2	D87757	polyprotein - rice	1383	77.5	2.0	317	2	T45984	hypothetical prote
1311	78.5	2.0	247	2	T27778	protein C44E4.1a l	1384	77.5	2.0	375	2	F70691	hypothetical prote
1312	78.5	2.0	334	2	T03157	hypothetical prote	1385	77.5	2.0	452	2	H84772	probable serine ca
1313	78.5	2.0	360	2	T26037	probable capid as	1386	77.5	2.0	476	2	T19786	hypothetical prote
1314	78.5	2.0	360	2	G82994	glycine-cleavage s	1387	77.5	2.0	500	2	AE2032	glycerol kinase [i
1315	78.5	2.0	372	2	T31060	hypothetical prote	1388	77.5	2.0	502	2	T41148	trp-asp repeat con
1316	78.5	2.0	385	2	A81926	hypothetical prote	1389	77.5	2.0	535	2	T19706	hypothetical prote
1317	78.5	2.0	401	2	C89102	hypothetical prote	1390	77.5	2.0	540	1	OYHUCR	natriuretic peptid
1318	78.5	2.0	404	2	T40553	protein P25E5.10 l	1391	77.5	2.0	591	2	S33542	catechol oxidase (
1319	78.5	2.0	415	2	E83377	Trp-Asp repeat pro	1392	77.5	2.0	713	2	T40729	wp repeat-containl
1320	78.5	2.0	441	2	AH2930	probable alcohol d	1393	77.5	2.0	729	2	A49120	fibroblast growth
1321	78.5	2.0	446	2	F98351	oxidoreductase Atu	1394	77.5	2.0	768	2	A87722	protein ZC13.1 [i
1322	78.5	2.0	454	1	GQWST1	tumor necrosis fac	1395	77.5	2.0	821	2	S06943	brain-derived neur
1323	78.5	2.0	468	2	B40228	neurexin I-beta pr	1396	77.5	2.0	1019	2	JC7538	neuronal different
1324	78.5	2.0	468	2	S25741	T-cell glycoprotei	1397	77.5	2.0	1302	2	T00038	hypothetical prote
1325	78.5	2.0	482	2	T17250	transmembrane glyc	1398	77.5	2.0	1498	2	B97355	DNA segregation AT
1326	78.5	2.0	522	2	A46103	hypothetical prote	1399	77.5	2.0	1552	2	G86344	T2211.2 protein -
1327	78.5	2.0	523	2	C95303	conserved hypobet	1400	77.5	2.0	1723	2	T26859	receptor DEC-205 -
1328	78.5	2.0	527	2	T04329	importin alpha - t	1401	77.5	2.0	1743	2	T26859	hypothetical prote
1329	78.5	2.0	527	2	C95303	importin alpha - t	1402	77.5	2.0	2165	2	T21371	hypothetical prote
1330	78.5	2.0	599	2	JH0259	integrin beta-3 ch	1403	77.5	2.0	2584	2	T24158	hypothetical prote
1331	78.5	2.0	725	2	T27148	hypothetical prote	1404	77.5	2.0	2606	2	T24157	hypothetical prote
1332	78.5	2.0	843	2	A27131	epidermal growth f	1405	77.5	2.0	2769	1	UIBO	thryoglobulin prec
1333	78.5	2.0	957	2	T15976	hypothetical prote	1406	77.5	2.0	3033	1	GNWV08	genome polyprotein
1334	78.5	2.0	989	2	T47503	hypothetical prote	1407	77.5	2.0	3660	1	S02041	dystrrophin, muscle
1335	78.5	2.0	1016	2	G86295	hypothetical prote	1408	77.5	2.0	4957	2	T03455	AR protein - huma
1336	78.5	2.0	1131	2	T38744	hypothetical prote	1409	77.5	2.0	5262	2	T03454	AR protein - huma
1337	78.5	2.0	1245	1	VHNVB	structural polypro	1410	77.5	1.9	771	2	A59413	platelet-aggregati
1338	78.5	2.0	1260	1	TVRTNU	protein-tyrosine k	1411	76.5	1.9	146	2	G95995	hypothetical prote
1339	78.5	2.0	1330	1	GQFFE	epidermal growth f	1412	76.5	1.9	216	2	JX0265	platelet aggregati
1340	78.5	2.0	1339	2	JC4387	epidermal growth f	1413	76.5	1.9	224	2	AD2115	phosphoribosylform
1341	78.5	2.0	1369	2	S70713	protein-tyrosine k	1414	76.5	1.9	254	2	I48603	insulin-like growt
1342	78.5	2.0	1658	2	D75489	hypothetical prote	1415	76.5	1.9	264	2	T22380	hypothetical prote
1343	78.5	2.0	3224	1	S58884	Ran-binding protei	1416	76.5	1.9	272	2	E97451	hypothetical prote

1417	76.5	1.9	272	2	AG2669	enoyl-(acyl)-carrie
1418	76.5	1.9	279	2	JC6565	four-and-a-half LI
1419	76.5	1.9	302	2	E86267	hypothetical prote
1420	76.5	1.9	322	1	S3734.9	chitinase (EC 3.2.
1421	76.5	1.9	323	2	T24836	hypothetical prote
1422	76.5	1.9	327	2	AC0156	probable cobalamin
1423	76.5	1.9	359	2	T36050	probable histidin
1424	76.5	1.9	359	2	E83262	hypothetical prote
1425	76.5	1.9	385	2	AH0793	probable lipopolys
1426	76.5	1.9	386	2	T12527	hypothetical prote
1427	76.5	1.9	388	1	EHMS	ig epsilon chain C
1428	76.5	1.9	420	2	S74398	gamma-glutamyl pho
1429	76.5	1.9	435	2	T25350	transcription prote
1430	76.5	1.9	481	2	A56346	importin alpha-lik
1431	76.5	1.9	483	2	T48338	hypothetical prote
1432	76.5	1.9	487	2	T21384	hypothetical prote
1433	76.5	1.9	504	2	T34304	hypothetical prote
1434	76.5	1.9	518	2	G88961	protein F59A7.8 (I
1435	76.5	1.9	520	2	C70311	hypothetical prote
1436	76.5	1.9	536	1	A39036	H+-transporting tw
1437	76.5	1.9	545	1	PMBYA	hypothetical prote
1438	76.5	1.9	601	2	T34396	probable membrane
1439	76.5	1.9	623	2	S56206	hypothetical prote
1440	76.5	1.9	658	2	T47960	finger protein - m
1441	76.5	1.9	707	2	S68858	hypothetical prote
1442	76.5	1.9	712	2	T16338	integrin beta 2 ch
1443	76.5	1.9	772	2	S32659	mucln-like peptide
1444	76.5	1.9	837	2	A42112	protein-tyrosine k
1445	76.5	1.9	849	2	I50617	starch phosphoryla
1446	76.5	1.9	1000	2	S47243	hypothetical prote
1447	76.5	1.9	1004	2	T31655	hypothetical prote
1448	76.5	1.9	1056	2	T33167	suppressor protein
1449	76.5	1.9	1071	2	T18307	DNA polymerase III
1450	76.5	1.9	1153	2	T00615	RNA polymerase (be
1451	76.5	1.9	1201	2	AD1107	acetyl-CoA carboxy
1452	76.5	1.9	1349	2	T01659	vitellogenin vit-6
1453	76.5	1.9	1561	2	T18561	hypothetical prote
1454	76.5	1.9	1660	2	C84507	hunc3-2 - rat
1455	76.5	1.9	1738	2	T18376	protein CTRP - mal
1456	76.5	1.9	1985	2	T18397	alpha tectorin - m
1457	76.5	1.9	2098	2	T30197	surface protein ty
1458	76.5	1.9	2155	2	S50820	xin protein - chic
1459	76.5	1.9	2395	1	T14266	erithorax protein
1460	76.5	1.9	2562	2	T13857	hypothetical prote
1461	76.5	1.9	3828	2	T18440	herc2 protein - mo
1462	76.5	1.9	4550	2	T18440	herc2 protein - mo
1463	76.5	1.9	4836	2	T14346	tissue kallikrein
1464	76	1.9	96	2	A05308	tearocarcinoma-de
1465	76	1.9	136	2	S72508	sperm motility inh
1466	76	1.9	171	2	T49612	hypothetical prote
1467	76	1.9	233	2	T22396	RNA methylase, YS
1468	76	1.9	261	2	G97180	paired box transcr
1469	76	1.9	269	2	S36166	conserved hypochet
1470	76	1.9	287	2	A11072	transcription fact
1471	76	1.9	333	2	T15257	membrane-associate
1472	76	1.9	349	1	I51739	hypothetical prote
1473	76	1.9	374	2	A42264	hypothetical prote
1474	76	1.9	415	2	T32467	oxidoreductase - D
1475	76	1.9	418	2	T24350	probable ADA-like
1476	76	1.9	454	2	D75446	purh bifunctional
1477	76	1.9	490	2	T35948	2-aminobenzonate-Co
1478	76	1.9	512	1	DTBSPH	metallopeptidase
1479	76	1.9	531	2	T22021	WD-repeat protein
1480	76	1.9	603	2	S22402	probable RNA-direc
1481	76	1.9	605	2	S71650	hypothetical prote
1482	76	1.9	612	2	T39666	probable DEAD box
1483	76	1.9	616	1	RRVQWA	transketolase (imp
1484	76	1.9	626	2	T09345	turin (EC 3.4.21.7
1485	76	1.9	634	2	AG0252	EBB kinase activa
1486	76	1.9	670	2	A12223	hypothetical prote
1487	76	1.9	837	2	S43656	
1488	76	1.9	860	2	JC5702	
1489	76	1.9	897	2	S67283	

1490	76	1.9	908	2	T27117	hypothetical prote
1491	76	1.9	925	2	T37475	lipoprotein recept
1492	76	1.9	926	1	OPPGIT	iodide peroxidase
1493	76	1.9	934	1	A34372	complement C6 prec
1494	76	1.9	967	2	T48210	hypothetical prote
1495	76	1.9	1001	2	AG1879	hypothetical prote
1496	76	1.9	1084	2	T18292	hypothetical prote
1497	76	1.9	1097	2	S17308	nicotinamide nucle
1498	76	1.9	1206	2	T18557	leukemia inhibitor
1499	76	1.9	1245	1	VHWVB2	probable hydrogena
1500	76	1.9	1385	2	S34230	structural polypro
						156k protein - pla

ALIGNMENTS

RESULT 1
 T08805
 hypothetical protein DKFZp566H2123.1 - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
 A:Accession: T08805
 R:Annotg, W.; Warkner, U.; Mewes, H.W.; Gaassenhuber, J.; Wiemann, S.
 Submitted to the Protein Sequence Database, May 1999
 A:Reference number: Z16472
 A:Accession: T08805
 A:Molecule type: mRNA
 A:Residues: 1-181 <ANS>
 A:Cross-references: UNIPROT:Q9Y432; EMBL:AL050214
 A:Experimental source: adult uterus; clone DKFZp566H2123
 C:Genetics:
 A>Note: DKFZp566H2123.1

Query Match 24.1%; Score 949; DB 2; Length 181;
 Best Local Similarity 99.4%; Pred. No. 2.2e-56;
 Matches 180; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	540	SLQISAIILHPNDPILLDADIAILKLDKARSTRVOPICLAASRDLSFQESHITVA	599
DB	1	SLAISAIILHPNDPILLDADIAILKLDKARSTRVOPICLAASRDLSFQESHITVA	60
QY	600	GNMVLADVRSPPGKNDTLRSGVSVVDSLLCEQHEHDGIPVSTVDMFCASNEPTAPSD	659
DB	61	GNMVLADVRSPPGKNDTLRSGVSVVDSLLCEQHEHDGIPVSTVDMFCASNEPTAPSD	120
QY	660	ICTAETGGIAAVSFPGRASPEPRMHLGLVSNVYDTCGHRISTATKVLPEQDVIERNM	719
DB	121	ICTAETGGIAAVSFPGRASPEPRMHLGLVSNVYDTCGHRISTATKVLPEQDVIERNM	180
QY	720	K 720	
DB	181	K 181	

RESULT 2

A38738
 coagulation factor C precursor - horseshoe crab (Tachyples tridentatus)
 N:Alternate names: coagulation-complement factor C; Limulus factor C
 N:Contains: coagulation factor C heavy chain; coagulation factor C light chain peptide A,
 C:Species: Tachyples tridentatus
 C:Date: 04-Oct-1991 #sequence_revision 04-Oct-1991 #text_change 09-Jul-2004
 A:Accession: A38738; B38738; S00105
 R:Mita, T.; Miyata, T.; Minami, Y.; Tokunaga, F.; Nakamura, T.; Toh, Y.; Ikehara, Y.; Iwe
 U. Biol. Chem. 266, 6534-6561, 1991
 A:Title: Limulus factor C. An endotoxin-sensitive serine protease zymogen with a mosaic
 A:Reference number: A38738; MIMD:91177916; PMID:2007602
 A:Accession: A38738
 A:Molecule type: mRNA
 A:Residues: 1-1019 <MUT>
 A:Cross-references: UNIPROT:P28175; GB:D90271; NID:g217396; PID:d1015020; PID:g217397
 A:Accession: B38738
 A:Molecule type: mRNA
 A:Residues: 1-466, 616, 'DN', 619-620, 'A', 622 <MUT>

A;Cross-references: GB:D90272
 R;Tokunaga, F.; Miyata, T.; Nakamura, T.; Morita, T.; Kuma, K.I.; Miyata, T.; Iwanaga, S
 Eur. J. Biochem. 167, 405-416, 1987
 A;Title: Lipopolysaccharide-sensitive serine-protease zymogen (factor C) of horseshoe cr
 is a novel type of serine protease.
 A;Reference number: S00105; MUID:88004461; PMID:3308457
 A;Accession: S00105
 A;Molecule type: protein
 A;Residues: 'S', 27-39, 'S', 41, 'T', 43-54, 'E', 691-782, 950-977 <TOK>
 A;Superfamily: C; C-type lectin homology; complement factor H repeat
 C;Keywords: alternative splicing; glycoprotein; hemolymph coagulation; hydrolase; serine
 F;1-25/Domain: signal sequence #status predicted <SIG>
 F;26-690/Product: coagulation factor C heavy chain #status experimental <RCH>
 F;136-195/Domain: complement factor H repeat homology <FH01>
 F;199-254/Domain: complement factor H repeat homology <FH02>
 F;260-321/Domain: complement factor H repeat homology <FH03>
 F;436-564/Domain: C-type lectin homology <LCH>
 F;576-634/Domain: complement factor H repeat homology <FH04>
 F;685-747/Domain: complement factor H repeat homology #status atypical <FH05>
 F;691-762/Product: coagulation factor C light chain peptide A #status experimental <PPA>
 F;763-1019/Product: coagulation factor C light chain peptide B #status experimental <PPB>
 F;523-534, 624-912/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;767/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F;809, 865, 966/Active site: His, Asp, Ser #status predicted

Query Match 17.0%; Score 672; DB 2; Length 1019;
 Best Local Similarity 25.6%; Pred. No. 4,5e-37;
 Matches 223; Conservative 117; Mismatches 308; Indels 222; Gaps 37;

34 PEAENWNT---CRECCYDIE---CYCPGKREYVGTTCRCNEHECSCLIHQCT 86
 184 PNCQMSRPPKICRECAKVSPEHGKVNAPSGNMIEGATL---RPSGDS---PYLL 233
 87 IFENCKSR-KGSMGCTL-----
 234 IGQELTQCGNQMSGQIPQCKKLVFCDDLPVNAHEQVKIGVEQKGGPPQGTETVYT 293
 104 --DFFVVGFCYCAECR--AGWYGG--DCMR-----CGQVLR--APKG 137
 294 CSGNVFLMGFTMLKCNPDGMSGSPSCVKAADREVDGDSKAVPLDVGSPVNIHCAG 353
 138 QILLES-----YPLAHCEWTHA---KPGVVI-----Q 163
 354 CSLTAGVGTGTAIYHELSSVCRAIHAACKLPNSGAVVNVNNGPYSDPLGSLNGIXSE 413
 164 LRFWMLSLFPIYM-----CQDYVEVND-----GMRDGIITKRVCGN--ERPAP 206
 414 LKSLARSRFPDVSSSTGRSGCCPDMGFEVEBNCVYTTSKORAMERAGCVCTNMAALAV 473
 207 IQS--IGSSLHVLFFHSDG-SKNFDFH-----AIYEITACSSSPCF 245
 474 LDKDLIPSLIETLAKGLITTTWIGLHRLDAEKPFVWELMRSNVNLNDNLTPMAGSEPG 533
 246 HDGTCV-LDKAGS---YKCACTAGYTGRCENLLEERN---CSDPGSPVNGYQKITGCP 297
 534 NETNVCVYDIDLDQLOPVWKTYSCEFPSSFACMMDDSDNKKAKCDPPGLENGHATLHQSS 593
 298 GLINRHAHKIGTVVSPFCNNSVYVLSGNEKRTCOQNGESGKOPICIK--ACREPKISLV 355
 594 --IDSFVA--GSSIVSCVLYLHLSGTETVTTCTTGTSAPRPKIKYITCONPVPVSYG 649
 356 RRRVLPVMOVSRETFHOLYSNAFSGKQLQ--SAPTKKPLPFSD-----LP 400
 650 SVEIRP---PRTNLSIRVSGPFLALPRLPLABAAPRPKPRSSQSPSTVDLASKVLP 706
 401 MGYOHLHTQLOYECISPFYRIRIGSSRRCTCLRTGKSGRAPSCIPICGIENITAP----- 455
 707 EGHVYVGRATYTCRSRYELLGSGRCRDSNGMSGPASCIPVCGRSDSPSPFIWNG 766
 456 -KTGCLRRPQWQAAIYRRTSGVHDSLHGAMFLVCSGALNERTVVAHAHCVTLDGKXTM 514
 767 NSTEIGQWPMQGISRWLA-----DHNMFLOCGGSLNEKWTIVTAHACVTSATAEI 819

QY 515 IKTADLKVTLGKRYRDDDEKTIQSLQISATILHPNYDPLLDADIDAIKLDKARIST 574
 DB 820 IDSOPFIYIGKRYRDRSDRDVYQVREALEIHVNPYDGNLNFIALIQLTPTVLT 879
 QY 575 RVQPICAASRDSISFQESH-----TVAGNVVLADVSPGPKNDLRSVGVSDSL 628
 DB 880 RVQPICLPT--DITL---RHLKEGLLAVVTGNG---LNNNTYSEMICQALDPVVAAS 930
 QY 629 LCEOHEDHGIPIVSDTDMFCASMEPTAPSDICTAETGIAAVSPGRASPEPRMHLGL 688
 DB 931 TCEGVYHEADLPITVENMFCAGYK-KGRYDACSBSGG--PLVFADDSRTERRWLEGI 987
 QY 689 VNSVSYDKTSGH-RLSTAFVLPFKWMIER 717
 DB 988 VSWGSPSGCGKANQYGFETKVNFLSMIRQ 1017

RESULT 3
 154763
 Ra-reactive factor (EC 3.4.21.-) 1 precursor - human
 N;Alternate names: mannose binding protein-associated serine proteinase 1 (MASP-1)
 C;Species: Homo sapiens (man)
 C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
 C;Accession: 154763; JN0883
 R;Sato, T.; Endo, Y.; Matsushita, M.; Fujita, T.
 Int. Immunol. 6, 665-669, 1994
 A;Title: Molecular characterization of a novel serine protease involved in activation of
 A;Reference number: 154763; MUID:94289349; PMID:8018603
 A;Accession: 154763
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-699 <SAT>
 A;Cross-references: UNIPROT:P48740; GB:D28593; NID:G790963; PIDN:BA05928.1; PID:G471128
 R;Takada, F.; Takayama, Y.; Hattuse, H.; Kawakami, M.
 Biochem. Biophys. Res. Commun. 196, 1003-1009, 1993
 A;Title: A new member of the C1s family of complement proteins found in a bactericidal fe
 A;Reference number: JN0883; MUID:94059062; PMID:8240317
 A;Accession: JN0883
 A;Molecule type: mRNA
 A;Residues: 1-234, 'E', 236-284, 'G', 286-498, 'K', 500-542, 'K', 544-642, 'S', 644-699 <TAK>
 A;Cross-references: DDBJ:D1752; NID:G439712; PIDN:BA04477.1; PID:G439713
 A;Experimental source: liver
 C;Comment: This is a serum bactericidal factor that activates complement C4 and C2 compor
 C;Genetics:
 A;Gene: GDB:MASP1; GDB:CRANF; CRANF1; PRSS5; MASP
 A;Map position: 3q27-3q28
 A;Cross-references: GDB:361104; GDB:330954; OMIM:600521
 C;Superfamily: complement-activating serine proteases C1r/C1s/MASP; C1r/C1s repeat homol
 C;Keywords: beta-hydroxyasparagine; complement pathway; duplication; glycoprotein; hydro
 F;1-17/Domain: signal sequence #status predicted <SIG>
 F;18-448, 449-699/Product: Ra-reactive factor #status predicted <MAT>
 F;19-135/Domain: C1r/C1s repeat homology <C1R1>
 F;143-181/Domain: EGF homology <EGF>
 F;185-294/Domain: C1r/C1s repeat homology <C1R2>
 F;301-362/Domain: complement factor H repeat homology <FH1>
 F;367-432/Domain: complement factor H repeat homology <FH2>
 F;449-691/Domain: trypsin homology <TRY>
 F;49-179, 407/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;73-91, 143-157, 153-166, 168-181, 185-212, 242-260, 301-349, 329-362, 367-414, 397-432, 436-572,
 F;159/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
 F;448-449/Cleavage site: Arg-11e (autolytic) #status predicted
 F;490, 552, 646/Active site: His, Asp, Ser #status predicted

Query Match 12.2%; Score 482; DB 1; Length 699;
 Best Local Similarity 24.9%; Pred. No. 1,4e-24;
 Matches 178; Conservative 93; Mismatches 215; Indels 228; Gaps 39;

QY 69 CRNEENCDSCLHPGCTIFRENCCKSNNGWGTTLDPFYVGFYCAECRAGWY-----CGD 124
 DB 143 CKHEDEBELSGDH-----CHN-----YIGGYCS-CRGOYLHTDNT 180
 QY 125 C-MRCGOVLRAPKQIILL-----ESYPLAHCEWTHAKGPFVQLRFWMLSLFPIYM-- 176

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Db      181 CRVECSNLTQKRGVITSPDFPNYPKSSCLTITLSEGFVNLQFEDI---FDIQDH 237
Qy      177 -----COYDVEVRDNDGDIIRKVCNERPAPISIGSSLAHLFSDSKNDFGFAI 232
Db      238 PEVPCPDIYIKIKKP-----KVLGPFCEKAPETISQSHSVLLFFSDSAENKGRRL- 292
Qy      233 YEETACSSPFCFHDGTCLVDKAGSYCACLAGYTGRCENLEERNCSDPGFVNGYOK 292
Db      293 -----SYRAA-----GNECEPL-----QP--PVH----- 309
Qy      293 ITGPGGLNGRHAIGTVVSFF-----CNSI-VLSGNEKR-----TCQNGESGCKQ 339
Db      310 -----GRIEBSQAKY-----FFKQOVLVSCDTGYKVLKDVNEMTPFOIECIKGTWSNKI 359
Qy      340 PIC-1KACREPKISDLVRRRLPMQVQSRETPLHLQVLSAFAKQKLSAPTKKKALPFGD 398
Db      360 PTCGIYDCRNP-----GE 372
Qy      399 LPMGYQHLMT-----OLQVECISPFYRLGSSR--RTCLRTGKMS-----GRA-PSC 442
Db      373 LEHGLIFSTRNMLTYKSEIKKSCQEPYKMLNNTGITYCSAQGVMAKVLGRLPLTC 432
Qy      443 IPICG-----KIENTAPKTOGLRMPMOAATIRRTSGVHDSLHGAMFLVCSGA 492
Db      433 LPVCGLPKFKRKLMAIFN-GRPAQKGT--PWIML-----SHLNGQPF--CGGS 478
Qy      493 LVNERTVVAHCV---TDIGKVT-----MIKTADLVNVLGKFRDDRDREKTIQSQIS 544
Db      479 LIGSSWTVTAHCHQSLDPPDLRSDLSLSPDFKILIGKMR--LRDENEQHLGVK 536
Qy      545 AILHPNVDPIILDADIAILKLDKARISTRVQPCICLAASRDLSFSQE--SHITVAGMNV 603
Db      537 HTLHPYDNTFENDVALVELLESPLVNAFVWICLPEBQ-----QEGAMVIVSGMK 591
Qy      604 LADVRSFGKNDITRSGVSVSDSLCEQHEHGIPIVSYTDNNFCASWEPTAPSDICTA 663
Db      592 QFLORFP-----ETLMEIETPIVDHSTQKAYAP--LKKKTVRDMICAG-EKEGGKACAG 644
Qy      664 ETGSIANVSFGRASPFRMHLMGVMSYDKTCSHRLSTAFVLPFKWMIR 717
Db      645 DSGGPMVTLNRRG---QWLVGTVSWGDGCKGRKYG--VSYTHNKWMIQIR 693

RESULT 4
C1HNRB
Complement subcomponent C1r (EC 3.4.21.41) precursor [validated] - human
C1Species: Homo sapiens (man)
C1Date: 15-Nov-1984 #sequence revision 30-Jun-1991 #text change 09-Jul-2004
C1Accession: A24170; A29768; A29769; S02422; A00916; A37820; S68830
R1Leysus, S.P.; Kurechi, K.; Sakataasen, K.S.; Davie, E.W.
Biochemistry 25, 4855-4863, 1986
A1Title: Nucleotide sequence of the cDNA coding for human complement C1r.
A1Reference number: A24170; MUID:87026566; PMID:3021205
A1Molecule type: mRNA
A1Residues: 1-705 <LEV>
A1Cross-references: UNIPROT:P00736; GB:M14058; NID:G179643; PIDN:AAA51851.1; PID:G179644
R1Journet, A.; Tobi, M.
Biochem. J. 240, 783-787, 1986
A1Title: Cloning and sequencing of full-length cDNA encoding the precursor of human comp
A1Reference number: A29768; MUID:87156625; PMID:3030286
A1Accession: A29768
A1Molecule type: mRNA
A1Residues: 1-151, 'L', 153-705 <JOU>
A1Cross-references: GB:X04701; NID:G29538; PIDN:CAA28407.1; PID:G29539
R1Arlaud, G.J.; Williams, A.C.; Gagnon, J.
Biochem. J. 241, 711-720, 1987
A1Title: Complete amino acid sequence of the A chain of human complement-claasical pathw
A1Reference number: A29769; MUID:87241246; PMID:3036070
A1Accession: A29769
A1Molecule type: protein
A1Residues: 18-166, 'X', 168-463 <ARL>

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A1Note: 152-Leu was also found
R1Arlaud, G.J.; van Dorselelaer, A.; Bell, A.; Mancini, M.; Aude, C.; Gagnon, J.
FEBS Lett. 222, 129-134, 1987
A1Title: Identification of erythro-beta-hydroxyasparagine in the EGF-like domain of humar
A1Reference number: S02422; MUID:88005128; PMID:2820791
A1Accession: S02422
A1Molecule type: protein
A1Residues: 152-186 <AR3>
A1Note: 152-Leu was also found
R1Arlaud, G.J.; Gagnon, J.
Biochemistry 22, 1758-1764, 1983
A1Title: Complete amino acid sequence of the catalytic chain of human complement subcomp
A1Reference number: A00916; MUID:83204782; PMID:6303394
A1Accession: A00916
A1Molecule type: protein
A1Residues: 464-705 <AR2>
R1Thieleens, N.M.; Aude, C.A.; Lacroix, M.B.; Gagnon, J.; Arlaud, G.J.
J. Biol. Chem. 265, 14469-14475, 1990
A1Title: Ca(2+) binding properties and Ca(2+)-dependent interactions of the isolated NH-;
A1Reference number: A37820; MUID:90354439; PMID:2387866
A1Accession: A37820
A1Molecule type: protein
A1Residues: 18-26, 'L', 153-160, 'X', 252-255 <TH1>
R1Pelloux, S.; Thieleens, N.M.; Hudry-Clergeon, G.; Pelliot, Y.; Fillhol, O.; Arlaud, G.J.
FEBS Lett. 386, 15-20, 1996
A1Title: Identification of a cryptic protein kinase CK2 phosphorylation site in human com
A1Reference number: S68830; MUID:96221263; PMID:8635594
A1Accession: S68830
A1Molecule type: protein
A1Residues: 133-137, 187-211, 610-613 <PEL>
A1Experimental source: Plasma
A1Comment: C1r is a dimer of identical chains, each of which is activated by cleavage int
C1Chain: while fragment gamma remains disulfide-bonded to the B chain to form C1r II.
C1Comment: This protein is a serine protease that combines with C1q and C1s to form C1, t
n, activate C2 and C4.
C1Genetics:
A1Gene: GDB:C1R
A1Cross-references: GDB:119729; OMIM:216950
A1Map position: 12p13-12p13
C1Superfamily: complement-activating serine proteases C1r/C1s/MASP, C1r/C1s repeat homol
C1Keywords: acute phase; beta-hydroxyasparagine; calcium binding; complement pathway; duf
F1-1-17/Domain: signal sequence #status predicted <SIG>
F1-1-138/Domain: C1r/C1s repeat homology <C1R1>
F1-18-463/Product: complement C1r chain A #status experimental <ACH>
F1-16-189/Domain: EGF homology <EGF>
F1-183-302/Domain: C1r/C1s repeat homology <C1R2>
F1-297-463/Product: C1r gamma fragment #status experimental <GFR>
F1-309-471/Domain: complement factor H repeat homology <FH1>
F1-376-447/Domain: complement factor H repeat homology <FH2>
F1-464-705/Product: complement C1r chain B #status experimental <BGH>
F1-464-697/Domain: trypsin homology <TRY>
F1-71-89, 146-165, 161-174, 176-189, 193-220, 250-268, 309-358, 338-371, 376-429, 406-447, 451-577,
F1-125, 221, 514, 581/Binding site: carbohydrate (Asn) (covalent) #status experimental
F1-167/Modified site: erythro-beta-hydroxyasparagine (Asn) #status experimental
F1-206/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status experimental
F1-463-464/Cleavage site: Arg-Ile (autolytic) #status experimental
F1-502, 557, 654/Active site: His, Asp, Ser #status predicted

Query Match 10.2%; Score 403.5; DB 1; Length 705;
Best Local Similarity 22.9%; Pred. No. 2,5e-19;
Matches 178; Conservative 96; Mismatches 259; Indels 245; Gaps 41;

Qy      44 ECEHYQIEC-----YC-----PKREVVGITPCC-----RNEVECD 77
Db      69 EGCFDYVYKISADKSLGRFCGLGSPGNPCKEFMSGGNMILLTFHTDFSENEN--G 126
Qy      78 SCLIHGCTIF--ENCKSCRNCSMGCTLD-----DFYKGYCAECRAGM----- 120
Db      127 TIMFYGFLAYVAVUDDEKASNSKSGEDPPOQCCHLCHNYGVGYFCS-CRGGYELQED 185
Qy      121 ---YGDCKRCQGVLRAPKQOI-LLE---SYLNAHCWTHIAKPGVQLARFVMSLEF 173
Db      186 RHSCQABC--SSRLYTEASGYISLSLEYPRSYPPDLRCNYSIRVERGLTILKLE---P 240

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Db      745 --ELTDHMLCAGFPSSKEDKACGDSGGLVQC-----NEKEPSTIYGLVSMG--EGCG- 794
Oy      700 RLST--AFTKVLPEKDWIERNMK 720
      795 RVSKPGVYTKRLPFTMIQNTQQ 817

RESULT 8
JC6554
complement subcomponent C1s (EC 3.4.21.42) precursor [similarity] - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 09-Jul-2004
C:Accession: JC6554
R:Sakai, H.; Nakashima, S.; Yoshimura, S.; Nishimura, Y.; Sakai, N.; Nozawa, Y.
Gene 209, 87-94, 1998
A:Title: Molecular cloning of a cDNA encoding a serine protease homologous to complement
A:Reference number: JC6554; MUID:98192519; PMID:9524231
A:Accession: JC6554
A:Molecule type: mRNA
A:Residues: 1-694 <SAK>
A:Cross-references: UNIPROT:O70542; DDBJ:D88250; NID:93080541; PIDN:BAA25797.1; PID:9308
C:Comment: This protein is involved in glial cell differentiation and cartilage remodeling
C:Genetic8:
A:Gene: r.99P
C:Superfamily: complement-activating serine proteases C1r/C1s/MASP, C1r/C1s repeat homo
C:Keywords: differentiation; glycoprotein; hydrolase; serine proteinase
F:1-21/Domin: signal sequence #status predicted <SIG>
F:17-133/Domin: C1r/C1s repeat homolog #status predicted <C1r>
F:12-694/Product: serine protease homolog #status predicted <MAT>
F:141-177/Product: EGF homology <EGF>
F:300-360/Domin: complement factor H repeat homology <FHR>
F:444-681/Domin: trypsin homology <TRY>
F:180,412/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:481,535,637/Active site: His, Asp, Ser #status predicted

Query Match      8.6%; Score 340.5; DB 2; Length 694;
Best Local Similarity 21.2%; Pred. No. 4e-15;
Matches 167; Conservative 98; Mismatches 244; Indels 277; Gaps 40;

Oy      44 ECCEEDOLECYCPGKRE-----VVGVTIPCCR-----NEE----- 73
Db      69 ENCAVDVQIISGIEERLCCGSSKSPNPTHEFPFNRLQVNTSPSNEERTG 128
Oy      74 -----NECDSCLIHPGCTIFENCKSCRNMGWGLTDFYVKGFCYCAECRAGWYG 123
Db      129 FAAYVASDVNVECTDFTDVP--CSHF-----CMN-----FIGVFCG--CPREYFLH 171
Oy      124 DCMR-----CGVILRAKGOILLES-----YPLNAHCWTHAKRGPYIQRFVNLSEF 173
Db      172 DDMRTCGVNCSDVFTALIGELASPNYPNPENSRCEYQIRLOEGF--RLVLTIRREDF 229
Oy      174 DYMCGVDVVEVRDDGNR-----DGOIIRKVCGRNRPAP--IQSISSILHVLPHSDG 222
Db      230 D-----VERADSEGNCHDSITFPAKNOQFPGYCGNPFPEBLTIKTSSNLTLDIVFQDL 282
Oy      223 SKNEDGFNAIY-----EETIACS-----SPCFHGTCTVLDKASYKACLAGYTG 268
Db      283 TGGNNGWMLRHYGDIIPCKEISANSIMEPEKAKVFD-----VVKITC----- 327
Oy      269 ORCENLLEERNCSDPGPGVNGYQKTGGPGLINGHAKIGIVVGFCCNNSVYLSGNEKRT 328
Db      328 -----VDGFEVEGNGV-----STSPY-----ST 346
Oy      329 COQNGMSGK-----OPICIKCREPKISDLVRRRLPMQVSRERPHQLVSAAFSKQL 384
Db      347 COSNQWNSRLIECPV--DCGVPE-----PIENGKVEDPETHVGSV----- 387
Oy      385 OSAPTKKDALPFGDLPNGYHLHTLOLEYECISPFY--RRLGSSRRTCRLRTKWSG----- 437
Db      388 -----IHTCEEPYLYMQEBSGEVHCANSAWSVWVDQGLV 422
Oy      438 RAPSCIPICG-----KIEN--ITAPKTOGLRWPMQAAIYRRRTSGVHDGSLHKGAWFLVC 489

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Db      423 ELKPCIPVCGVPEPEPKVQORIRFGYSTKIQSPFMQVYESPRG----- 467
Oy      490 SGALVNERIVVAACVLT-DLGRVTMIKTADLKNVLGKFEYRDDDEKTIQSLQISAIL 548
Db      468 -GALIDEVVLTFAHIVEGNSDPVMVGSITLKI-----ERLRNQRLITERVIL 516
Oy      549 HENVYD-----ILLDADAILKLDKARISIRVQPCIAASRDISTSQESHI---TV 598
Db      517 HPSWKQEDDLNRTNFDNDIALVOLKDPVMGPTVAPICLP--ETPSDYNPSBVDGLI 573
Oy      599 AGNNVLADVRSFGKNDITLRSGVSVSDSLCE-----EGHEDHGPVSVTDNMFCASWEP 654
Db      574 SGWG-RTEIRTNVQ--LRGALCPITLSLEKCOQVVENPKASNDVFTDNMIGAGEKG 629
Oy      655 TAPSDICTAETGIGIAVSPFGRASPEPRMHLMLGVMSYDKTCSHRLSTAFYVLPFKW 714
Db      630 V--DSCEBGSGCAFALPVN--VKDPKFVAGLVSMG--KKCG--TYGIYTKVKNVVDW 680
Oy      715 IERNMK 720
Db      681 ILKTMQ 686

RESULT 9
C1HUS
complement subcomponent C1s (EC 3.4.21.42) precursor [validated] - human
N:Alternate names: C1 esterase precursor
C:Species: Homo sapiens (man)
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-May-2004
C:Accession: A04966; A27381; S00224; S26732; S05634; A05140; A25396; A38407; B37820
R:Kusunoto, H.; Hirozawa, S.; Sailer, J.P.; Hagen, F.S.; Kurechi, K.
Proc. Natl. Acad. Sci. U.S.A. 85, 7307-7311, 1988
A:Title: Human genes for complement components C1r and C1s in a close tail-to-tail arrang
A:Reference number: A40496; MUID:89017187; PMID:2459702
A:Accession: A40496
A:Molecule type: mRNA
A:Residues: 1-688 <KUS>
A:Cross-references: GB:M18767; NID:g179645; PIDN:AAA51852.1; PID:g179646
R:Tosi, M.; Duponchel, C.; Meo, T.; Jullier, C.
Biochemistry 26, 8516-8524, 1987
A:Title: Complete cDNA sequence of human complement C1s and close physical linkage of the
A:Reference number: A27381; MUID:88163522; PMID:2831944
A:Accession: A27381
A:Molecule type: mRNA
A:Residues: 1-688 <TOS>
A:Cross-references: GB:M18767; NID:g179647; PIDN:AAA51853.1; PID:g179648
R:MacKinnon, C.M.; Carter, P.B.; Smyth, S.J.; Dunbar, B.; Fothergill, J.E.
Eur. J. Biochem. 169, 547-553, 1987
A:Title: Molecular cloning of cDNA for human complement component C1s. The complete amin
A:Reference number: S00224; MUID:88082788; PMID:3500856
A:Accession: S00224
A:Molecule type: mRNA
A:Residues: 1-688 <MAC>
A:Cross-references: EMBL:X06596; NID:g29542; PIDN:CAA29817.1; PID:g763110
A:Accession: S26732
A:Molecule type: Protein
A:Residues: 16-38;68-116;170-236;246-262;265-280;282-284;287-308;315-363;384-394;421-435
R:Tosi, M.; Duponchel, C.; Meo, T.; Couture-Tosi, E.
J. Mol. Biol. 208, 709-714, 1989
A:Title: Complement genes C1r and C1s feature an intronless serine protease domain close
A:Reference number: S05634; MUID:90040704; PMID:2553984
A:Accession: S05634
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 356-513 'G', 514-688 <TOS>
R:Carter, P.B.; Dunbar, B.; Fothergill, J.E.
Biochem. J. 215, 565-571, 1983
A:Title: The serine proteinase chain of human complement component C1s. Cyanogen bromide
A:Reference number: A05140; MUID:84104122; PMID:6362661
A:Accession: A05140
A:Molecule type: protein
A:Residues: 438-483 'X', 485-500;503-534;542-558;561-572 'A', 574-601;617-623;626-644;647-
R:Spycher, S.E.; Nick, H.; Rickli, E.B.

```


OY 295 GGPGLIN-----GHAK--I 307
|||
:
Db 254 GPFGPLNLETKSNALDIIFOTDLTGQKGWKLRYHGDPMPCPKEDTPNSWEPAKAAYVF 313
|||
:
OY 308 GTVVAFPPCNNSV-YLSSG-----NEKRTCOONGESMGK----OPICIMACEPRKSIDLVR 357
|||
:
Db 314 RDVOQTCLLDGEVEEGRVGATSFYSTCGSNGMSNSKKCPF---DGGIP----- 362
|||
:
OY 358 RVLPMQVOSRETRPHQLYSAAFSKQKLGSAFTKKP-ALPEGDLPMGYOHLHTLOLEYCIS 416
:::
:
Db 363 -----ESIENGKVDEPSTLLGSV-----IRYCEE 388
:
:
OY 417 PFY--RLIGSSRRCTLRGKMSGRA-----PSCIPICGKIENITAPTKOGLRMPWOAIY 469
|||
:
Cd 389 PYYVMENGGGEGHYHCAGSGSWMEVLGAPELLFKCVPGV-----VP-----REPFEER- 435
|||
:
OY 470 RTSGVTHQSJLKGMGFVY-----CSGAVNETTVVAACVTMDLGVMTIKTADLKVYL 524
|||
:
Db 436 QGITGSDDIDKNFPQQVFPDPNPAGCALINEXHWLVLAHVHGNNRPPTM-----YV 487
|||
:
OY 525 GKFRVDDRDEKTIOSLQISAIIHPNYDPLL-----DAIDAILDKLARKISTRVQ 577
|||
:
Db 488 GSTSVQTSRLAAS-KMLTEPHFIHPGWKLELPBGRNTDNIDIALVRLDPMVCMGPTVS 546
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:
Db 547 PICLTGSTSDYNIMDGDLGISWG-----RTE--KRDRVRLKAARLPVALRKCKEVK 599
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OY 635 EDHGIPVS-----VTDMNFCAEMPTAPSDTICTATGTGIAIVSPFRASBERPMHLMGL 688
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:
Db 600 VEK--FLTDAAEAAYVFPPNMICAGE--KGMDSCKSGGFAVQDP---NDKTFYAAGL 652
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:
OY 689 VSMXYDKTCSHRLSTAFTKYLFPFKDWERNNMK 720
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:
Db 653 VSWG--POCG--TYGLYTTRYKXNVDMINKTMQ 680
|||
:

RESULT 10
A56318
enteropeptidase (EC 3.4.21.9) precursor [validated] - human
N/Aternate names: enterokinase
C/Species: Homo sapiens (man)
C/cdate: 19-May-1995 #sequence__revision 09-Aug-1996 #text_change 09-Jul-2004
C/accession: A56318; B43090
R/Kitamotoo, Y.; Veille, R.A.; Donis-Keller, H.; Sadler, J.E.
Biochemistry 34, 4562-4568, 1995
A/RTitle: cDNA sequence and chromosomal localization of human enterokinase, the proteolytic
A/Reference number: A56318; NUID:95234679; PMID:7718557
A/Accession: A56318
A/Molecule type: mRNA
A/Residues: 1-1019 <KIT>
A/Cross-references: UNIPROT:P98073; GB:U09860; NID:g746412; PID:NACC50138.1; PID:g746413
R/Kitamotoo, Y.; Yuan, X.; Wu, Q.; McCourt, D.W.; Sadler, J.E.
Proc. Natl. Acad. Sci. U.S.A. 91, 7588-7592, 1994
A/RTitle: Enterokinase, the initiator of intestinal digestion, is a mosaic proclease composed
A/Reference number: A43090; NUID:94329561; PMID:8052624
A/Accession: B43090
A>Status: nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 749-1019 <KIT>
A/Cross-references: GB:U09860
C/Comment: The mechanism of association with the membrane of the intestinal brush border
coated below) or with amino-terminal myristoylation of the heavy chain.
C/Genetics:
A/Gene: GDB:PRS7
A/Cross-references: GDB:384083; OMIM:226200
A/Map position: 21q21-21q21
C/Complex: Mature enteropeptidase is variously reported to contain two (heavy and light)
chain by a disulfide bond. Possibly, conversion from membrane-bound to soluble forms involve
cleavage.

protein C (activated) (EC 3.4.21.69) precursor - mouse
 UniProt accession: P3J387; GI:10445; NID:9220385; PID:BA01235.1; PID:9220386
 N/Alternate names: vitamin K-dependent serine proteinase
 C/Species: Mus musculus (house mouse)
 C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C/Accession: JX0210
 R/Author: N.; Sato, M.; Tsujimura, A.; Iwase, R.; Hashimoto-Gotoh, T.
 J. Biochem. 111, 491-495, 1992
 A/Title: Isolation and characterization of a mouse protein C cDNA.
 A/Reference number: JX0210; MUID:92316897; PMID:1618739
 A/Accession: JX0210
 A/Molecule type: mRNA
 A/Residues: 1-461 <TAD>
 A/Cross-references: UNIPROT:P3J387; GI:10445; NID:9220385; PID:BA01235.1; PID:9220386
 A/Experimental source: liver
 C/Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that re-
 8.
 C/Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 C/Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutamate
 F/1-33/Domain: signal sequence #status predicted <SIG>
 F/127-85/Domain: Gla domain homology <GLA>
 F/334-41/Domain: propeptide #status predicted <PRO>
 F/442-196,199-461/Product: protein C #status predicted <PRC>
 F/442-196/Domain: light chain #status predicted <PCL>
 F/91-130/Domain: EGF homology <EG1>
 F/139-174/Domain: EGF homology <EG2>
 F/199-461/Domain: heavy chain #status predicted <PCH>
 F/199-211/Domain: activation peptide #status predicted <ACT>
 F/212-461/Product: vitamin K-dependent serine proteinase #status predicted <VIT>
 F/212-445/Domain: trypsin homology <TRY>
 F/447/48,55,57,60,61,66,67,70,76/Modified site: gamma-carboxylglutamic acid (Glu) #status
 F/117/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
 F/121-130,139-150,146-151,161-174,182-219,238-254,373-387,398-426/Disulfide bonds: #status
 F/212,230,355/binding site: carbohydrate (Asn) (covalent) #status predicted
 F/253,299,402/Active site: His, Asp, Ser #status predicted

Query Match 8.1%; Score 320; DB 1; Length 461;
 Best Local Similarity 23.9%; Pred. No. 6e-14;
 Matches 145; Conservative 70; Mismatches 174; Indels 218; Gaps 29;

QY	152	WTI-----HAKRGF-----	V I Q L R F V M L S L E P D Y M C O Y D V E V R D G R D G Q I I K R V	198
DB	14	WGISSTPHHPDPVSSSSHAHQVLKVRANSEFL-----	E M R P G - S L E R C H E E I	62
QY	199	CGNERPAP I -QSIGSSHLVLFPHSDGSKNPFDFHAIYEEITACSSPCHDTCVLADKAS	257	
DB	63	CDPEBAQGI PQNVEDTLAFWI-----	K Y F D D Q C S A P P L D H Q C S P C C G H G T C I - D G I G S	116
QY	258	YKCACTAGYTGRCENLLEERNCSDPGSPVNGYKITGGPGL-----	I N G R H A K I G T V	311
DB	117	FSCSCDCKMEGKFCQQLERFPDC-----	R V N N G G C L H Y C L E E S N G R C A - - - -	160
QY	312	SFFCNKSVVLSGNER-----	T C Q N G E W S G K P I C I K A C R E P K I S D V Y R R V L P M Q V	364
DB	161	---CAPGELDDDHMRCKSVTFPCGKLGRIE K-----	K R K I L - - - - -	196
QY	365	QSRETPHLQLYSAFSSKOKLSAPTKKPALPFGDLPDMGYQHILHTQLYECISPYRRLLGS	424	
DB	197	-KRQIDL-----	E D E L E R P D - - - - -	210
QY	425	SRRTCLRTGKMGSRAPSCPIPGCKIENTAPRTQGLRPMQAOAIYRRTSGVHDSGLHKA	484	
DB	211	-----	R I V N G T L R K - Q G - D S P M Q A I L L - - - - -	235
QY	485	WFLVSGSLVNERTVVAACHVTDLGKVTMKITADLKVLVGLKFRDDEKRTQSLQIS	544	
DB	236	--LACGGVLHRTSWLTAHCEGTGKLT-----	V R L G E Y - D L R R R H W E L D I K	283
QY	545	AIILHPNDPILTLADIAILKLLDKARISTRVOPICL-----	A A S R D I S T S F Q E S H I T V A G	600
DB	284	EIVHPNTRRSSDDIDALLRLRAQPAITSLKTIIVPICLPNNGLAQDELTLQAQGEIVVT--G	341	
QY	601	WNLVDVRSPEGKNDTL-----	R S G V S V V D S Y L L C E Q H E D H G I P V S Y T D N M F C	649

[illegible]

A/Cross-references: UNIPROT:Q9JUI7; DDBJ:AB049189

A/Experimental source: strain Male, 7-week-old

R/Satom, S.; Yamasaki, Y.; Tazuki, S.; Hitomi, Y.; Iwanaga, T.; Fushiki, T.

Biochem. Biophys. Res. Commun. 287, 995-1002, 2001

A/Title: A role for membrane-type serine protease (MT-Sp1) in intestinal epithelial turn

A/Reference number: JC7775; PMID:11573963

A/Contents: Small intestine

A/Accession: JC7775

A/Molecule type: mRNA

A/Reads: 1-855 <SAT>

A/Cross-references: DDBJ:AB037898

C/Comment: This enzyme, an epithelial-derived, type II integral membrane serine protease of specific proteins or peptides on the brushborder membranes. It also participates in 11a1 migration and/or cell loss.

C/Genetics:

A/Genes: mt-spl

A/Map position: basolateral cell surface

C/Superfamily: membrane-bound arginine-specific serine proteinase

C/Keywords: protein digestion

Query Match 7.9%; Score 313; DB 2; Length 855;

Best Local Similarity 21.4%; Pred. No. 3.4e-13;

Matches 151; Conservative 78; Mismatches 227; Indels 250; Gaps 33;

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QY 82 HPG--CTIFENCKSCRNQSGTLDPFYKGYCAECRAGWYGDCKRCQVLAAPKQI 139
DB 324 HPGFATFFQLPKM---SSCGGLSE--AQTFSSP---YYPG----- 358
QY 140 LLESYPLNANCEWTIHAKEGVVQLRFVMSLEFDY---CQDYVEVRDGNRQGIT 195
DB 359 ---HYPPNICTWNKIKVNNNNVAKRFELFYLVDPNIPVSGCTKDYVEING----- 406
QY 196 KRVGNERPAPIQISLSHLFHSDSKNDGFHAYEETACSSSP-----FHDGTC 250
DB 407 EKFCGERSQFVSSNSKITVHFSDHSYDTGTFLAEY--LSYSDNDCPMFMCKTGRC 464
QY 251 VL-----DKAGSYKACLAGY---TGRCENLY-----ERNCS 281
DB 465 IRKDLRCGDGADCDYDERHRCNATHQFCKKQFCKPLFWCDSDVNDGDSDESGS 524
QY 282 DPGGPNVGYOKITGGFGLINGRAKIGTVASFCCNSYVL---SGNEKTCQONGEMSG 337
DB 525 CPAG-----SFKCSNGKCLPQSQQCNGKDCDGDSDSAS 558
QY 338 KQPCICAKREPKSDLVRRRVLPQVQSRTPHQLYSAFQKXKQASAPTKKPLPFG 397
DB 559 CDVNAVSC----- 567
QY 398 DLPWGYOHLHTQYECISPEYRLGSSRRCTLRGKMGRAPEICPICIKENITAPKT 457
DB 568 -----TKYTYRC-----QNGCLANKN-----PBC--DGKDCSDGSDE 599
QY 458 Q---GLR-----WPMQAIYRTSGVHDSGLHKGAMFLVCSGALVN 495
DB 600 KNCDCGLRSFTQARVVGTVNADGEWPMQVSLHALGQ-----H-----LCGASLIS 647
QY 496 ERTVVAACHCTDGLKTYMTIAD---LKVVLGKPYRDDDEKTIOSLQISAILLHPNY 552
DB 648 PDWLVSAAHCPQD---ETIFKYSHTWTAFGL--LLDOSKRSASAGVQEHKLRITHPSP 703
QY 553 DPILLDDADIALIKLLDKARISTRVOPICIASRDLSTSPQESHITVAGMNVLAIVRSPGF 612
DB 704 NDFPFDDIALLELEKPAEYISTVVRPICLPDNTHTVPAGKA--IWTGWM---GHTKEGGT 758
QY 613 KNDTLRSGVSVVDSLCEQHEHDGIPVSVTDNMFCASWEPTAPSDICTAETGG-IAAV 671
DB 759 GALLIGKEIRVINGTCEEL---LPQGITPRMVCVGF--LSGGVDSQCGDSGGLPSV 812
QY 672 SFPRASPEPRNMLMGLVMSYDKTCSRLST-AFTKVLPRKDWIE 716
DB 813 EKDGRI-----FQAGVWSG--EGCAQRNKPQVTRIPVTRDVIK 850
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Job time : 55 secs

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: July 12, 2005, 17:08:16 ; Search time 173 Seconds
(without alignments)
2131.197 Million cell updates/sec

Title: US-10-063-546-38

Perfect score: 3945
Sequence: 1 MEIGCWTLQTLFLLQLLLIS.....LSTAFKVLFPKDIERNMK 720

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 1500 summaries

Database : UniProt_03:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	3945	100.0	2 O6UXH9	O6UXH9 homo sapien
2	3936	99.8	2 O6N062	O6N062 homo sapien
3	3921.5	99.4	2 O96JW2	O96JW2 homo sapien
4	3612	91.6	2 O8BU25	O8BU25 m mus muscu
5	3612	91.6	2 O8K2B8	O8K2B8 mus muscu
6	2823	71.6	2 O6DIV5	O6DIV5 xenopus tro
7	2059	52.2	2 O71RE9	O71RE9 homo sapien
8	949	24.1	2 O9Y432	O9Y432 homo sapien
9	678	17.2	2 O8T981	O8T981 tachypleus
10	672	17.0	1 LFC_TACTR	LFC_TACTR
11	665	16.9	1 LFC_CARRO	LFC_CARRO
12	665	15.4	2 O26423	O26423 carcinoscor
13	608.5	15.4	2 O868H7	O868H7 branchiosto
14	604	15.3	2 O868H5	O868H5 branchiosto
15	597	15.1	2 O868H6	O868H6 branchiosto
16	576.5	14.6	2 O868H4	O868H4 branchiosto
17	507.5	12.9	2 O6GPF9	O6GPF9 xenopus lae
18	490.5	12.4	2 O6Q1O8	O6Q1O8 gallus gall
19	489.5	12.4	2 O9PU17	O9PU17 xenopus lae
20	483	12.2	2 O9JIS9	O9JIS9 rattus norv
21	482.5	12.2	2 O8CHN8	O8CHN8 rattus norv
22	482	12.2	2 O8AXR1	O8AXR1 xenopus lae
23	478	12.1	1 CRAR_HUMAN	CRAR_HUMAN
24	475	12.0	1 CRAR_MOUSE	CRAR_MOUSE
25	468	11.9	2 O96RS4	O96RS4 mus musculu
26	467	11.8	2 O8CG43	O8CG43 rattus norv
27	466	11.8	2 O8AXR0	O8AXR0 xenopus lae
28	459	11.6	2 O8CD27	O8CD27 mus musculu
29	457	11.6	2 O9PVY2	O9PVY2 triakis ecy
30	452	11.5	2 O920S0	O920S0 mus musculu
31	448	11.4	2 O9PVY3	O9PVY3 cyprinus ca

32	447	11.3	2 O6Q1O9	O6Q1O9 gallus gall
33	436.5	11.1	2 O7CT70	O7CT70 lampetra ja
34	428	10.8	1 C1R_MOUSE	C1R_MOUSE
35	424	10.7	2 O9JIS8	O9JIS8 rattus norv
36	421.5	10.7	2 O9PVY4	O9PVY4 xenopus lae
37	420	10.6	2 O9QX84	O9QX84 rattus norv
38	417	10.6	2 O91MP0	O91MP0 mus musculu
39	416.5	10.6	2 O8CFG9	O8CFG9 mus musculu
40	412	10.4	2 O923J8	O923J8 mus musculu
41	403.5	10.2	1 C1R_HUMAN	C1R_HUMAN
42	401.5	10.2	2 O8CHP7	O8CHP7 cavia porce
43	401.5	10.2	2 O81ND8	O81ND8 halocynthia
44	400.5	10.2	2 O01654	O01654 halocynthia
45	400.5	10.2	2 O9DGC2	O9DGC2 cyprinus ca
46	398.5	10.1	2 O7ZT69	O7ZT69 lampetra ja
47	395	10.0	2 O8CRG8	O8CRG8 mus musculu
48	384	9.7	2 O01655	O01655 halocynthia
49	382.5	9.7	2 O8AW90	O8AW90 lampetra ja
50	382	9.7	2 O9PS25	O9PS25 sus scrofa
51	381	9.7	2 O69DK8	O69DK8 sus scrofa
52	380.5	9.6	2 O9DGC1	O9DGC1 cyprinus ca
53	378.5	9.6	2 O9DGC1	O9DGC1 cyprinus ca
54	376	9.5	2 O9JIB3	O9JIB3 rattus norv
55	372.5	9.4	2 O81AD7	O81AD7 halocynthia
56	371.5	9.4	2 O9QX90	O9QX90 rattus norv
57	370	9.4	2 O8CG14	O8CG14 mus musculu
58	369	9.4	2 O8BJC4	O8BJC4 mus musculu
59	368	9.3	2 O9DGC1	O9DGC1 cyprinus ca
60	366	9.3	2 O9DGC0	O9DGC0 cyprinus ca
61	364	9.2	2 O8CH28	O8CH28 mus musculu
62	364	9.2	2 O8VBV4	O8VBV4 mus musculu
63	357	9.0	2 O6DUJ6	O6DUJ6 cyprinus ca
64	354	9.0	2 O91674	O91674 xenopus lae
65	342	8.7	2 O8R099	O8R099 mus musculu
66	340.5	8.6	2 O70542	O70542 rattus norv
67	340.5	8.6	2 O6PET1	O6PET1 rattus norv
68	339.5	8.6	2 O70W31	O70W31 oncorhynch
69	335	8.5	2 O7PY92	O7PY92 anopheles g
70	335	8.5	2 O69BL0	O69BL0 manduca sex
71	334	8.5	2 O8AYE4	O8AYE4 brachydanio
72	334	8.5	2 C1S_HUMAN	C1S_HUMAN
73	331.5	8.4	1 ENTX_HUMAN	ENTX_HUMAN
74	330.5	8.4	1 ENTX_PIG	ENTX_PIG
75	329.5	8.4	1 CSM1_HUMAN	CSM1_HUMAN
76	329	8.3	1 CSM1_MOUSE	CSM1_MOUSE
77	328	8.3	1 ST14_HUMAN	ST14_HUMAN
78	318	8.1	1 CSM2_HUMAN	CSM2_HUMAN
79	317.5	8.0	1 ENTX_BOVIN	ENTX_BOVIN
80	316.5	8.0	1 PRTC_MOUSE	PRTC_MOUSE
81	315	8.0	1 FA10_RABIT	FA10_RABIT
82	314.5	8.0	1 ST14_MOUSE	ST14_MOUSE
83	314	8.0	1 C1S_HUMAN	C1S_HUMAN
84	313	7.9	2 O9JUI7	O9JUI7
85	311	7.9	1 FA7_RAT	FA7_RAT
86	310.5	7.9	2 O7T3B6	O7T3B6
87	310.5	7.9	1 PRTC_HUMAN	PRTC_HUMAN
88	309.5	7.8	2 O6PF94	O6PF94 mus musculu
89	309.5	7.8	1 TMS6_MOUSE	TMS6_MOUSE
90	305	7.7	1 PRTC_CANFA	PRTC_CANFA
91	304	7.7	1 ENTX_MOUSE	ENTX_MOUSE
92	302.5	7.7	1 FA7_MOUSE	FA7_MOUSE
93	301.5	7.6	2 O8JHD0	O8JHD0 brachydanio
94	300.5	7.6	2 O6T1T0	O6T1T0
95	299.5	7.6	2 O6T1O9	O6T1O9 pseudonaja
96	299	7.6	2 O80YN4	O80YN4 rattus norv
97	298.5	7.6	2 O90YK1	O90YK1 brachydanio
98	298.5	7.6	2 O6P7I9	O6P7I9 xenopus lae
99	297.5	7.5	2 O9BU99	O9BU99 homo sapien
100	297.5	7.5	2 O8CAN9	O8CAN9 mus musculu
101	297	7.5	1 PRTC_PIG	PRTC_PIG
102	296	7.5	1 PRTC_RABIT	PRTC_RABIT
103	295.5	7.5	2 O8CIR9	O8CIR9 mus musculu
104	295.5	7.5	2 O804X2	O804X2 fugu rubrip

105	295	7.5	425	2	Q804X7	Q804X7 gallus gall	178	263	6.7	553	2	Q8VCS4	Q8VCS4 mus musculus
106	294	7.5	461	2	Q68FY8	Q68FY8 rattus norv	179	262.5	6.7	300	2	Q81P94	Q81P94 mus musculus
107	293.5	7.4	407	1	FA7_BOVIN	P22457 bos taurus	180	262.5	6.7	461	1	FA9_HUMAN	P00740 homo sapien
108	293	7.4	430	2	Q804X0	Q804X0 figu rubrip	181	262.5	6.7	461	1	FA9_PANTR	Q95n67 pan troglod
109	292	7.4	461	1	PRTC_RAT	P31394 rattus norv	182	262.5	6.7	1042	1	CORI_HUMAN	Q95n65 homo sapien
110	291.5	7.4	390	2	Q69DJ3	Q69DJ3 sus scrofa	183	262	6.6	477	1	URRT_DESRO	P15638 desmodus ro
111	291	7.4	376	1	FA10_TROCA	P81428 tropidechis	184	261.5	6.6	284	2	Q8aX08	Q8aX08 xenopus lae
112	291	7.4	475	1	Q804W9	Q804W9 figu rubrip	185	261.5	6.6	442	1	UROK_PIG	P04155 sus scrofa
113	289.5	7.3	466	2	Q6SA95	Q6SA95 felis silve	186	261.5	6.6	551	2	Q7QDT9	Q7QDT9 homo sapien
114	288.5	7.3	802	2	Q6UXD8	Q6UXD8 homo sapien	187	261	6.6	431	1	UROK_HUMAN	P00749 homo sapien
115	287.5	7.3	811	1	TMS6_HUMAN	Q81u80 homo sapien	188	260.5	6.6	433	1	UROK_BOVIN	Q95589 bos taurus
116	285.5	7.2	300	2	Q7P2D2	Q7P2D2 mus musculus	189	260.5	6.6	254	2	Q9EQZ8	Q9EQZ8 rattus norv
117	285.5	7.2	452	1	FA9_CANFA	P18540 canis famli	190	260.5	6.6	456	2	Q7TT43	Q7TT43 mus musculus
118	285	7.2	504	2	Q6PGW7	Q6PGW7 brachydanio	191	260.5	6.6	452	2	Q6PAG2	Q6PAG2 xenopus lae
119	284	7.2	432	2	Q6GNM2	Q6GNM2 xenopus lae	192	259	6.6	245	1	CTRB_GADMO	P80646 gadus morhu
120	284	7.2	974	2	Q9OWD8	Q9OWD8 bufo japoni	193	259	6.6	416	1	FA9_BOVIN	P00741 bos taurus
121	283.5	7.2	482	1	FA10_RAT	Q63207 rattus norv	194	259	6.6	474	2	Q8JHC8	Q8JHC8 brachydanio
122	283.5	7.2	589	2	Q6PBJ5	Q6PBJ5 homo sapien	195	259	6.6	581	2	Q9XZM7	Q9XZM7 strongyloce
123	283	7.2	376	1	FA10_HOPST	P83370 hoplocephal	196	258.5	6.6	683	2	Q8MRH5	Q8MRH5 drosophila
124	282.5	7.2	320	2	Q6CIR7	Q6CIR7 rattus norv	197	258.5	6.6	786	1	STUB_DROME	Q05319 drosophila
125	282	7.1	456	1	PRTC_BOVIN	Q9MD9 ornithorhyn	198	258.5	6.6	787	2	Q9VEY6	Q9VEY6 drosophila
126	282	7.1	469	2	Q9GMD9	Q9GMD9 ornithorhyn	199	258	6.5	263	2	Q9PWQ6	Q9PWQ6 gadus morhu
127	282	7.1	1466	2	Q6GKX4	Q6GKX4 xenopus lae	200	258	6.5	433	1	UROK_PAPCY	P16227 papio cynoc
128	281.5	7.1	476	2	Q6L7I1	Q6L7I1 rattus norv	201	258	6.5	545	2	Q7OKS0	Q7OKS0 anopheles g
129	281.5	7.1	558	2	Q6L7I1	Q6L7I1 rattus norv	202	258	6.5	612	2	Q804W7	Q804W7 figu rubrip
130	281	7.1	481	1	FA10_MOUSE	Q88947 mus musculu	203	257.5	6.5	1004	2	P79953	P79953 xenopus lae
131	281	7.1	492	1	FA10_BOVIN	P00743 bos taurus	204	257	6.5	568	2	Q7Q8L2	Q7Q8L2 anopheles g
132	280.5	7.1	264	1	CTRL_HUMAN	P40313 homo sapien	205	256.5	6.5	254	2	Q9D7P8	Q9D7P8 mus musculus
133	280.5	7.1	269	2	Q8IUM0	Q8IUM0 homo sapien	206	256.5	6.5	254	2	Q9EROS	Q9EROS mus musculus
134	280	7.1	562	1	TPA_HUMAN	P00750 homo sapien	207	255.5	6.5	268	2	Q64ZS8	Q64ZS8 xenopus tro
135	278.5	7.1	466	1	FA7_HUMAN	P08709 homo sapien	208	255.5	6.5	753	2	Q31430	Q31430 lampetra ja
136	278.5	7.1	824	2	Q6ICC2	Q6ICC2 homo sapien	209	255	6.5	325	2	Q15944	Q15944 sarcophaga
137	278	7.0	408	2	Q9VW19	Q9VW19 drosophila	210	255	6.5	845	2	Q6GRS4	Q6GRS4 xenopus lae
138	278	7.0	433	2	Q804X5	Q804X5 gallus gall	211	254.5	6.5	315	2	Q7TT44	Q7TT44 mus musculus
139	278	7.0	488	1	FA10_HUMAN	P00742 homo sapien	212	254.5	6.5	374	2	Q7OCC5	Q7OCC5 anopheles g
140	278	7.0	1113	1	CORI_MOUSE	Q93319 mus musculu	213	254.5	6.5	461	2	Q95ND6	Q95ND6 pan troglod
141	277	7.0	539	1	TPA_RAT	P19637 rattus norv	214	254	6.4	314	2	Q9VR15	Q9VR15 drosophila
142	276.5	7.0	655	1	HGFA_HUMAN	Q04756 homo sapien	215	254	6.4	617	1	THRB_RAT	P18232 rattus norv
143	276.5	7.0	679	2	Q96PQ8	Q96PQ8 homo sapien	216	253.5	6.4	487	2	Q9NZP8	Q9NZP8 homo sapien
144	276	7.0	559	2	Q6P7U0	Q6P7U0 mus musculu	217	253.5	6.4	618	2	Q6GNK4	Q6GNK4 xenopus lae
145	275.5	7.0	1134	2	Q7RTY7	Q7RTY7 homo sapien	218	253.5	6.4	628	2	Q9VER6	Q9VER6 drosophila
146	274.5	7.0	625	1	THRB_BOVIN	P00735 bos taurus	219	253	6.4	471	2	Q804X6	Q804X6 gallus gall
147	274.5	7.0	654	2	Q6ONF4	Q6ONF4 canis famli	220	253	6.4	616	2	Q97507	Q97507 sus scrofa
148	274.5	7.0	1235	2	Q659T9	Q659T9 clona intes	221	253	6.4	1070	2	P91972	P91972 aplysia cal
149	274.5	7.0	3670	1	CHMC3_HUMAN	Q72407 homo sapien	222	252	6.4	260	2	Q6P2V9	Q6P2V9 xenopus tro
150	273.5	6.9	443	1	Q8JHC3	Q8JHC3 brachydanio	223	252	6.4	261	2	Q66HW9	Q66HW9 brachydanio
151	273.5	6.9	517	2	Q8K0D2	Q8K0D2 mus musculu	224	252	6.4	607	2	Q6DFJ5	Q6DFJ5 xenopus lae
152	273.5	6.9	566	1	TPA_BOVIN	Q82198 bos taurus	225	251.5	6.4	261	2	Q7PC94	Q7PC94 anopheles g
153	273	6.9	366	2	Q9QX85	Q9QX85 rattus norv	226	251	6.4	295	2	Q8CIP7	Q8CIP7 rattus norv
154	273	6.9	560	2	Q14520	Q14520 homo sapien	227	251	6.4	537	2	Q804W8	Q804W8 figu rubrip
155	273	6.9	2796	1	CSM3_MOUSE	Q80C79 mus musculu	228	250.5	6.3	347	1	HPT_RABIT	P19007 oryctolagus
156	272.5	6.9	321	2	Q6WZL2	Q6WZL2 homo sapien	229	250	6.3	306	1	BSS4_MOUSE	Q9ER10 mus musculu
157	271.5	6.9	244	1	KLKE_HUMAN	Q92876 homo sapien	230	250	6.3	562	2	Q8S0Z3	Q8S0Z3 sus scrofa
158	271.5	6.9	461	2	Q6IEE4	Q6IEE4 rattus norv	231	250	6.3	845	2	Q63Z06	Q63Z06 xenopus lae
159	271	6.9	433	2	Q8MHY7	Q8MHY7 oryctolagus	232	250	6.3	1379	2	Q9V4N6	Q9V4N6 drosophila
160	271	6.9	433	2	Q8MHY7	Q8MHY7 oryctolagus	233	250	6.3	1397	2	Q7KQO9	Q7KQO9 drosophila
161	270	6.8	559	1	TPA_MOUSE	P11214 mus musculu	234	249.5	6.3	400	2	Q27081	Q27081 cachypleus
162	270	6.8	477	1	URRT_DESRO	P98119 desmodus ro	235	249.5	6.3	875	1	NETR_HUMAN	P56730 homo sapien
163	270	6.8	490	1	FA10_RABIT	Q19045 oryctolagus	236	249	6.3	263	2	Q6GPI1	Q6GPI1 homo sapien
164	269	6.8	261	2	Q6DH05	Q6DH05 brachydanio	237	249	6.3	263	2	Q9CRJ5	Q9CRJ5 m mus muscu
165	269	6.8	643	2	Q97506	Q97506 sus scrofa	238	248.5	6.3	459	1	FA9_MOUSE	P16234 mus musculu
166	269	6.8	833	2	Q96442	Q96442 strongyloce	239	248.5	6.3	645	2	Q7PWE4	Q7PWE4 anopheles g
167	267.5	6.8	268	2	Q6G0E9	Q6G0E9 xenopus lae	240	248.5	6.3	1135	2	Q7QI37	Q7QI37 anopheles g
168	267	6.8	339	2	Q9QX91	Q9QX91 rattus norv	241	248	6.3	259	2	Q6AZC2	Q6AZC2 brachydanio
169	267	6.8	455	2	Q7SY86	Q7SY86 xenopus lae	242	248	6.3	261	2	Q9W7O4	Q9W7O4 paralichthy
170	267	6.8	868	2	Q9Y1V3	Q9Y1V3 polyanthroca	243	248	6.3	263	1	CTRB_HUMAN	P17538 homo sapien
171	266	6.7	352	2	Q7KVM3	Q7KVM3 drosophila	244	248	6.3	340	2	Q800T7	Q800T7 meleagris g
172	265.5	6.7	250	2	Q9V514	Q9V514 drosophila	245	248	6.3	638	1	KAL_HUMAN	P03952 homo sapien
173	264.5	6.7	431	1	URTB_DESRO	P98121 desmodus ro	246	248	6.3	764	1	CFAB_PANTR	Q86440 pan troglod
174	264.5	6.7	618	1	THRB_MOUSE	P19221 mus musculu	247	248	6.3	775	2	Q6P550	Q6P550 mus musculu
175	264	6.7	653	1	HGFA_MOUSE	Q97098 mus musculu	248	248	6.3	991	2	Q6N7M2	Q6N7M2 mus musculu
176	263.5	6.7	263	2	Q7SX97	Q7SX97 brachydanio	249	247.5	6.3	307	2	Q7TKM0	Q7TKM0 mus musculu
177	263	6.7	270	2	Q7QI44	Q7QI44 anopheles g	250	247.5	6.3	311	2	Q9W2C2	Q9W2C2 drosophila

251	247.5	6.3	991	1	BMP1_MOUSE	P98063	mus musculus	324	237.5	6.0	415	2	Q7PY21	Q7PY21	anopheles g
252	247	6.3	235	2	Q28731	Q28731	oryctolagus	325	237.5	6.0	735	2	O57381	O57381	xenopus lae
253	247	6.3	270	2	Q7PK67	Q7PK67	anopheles g	326	237.5	6.0	735	2	O66K13	O66K13	xenopus lae
254	247	6.3	275	1	TRYT_CANFA	P15944	canis famli	327	237.5	6.0	810	1	PLMN_ERIEU	Q29485	eritaceus e
255	247	6.3	364	2	Q917V4	Q917V4	drosoophila	328	237	6.0	237	2	O91515	O91515	fugu rubrip
256	247	6.3	366	2	Q81924	Q81924	domlyx mori	329	237	6.0	263	1	CTRB_RAT	P07338	rattus norv
257	247	6.3	764	1	CFAB_HUMAN	P00751	homo sapien	330	237	6.0	263	2	O6P6S4	O6P6S4	xenopus lae
258	247	6.3	966	1	BMP1_HUMAN	P13497	homo sapien	331	236.5	6.0	251	2	O7Q9W2	Q7Q9W2	anopheles g
259	246.5	6.2	235	2	Q90387	Q90387	cynops pyr	332	236.5	6.0	274	1	MCTE_RAT	P50343	rattus norv
260	246.5	6.2	264	2	Q9D960	Q9D960	mus musculu	333	236.5	6.0	707	1	BMP1_XENLA	P98070	xenopus lae
261	246.5	6.2	297	2	Q88781	Q88781	rattus ratt	334	236.5	6.0	761	2	O99JCB	Q99JCB	rattus norv
262	246.5	6.2	323	2	Q960C4	Q960C4	homo sapien	335	236.5	6.0	1013	2	O62381	O62381	mus musculu
263	246.5	6.2	347	1	HPT_ATEGE	P50417	ateles geof	336	236	6.0	239	2	Q7Q057	Q7Q057	anopheles g
264	246.5	6.2	622	1	THRB_HUMAN	P00734	homo sapien	337	236	6.0	812	1	PLMN_MOUSE	P20918	mus musculu
265	246.5	6.2	622	2	Q727B3	Q727B3	homo sapien	338	235.5	6.0	260	2	O9W7Q3	Q9W7Q3	paralichthy
266	246	6.2	243	2	Q7PK66	Q7PK66	anopheles g	339	235.5	6.0	369	2	O6AXZ6	O6AXZ6	rattus norv
267	246	6.2	263	2	Q9D8X8	Q9D8X8	mus musculu	340	235.5	6.0	453	2	O812A6	O812A6	mus musculu
268	246	6.2	764	1	CFAB_GORGO	Q864V9	gorilla gor	341	235	6.0	270	1	TRIT_MERUN	P50342	meriones un
269	246	6.2	812	1	PLMN_BOVIN	P06868	bos taurus	342	235	6.0	336	2	Q7RTY5	Q7RTY5	homo sapien
270	245.5	6.2	255	2	Q804G1	Q804G1	brachydanio	343	235	6.0	345	2	O28800	Q28800	pan troglod
271	245.5	6.2	369	2	Q7OKL1	Q7OKL1	anopheles g	344	235	6.0	524	2	O7SXH8	Q7SXH8	brachydanio
272	245.5	6.2	467	2	Q967X8	Q967X8	panilius a	345	235	6.0	812	1	PLMN_RAT	Q01177	rattus norv
273	245	6.2	248	2	Q7PK68	Q7PK68	anopheles g	346	235	6.0	1430	1	APOA_MACMU	P14417	macaca mula
274	245	6.2	263	2	Q6GNF7	Q6GNF7	xenopus lae	347	234.5	5.9	335	2	O9BZM1	Q9BZM1	homo sapien
275	245	6.2	638	2	Q8R0P5	Q8R0P5	mus musculu	348	234.5	5.9	453	1	TMS3_MOUSE	O6NP02	mus musculu
276	245	6.2	639	1	BMPH_STRPU	P98069	strongyloca	349	234.5	5.9	489	2	O7Q432	Q7Q432	anopheles g
277	244.5	6.2	608	2	Q9PTM7	Q9PTM7	strophio ca	350	234.5	5.9	624	2	O9DPA3	Q9DPA3	mus musculu
278	244	6.2	263	2	Q9DC66	Q9DC66	mus musculu	351	234.5	5.9	575	2	O9DPA3	Q9DPA3	mus musculu
279	244	6.2	322	2	Q920S2	Q920S2	mus musculu	352	234	5.9	253	1	CTRA_GADMO	P47796	gadus morhu
280	244	6.2	638	1	KAL_MOUSE	P26262	mus musculu	353	233.5	5.9	267	2	O7S2S1	Q7S2S1	brachydanio
281	243.5	6.2	285	2	Q7PJQ0	Q7PJQ0	anopheles g	354	233.5	5.9	420	2	O90504	Q90504	epitetracus
282	243.5	6.2	245	2	O8CG42	O8CG42	rattus norv	355	233.5	5.9	273	2	O9XSM1	Q9XSM1	ovis aries
283	243.5	6.2	435	1	SNAK_PROME	P05049	drosoophila	356	233	5.9	445	2	O8CJ17	O8CJ17	rattus norv
284	243.5	6.2	764	1	CFAB_PONYE	Q864V1	pongo pygma	357	233	5.9	936	2	O81FX2	O81FX2	crasostrea
285	243	6.2	273	1	TRIT_SKEP	Q9XAM2	ovis aries	358	232.5	5.9	270	2	O81FX2	O81FX2	gadus morhu
286	243	6.2	282	2	Q9D4I3	Q9D4I3	mus musculu	359	232.5	5.9	1013	2	O43897	Q43897	homo sapien
287	243	6.2	442	2	Q804X1	Q804X1	fugu rubrip	360	232.5	5.9	1013	2	O9NQS4	Q9NQS4	homo sapien
288	242.5	6.1	564	2	Q8MKX1	Q8MKX1	oryctolagus	361	232	5.9	283	2	Q7Q0S6	Q7Q0S6	anopheles g
289	242.5	6.1	574	2	Q86R18	Q86R18	ilyanassa o	362	232	5.9	416	1	HEPS_RAT	P14272	rattus norv
290	242.5	6.1	691	2	O57658	O57658	gallus gall	363	232	5.9	638	1	KAL_RAT	Q29461	bos taurus
291	242.5	6.1	1019	2	O57382	O57382	xenopus lae	364	231.5	5.9	269	1	BL2_BOVIN	Q91039	gadus morhu
292	242	6.1	247	2	Q7PK69	Q7PK69	anopheles g	365	231.5	5.9	270	2	O91039	Q91039	gadus morhu
293	241.5	6.1	279	2	Q9SM64	Q9SM64	mus musculu	366	231.5	5.9	371	2	O8CJ16	O8CJ16	rattus norv
294	241.5	6.1	314	2	Q7QLC2	Q7QLC2	anopheles g	367	231.5	5.9	483	2	O8T8X4	O8T8X4	drosoophila
295	241.5	6.1	416	2	Q86T26	Q86T26	homo sapien	368	231.5	5.9	483	2	O9VK10	Q9VK10	drosoophila
296	241	6.1	306	2	Q7Q058	Q7Q058	anopheles g	369	231.5	5.9	624	2	O9SME7	O9SME7	oryctolagus
297	241	6.1	346	1	HPT_MESAU	Q35086	mesocricetu	370	231.5	5.9	666	2	O6VPJ8	O6VPJ8	drosoophila
298	241	6.1	818	2	O6PBA6	O6PBA6	brachydanio	371	231	5.9	242	2	O93266	Q93266	pseudopleur
299	241	6.1	1415	2	Q8MJ16	Q8MJ16	bos taurus	372	231	5.9	1008	2	Q9D8R7	Q9D8R7	gallus gall
300	240.5	6.1	238	2	Q9WT06	Q9WT06	paralichthy	373	231	5.9	1012	2	O9W7M6	Q9W7M6	mus musculu
301	240.5	6.1	422	2	Q8WVCI	Q8WVCI	homo sapien	374	230.5	5.8	235	2	O69E28	O69E28	homo sapien
302	240.5	6.1	441	2	Q7QKX8	Q7QKX8	anopheles g	375	230.5	5.8	244	2	O8Q6W3	O8Q6W3	anguilla ja
303	240	6.1	242	2	Q92099	Q92099	paranotoche	376	230	5.8	265	2	O9VVT3	Q9VVT3	drosoophila
304	240	6.1	1059	2	Q72411	Q72411	homo sapien	377	230	5.8	318	2	Q7RTY9	Q7RTY9	homo sapien
305	239.5	6.1	240	2	Q98TH0	Q98TH0	engraulis j	378	230	5.8	372	2	O9YIK6	Q9YIK6	anopheles g
306	239.5	6.1	405	1	HPT_HUMAN	P00738	homo sapien	379	230	5.8	607	2	O91001	Q91001	gallus gall
307	239.5	6.1	1015	2	Q9Y6L7	Q9Y6L7	homo sapien	380	230	5.8	329	1	HPT_CANFA	P19006	canis famli
308	239.5	6.1	1078	2	Q9U0U0	Q9U0U0	homo sapien	381	229.5	5.8	374	2	Q9VUG2	Q9VUG2	drosoophila
309	239.5	6.1	3567	2	Q9SE77	Q9SE77	mus musculu	382	229.5	5.8	624	1	FALL_MOUSE	Q9BK47	luidia foli
310	239	6.1	245	1	CTRA_BOVIN	Q7PZ03	anopheles g	383	229	5.8	267	2	O9BK47	Q9BK47	mus musculu
311	239	6.1	314	2	Q7PZ03	Q7PZ03	anopheles g	384	229	5.8	274	2	O924N9	Q924N9	mus musculu
312	239	6.1	436	1	HEPS_MOUSE	Q35453	mus musculu	385	229	5.8	722	2	O6NUP5	O6NUP5	xenopus lae
313	239	6.1	456	2	Q7QC30	Q7QC30	anopheles g	386	229	5.8	733	2	O6NUP5	O6NUP5	xenopus lae
314	239	6.1	977	2	Q91925	Q91925	xenopus lae	387	229	5.8	845	2	O9D8R1	Q9D8R1	gadus morhu
315	238.5	6.0	268	2	O46151	O46151	pacifastacu	388	229	5.8	347	2	O63927	Q63927	mus sp. hap
316	238.5	6.0	578	2	O6Q017	O6Q017	bos taurus	389	228.5	5.8	352	2	O6UMB4	Q6UMB4	homo sapien
317	238	6.0	237	1	TRYP_ASTFL	P00765	atactus flu	390	228.5	5.8	513	2	O7PKB9	Q7PKB9	anopheles g
318	238	6.0	263	1	CTR2_CANFA	P04813	canis famli	391	228.5	5.8	600	2	O17490	Q17490	anopheles g
319	238	6.0	275	1	TRIT_PIG	Q9N241	bis scrofa	392	228.5	5.8	600	2	O7PV58	Q7PV58	anopheles g
320	238	6.0	375	1	PCE_FACIR	P19102	tachypleus	393	228.5	5.8	1084	2	Q9BP40	Q9BP40	halocynthia
321	238	6.0	435	2	O9NFY2	Q9NFY2	anopheles lae	394	228.5	5.8	2516	2	Q7TQ52	Q7TQ52	mus musculu
322	238	6.0	767	2	Q9DGR2	Q9DGR2	xenopus lae	395	228.5	5.8	2526	2	Q7TQ51	Q7TQ51	mus musculu
323	237.5	6.0	286	2	Q7QAX5	Q7QAX5	anopheles g	396	228.5	5.8					

397	228.5	5.8	2531	1	NTC1_MOUSE	Q01705	mus musculus	470	223	5.7	529	2	Q7Q299	Q7q299	anopheles g
398	228.5	5.8	2531	2	Q8K428	Q8k428	mus musculus	471	222.5	5.6	411	2	Q9VUF0	Q9vuf0	drosohilla
399	228.5	5.8	2531	2	Q7T050	Q7t050	mus musculus	472	222.5	5.6	417	1	HEPS_HUMAN	P05961	homo sapien
400	228	5.8	3687	2	Q9W332	Q9w332	drosohilla	473	222.5	5.6	434	1	UROK_CHICK	P15120	gallus gall
401	227.5	5.8	2635	2	Q91004	Q91004	gessco gessco	474	222.5	5.6	455	1	TMS5_MOUSE	Q9e074	mus musculus
402	227.5	5.8	242	1	TRV1_SALSA	P35031	salmo salar	475	222.5	5.6	790	1	PLMN_PIG	P06867	sus scrofa
403	227.5	5.8	251	1	KUKE_HUMAN	Q9P093	homo sapien	476	222.5	5.6	954	2	Q75UQ6	Q75uq6	acheaearnea
404	227.5	5.8	251	1	Q6B089	Q6b089	homo sapien	477	222	5.6	267	2	Q9V942	Q9v942	drosohilla
405	227.5	5.8	349	2	Q28802	Q28802	pan troglod	478	222	5.6	269	1	EL2_PIG	P08419	sus scrofa
406	227.5	5.8	385	2	Q92659	Q92659	homo sapien	479	222	5.6	273	2	Q921N4	Q921n4	mus musculus
407	227.5	5.8	418	2	Q61E15	Q61e15	rattus norv	480	222	5.6	275	1	TRB2_HUMAN	P20231	homo sapien
408	227.5	5.8	714	2	Q7PWES	Q7pwe5	rattus norv	481	222	5.6	275	1	TRV1_HUMAN	P15157	homo sapien
409	227	5.8	242	2	Q6R179	Q6r179	taucogolabr	482	222	5.6	275	2	Q6RTM8	Q6rtm8	homo sapien
410	227	5.8	263	2	Q7YS64	Q7ys64	xenopus lae	483	222	5.6	276	2	Q6BUD5	Q6bud5	homo sapien
411	227	5.8	275	2	Q7YS62	Q7ys62	equus caball	484	222	5.6	282	2	Q6NZY1	Q6nzy1	homo sapien
412	227	5.8	324	1	TEST_MOUSE	Q9jh17	mus musculus	485	222	5.6	422	1	DESI_HUMAN	Q9u152	homo sapien
413	227	5.8	336	2	Q80YD8	Q80yd8	mus musculus	486	222	5.6	433	2	Q6WJ31	Q6wuj1	homo sapien
414	227	5.8	417	2	Q8B210	Q8b210	mus musculus	487	222	5.6	561	2	Q7PN97	Q7pn97	anopheles g
415	227	5.8	488	2	Q9TYH4	Q9tyh4	schistosoma	488	222	5.6	860	2	Q7QAH1	Q7qah1	anopheles g
416	227	5.8	1464	2	Q23995	Q23995	drosohilla	489	221.5	5.6	271	2	Q803Z4	Q803z4	brachydanio
417	227	5.8	1464	2	Q24132	Q24132	drosohilla	490	221.5	5.6	453	2	Q6ZMC3	Q6zmc3	homo sapien
418	227	5.8	1464	2	Q9VC47	Q9vc47	drosohilla	491	221.5	5.6	2531	1	NTC1_RAT	Q07008	rattus norv
419	227	5.7	238	1	TRV3_SALSA	P35033	salmo salar	492	221.5	5.6	3620	2	Q9TUS3	Q9tus3	canis famli
420	226.5	5.7	257	2	Q8B204	Q8b204	mus musculus	493	221	5.6	227	2	Q7PHB4	Q7phb4	anopheles g
421	226.5	5.7	371	2	Q8MS52	Q8ms52	drosohilla	494	221	5.6	221	1	TRV2_SALSA	P35032	salmo salar
422	226.5	5.7	761	1	NETR_MOUSE	Q8m562	mus musculus	495	221	5.6	268	2	Q97399	Q97399	phaedon coc
423	226.5	5.7	855	2	Q7Z410	Q7z410	homo sapien	496	221	5.6	288	1	CLCR_RAT	P55091	rattus norv
424	226.5	5.7	1429	1	ATRN_HUMAN	Q75882	homo sapien	497	221	5.6	273	2	MCT7_RAT	P27435	rattus norv
425	226.5	5.7	394	1	URTG_DESRO	PA9150	desmodus ro	498	221	5.6	273	1	Q6PEW8	Q6pew8	rattus norv
426	226	5.7	432	2	Q6UX37	Q6ux37	homo sapien	499	221	5.6	314	2	Q6RUT2	Q6rut2	mus musculus
427	226	5.7	437	2	TMS4_HUMAN	Q9mrx4	homo sapien	500	221	5.6	974	2	Q6RUT2	P91658	drosohilla
428	226	5.7	490	2	Q6P7D7	Q6p7d7	rattus norv	501	221	5.6	1234	2	Q7P1Q7	Q7p1q7	anopheles g
429	226	5.7	625	1	FA11_HUMAN	P03951	homo sapien	502	221	5.6	1332	2	Q7PNR7	Q7pnr7	anopheles g
430	225.5	5.7	312	2	Q7M755	Q7m755	mus musculus	503	220.5	5.6	242	2	Q80VS4	Q80vs4	mus musculus
431	225.5	5.7	347	1	HPT_PIG	Q8bep7	sus scrofa	504	220.5	5.6	250	2	Q8CGR5	Q8cgr5	anopheles g
432	225.5	5.7	418	2	Q8SZK2	Q8szk2	drosohilla	505	220.5	5.6	272	2	Q7Q9W5	Q7q9w5	mus musculus
433	225.5	5.7	418	2	Q9VAB7	Q9vab7	drosohilla	506	220.5	5.6	277	2	Q80MW7	Q80mw7	mus musculus
434	225.5	5.7	429	2	Q8AVB0	Q8avb0	brachydanio	507	220.5	5.6	360	2	Q17489	Q17489	anopheles g
435	225.5	5.7	445	2	Q7Q956	Q7q956	anopheles g	508	220.5	5.6	360	2	Q7PEV7	Q7pev7	anopheles g
436	225.5	5.7	457	1	TMS5_HUMAN	Q91363	homo sapien	509	220.5	5.6	468	2	Q9U0G3	Q9u0g3	pacifastacu
437	225	5.7	243	2	Q7PY20	Q7py20	anopheles g	510	220.5	5.6	506	2	Q7PR64	Q7pr64	anopheles g
438	225	5.7	328	2	Q80Z40	Q80z40	rattus norv	511	220.5	5.6	808	2	Q7YU36	Q7yuj36	drosohilla
439	225	5.7	387	2	Q9XY57	Q9xy57	clenocephal	512	220.5	5.6	1067	1	TLD_DROME	P25723	drosohilla
440	225	5.7	393	2	Q6RX66	Q6rx66	armigeres s	513	220	5.6	260	2	Q9W7P9	Q9w7p9	paralichthy
441	225	5.7	432	2	Q7QKL4	Q7qkl4	anopheles g	514	220	5.6	261	2	Q962G7	Q962g7	culex pipie
442	225	5.7	455	2	Q8CDRO	Q8cdro	mus musculus	515	220	5.6	275	1	TRB1_HUMAN	Q6b051	homo sapien
443	225	5.7	490	2	Q920K3	Q920k3	rattus norv	516	220	5.6	275	2	Q6B051	Q6b051	homo sapien
444	225	5.7	490	2	Q7TN04	Q7tn04	mus musculus	517	220	5.6	331	2	Q8B1A6	Q8b1a6	mus musculus
445	225	5.7	615	1	FA12_HUMAN	P00748	homo sapien	518	220	5.6	331	2	Q80X17	Q80x17	mus musculus
446	224.5	5.7	246	2	Q88301	Q88301	mus musculus	519	220	5.6	368	2	Q7Q064	Q7q064	anopheles g
447	224.5	5.7	251	2	Q54854	Q54854	rattus norv	520	219.5	5.6	244	1	TRY2_XENTLA	P70059	xenopus lae
448	224.5	5.7	253	2	Q91Y82	Q91y82	mus musculus	521	219.5	5.6	248	2	Q7OAX4	Q7qax4	anopheles g
449	224.5	5.7	271	1	EL2_RAT	P00774	rattus norv	522	219.5	5.6	248	2	Q7SZT1	Q7szt1	xenopus lae
450	224.5	5.7	274	1	TRV1_ANOGA	P35035	anopheles g	523	219.5	5.6	255	2	Q6GNY0	Q6gny0	galleria lae
451	224.5	5.7	347	1	HPT_MOUSE	Q61646	mus musculus	524	219.5	5.6	255	2	Q6GNY2	Q6gny2	xenopus lae
452	224.5	5.7	1022	1	TLD_BRARE	Q57460	brachydanio	525	219.5	5.6	271	1	EL2_MOUSE	P05208	mus musculus
453	224.5	5.7	1427	2	Q8V1B7	Q8v1b7	mesocricetu	526	219.5	5.6	347	1	HPT_MOUSE	Q60574	mus caroli
454	224	5.7	222	2	Q8AV18	Q8av18	oncorhynch	527	219.5	5.6	761	1	CPAB_MOUSE	P04166	mus musculus
455	224	5.7	242	2	Q7TIR8	Q7t1r8	pangasius h	528	219.5	5.6	1378	2	Q6BH72	Q6bhv2	mus musculus
456	224	5.7	245	2	CTRB_BOVIN	P00767	bos taurus	529	219.5	5.6	1444	2	Q6A051	Q6a051	mus musculus
457	224	5.7	248	2	O16126	O16126	bolletia vi	530	219	5.6	276	2	Q7QAM5	Q7qam5	anopheles g
458	224	5.7	261	1	KLK2_HORSE	Q61321	equus caball	531	219	5.6	318	2	Q80UR4	Q80ur4	mus musculus
459	224	5.7	490	1	TMS2_MOUSE	Q91i98	mus musculus	532	219	5.6	343	1	PSS8_HUMAN	Q16651	homo sapien
460	224	5.7	1174	2	Q9VYR4	Q9vyr4	drosohilla	533	219	5.6	365	2	Q97366	Q97366	holocricitia
461	224	5.7	262	2	Q9PSV8	Q9psv8	anopheles g	534	218.5	5.5	374	2	Q81B62	Q81b62	dermacentor
462	223.5	5.7	234	2	Q90244	Q90244	acipenser c	535	218.5	5.5	375	2	Q81TW8	Q81tw8	dermacentor
463	223.5	5.7	366	1	Q9W7Q0	Q9w7q0	paralichthy	536	218.5	5.5	435	2	TMS4_MOUSE	Q9vc55	mus musculus
464	223.5	5.7	248	1	HPT_HUMAN	P00739	homo sapien	537	218.5	5.5	787	2	Q6S1G0	Q6s1g0	naja kaouch
465	223.5	5.7	1242	1	JAG1_BRARE	Q9Y57	brachydanio	538	218.5	5.5	1007	2	Q8UJ28	Q8uj28	xenopus lae
466	223.5	5.7	1629	2	Q9V513	Q9v513	drosohilla	539	218.5	5.5	1379	2	Q6T256	Q6t256	homo sapien
467	223.5	5.7	1674	2	Q8SY35	Q8sy35	drosohilla	540	218	5.5	232	2	Q7PG16	Q7pg16	anopheles g
468	223	5.7	242	2	Q9W7Q7	Q9w7q7	paralichthy	541	218	5.5	242	2	Q7SX90	Q7sx90	brachydanio
469	223	5.7	454	1	TMS3_HUMAN	P57727	homo sapien	542	218	5.5	271	2	Q54213	Q54213	streptomyce

543	217.5	5.5	243	2	Q7M413	Q7M413	megabombus	616	212.5	5.4	339	2	Q99144	Q99144	mus musculus
544	217.5	5.5	269	2	Q6IS05	Q6IS05	homo sapien	617	212.5	5.4	420	2	Q6IB14	Q6IE14	rattus norv
545	217.5	5.5	324	2	Q7PXE3	Q7PXE3	anopheles g	618	212.5	5.4	425	2	Q7PZ85	Q7PZ85	anopheles g
546	217.5	5.5	3646	5	Q7Q737	Q7Q737	anopheles g	619	212.5	5.4	778	2	Q9V519	Q9V519	drosoophila
547	217	5.5	239	1	KLK2_CAVPO	P13133	cavia porce	620	212	5.4	260	1	NRPN_MOUSE	Q6GNF0	mus musculus
548	217	5.5	268	1	CLCR_HUMAN	Q99885	homo sapien	621	212	5.4	274	2	Q6GNF0	Q6GNF0	anopheles lae
549	217	5.5	273	1	MCT7_MOUSE	Q02844	mus musculus	622	212	5.4	340	2	Q8BV6	Q8BV6	mus musculus
550	217	5.5	275	2	Q96R26	Q96R26	homo sapien	623	212	5.4	1322	2	Q9NJS5	Q9NJS5	anopheles g
551	217	5.5	280	2	Q6GLK1	Q6GLK1	anopheles lae	624	211.5	5.4	418	1	HATT_HUMAN	Q60235	homo sapien
552	217	5.5	597	2	Q35727	Q35727	mus musculus	625	211.5	5.4	501	2	Q7OCV0	Q7OCV0	anopheles g
553	217	5.5	603	1	FA12_CAVPO	Q04962	cavia porce	626	211.5	5.4	629	2	Q6AZS7	Q6AZS7	anopheles lae
554	217	5.5	2703	1	NOTC_DROME	P07207	drosoophila	627	211.5	5.4	719	2	Q6BDY0	Q6BDY0	anopheles tro
555	216.5	5.5	235	2	Q6B4R4	Q6B4R4	bos taurus	628	211	5.3	237	2	Q29464	Q29464	bos taurus
556	216.5	5.5	277	2	Q96899	Q96899	scolopendra	629	211	5.3	276	1	MCTE_MOUSE	P21845	mus musculus
557	216.5	5.5	346	2	Q7LE20	Q7LE20	homo sapien	630	211	5.3	681	2	Q7O554	Q91545	anopheles g
558	216.5	5.5	346	2	Q28801	Q28801	pan troglod	631	211	5.3	1218	1	JAG1_HUMAN	P78504	homo sapien
559	216.5	5.5	2528	2	Q8AXP0	Q8AXP0	cynops pyrr	632	211	5.3	2447	2	Q13149	Q13149	fugu rubrip
560	216.5	5.5	2618	1	NDL_DROME	P81159	drosoophila	633	210.5	5.3	247	1	TRIP_STMVI	P35048	simulium vi
561	216	5.5	255	2	Q7TN10	Q7TN10	mus musculus	634	210.5	5.3	275	2	Q7PNF7	Q7PNF7	anopheles g
562	216	5.5	269	2	Q9C052	Q9C052	m mus muscu	635	210.5	5.3	280	2	Q8N171	Q8N171	homo sapien
563	216	5.5	269	2	Q9D779	Q9D779	mus musculus	636	210.5	5.3	342	1	PS58_MOUSE	Q9641	mus musculus
564	216	5.5	355	2	Q7PEW0	Q7PEW0	anopheles g	637	210.5	5.3	357	2	Q7OKX6	Q7OKX6	anopheles g
565	216	5.5	355	2	Q7PQR9	Q7PQR9	anopheles g	638	210.5	5.3	360	2	Q9M1X6	Q9M1X6	drosoophila
566	216	5.5	404	2	Q7QKJ2	Q7QKJ2	anopheles g	639	210.5	5.3	572	2	Q7RTY8	Q7RTY8	homo sapien
567	216	5.5	418	2	Q7PGU3	Q7PGU3	anopheles g	640	210.5	5.3	754	2	Q28290	Q28290	canis fami
568	216	5.5	1218	1	JAG1_MOUSE	Q9XX40	mus musculus	641	210.5	5.3	1219	1	JAG1_HUMAN	P63722	rattus norv
569	215.5	5.5	243	2	Q9TXD8	Q9TXD8	agelenopsis	642	210	5.3	2437	1	NTC1_BRABE	P46510	brachydanio
570	215.5	5.5	247	1	TRY3_CHICK	P06872	canis fami	643	209.5	5.3	280	2	Q6MXK6	Q6MXK6	canis fami
571	215.5	5.5	248	1	TRY3_CHICK	Q90629	gallus gall	644	209.5	5.3	313	2	Q8IN51	Q8IN51	drosoophila
572	215.5	5.5	254	2	Q8CGR4	Q8CGR4	mus musculus	645	209.5	5.3	321	2	Q96RZ8	Q96RZ8	homo sapien
573	215.5	5.5	269	2	Q6GN82	Q6GN82	anopheles lae	646	209.5	5.3	347	1	HPT_MUSSA	Q62558	mus saxicol
574	215.5	5.5	317	1	BSS4_HUMAN	Q9GN24	homo sapien	647	209.5	5.3	1441	2	Q723G3	Q723G3	homo sapien
575	215.5	5.5	321	2	Q80YJ8	Q80YJ8	mus musculus	648	209	5.3	245	2	Q7PEF6	Q7PEF6	anopheles g
576	215.5	5.5	326	2	Q9D9W0	Q9D9W0	mus musculus	649	209	5.3	263	2	Q6JZK0	Q6JZK0	anopheles lae
577	215.5	5.5	334	2	Q6UXE0	Q6UXE0	homo sapien	650	209	5.3	307	2	Q6ZND6	Q6ZND6	homo sapien
578	215.5	5.5	562	2	Q675X7	Q675X7	olkopleura	651	209	5.3	384	2	Q9W630	Q9W630	cyprinus ca
579	215.5	5.5	669	2	Q7PWE1	Q7PWE1	anopheles g	652	209	5.3	410	2	Q7QKD2	Q7QKD2	anopheles g
580	215.5	5.5	761	2	Q6MG74	Q6MG74	rattus norv	653	209	5.3	433	1	UROK_MOUSE	P06869	mus musculus
581	215	5.4	241	1	TRYX_GADMO	Q91041	gadus morhu	654	208.5	5.3	236	2	Q9TYH3	Q9TYH3	schistosoma
582	215	5.4	256	2	Q25081	Q25081	hypoderma 1	655	208.5	5.3	258	2	Q28803	Q28803	pan troglod
583	215	5.4	285	2	Q7QSK4	Q7QSK4	anopheles g	656	208.5	5.3	279	2	Q7TNX3	Q7TNX3	mus musculus
584	215	5.4	301	2	Q7PXG5	Q7PXG5	anopheles g	657	208.5	5.3	311	2	Q80XZ3	Q80XZ3	rattus norv
585	215	5.4	389	2	Q9PVX7	Q9PVX7	anopheles lae	658	208.5	5.3	417	2	Q8VHK8	Q8VHK8	mus musculus
586	215	5.4	597	2	Q6PER0	Q6PER0	mus musculus	659	208.5	5.3	417	2	Q8VDV1	Q8VDV1	mus musculus
587	215	5.4	609	2	Q80YCS	Q80YCS	mus musculus	660	208.5	5.3	444	2	Q9V4W6	Q9V4W6	drosoophila
588	215	5.4	749	2	Q9YGE8	Q9YGE8	oncothynchu	661	208.5	5.3	464	2	Q6L7Z5	Q6L7Z5	haemaphysal
589	215	5.4	760	2	Q8UG08	Q8UG08	teliraodon n	662	208.5	5.3	471	2	Q8CFE0	Q8CFE0	mus musculus
590	215	5.4	810	1	PLMN_HUMAN	P00747	homo sapien	663	208	5.3	256	2	Q25082	Q25082	hypoderma 1
591	215	5.4	1116	2	Q7TPO5	Q7TPO5	rattus norv	664	208	5.3	271	2	Q8HYJ2	Q8HYJ2	bos taurus
592	214.5	5.4	195	2	Q819P3	Q819P3	aurelia aur	665	208	5.3	275	2	Q8IXD7	Q8IXD7	homo sapien
593	214.5	5.4	247	1	TRY2_BOVIN	Q29463	bos taurus	666	208	5.3	282	2	Q7PX30	Q7PX30	anopheles g
594	214.5	5.4	249	2	Q6DIT2	Q6DIT2	anopheles tro	667	208	5.3	292	2	Q7Q6S2	Q7Q6S2	anopheles g
595	214.5	5.4	357	2	Q7Q092	Q7Q092	anopheles g	668	208	5.3	326	2	Q7RTY6	Q7RTY6	homo sapien
596	214.5	5.4	366	2	Q7O170	Q7O170	mus musculus	669	208	5.3	358	2	Q86WY4	Q86WY4	homo sapien
597	214.5	5.4	505	2	Q966V4	Q966V4	halocynthia	670	207.5	5.3	195	2	Q8J706	Q8J706	homo sapien
598	214.5	5.4	593	1	FA12_BOVIN	P98140	bos taurus	671	207.5	5.3	239	2	Q91218	Q91218	oncothynchu
599	214.5	5.4	1130	2	Q7QIT7	Q7QIT7	anopheles g	672	207.5	5.3	256	1	TRIV_MANSE	P35046	manduca sex
600	214.5	5.4	1322	2	Q9NAT0	Q9NAT0	anopheles g	673	207.5	5.3	266	2	Q92077	Q92077	gadus morhu
601	214.5	5.4	275	2	Q6FHB8	Q6FHB8	mus musculus	674	207.5	5.3	269	1	EL2A_HUMAN	P08217	homo sapien
602	214	5.4	342	1	PS58_RAT	Q6FHB8	homo sapien	675	207.5	5.3	289	2	Q6ISN8	Q6ISN8	homo sapien
603	214	5.4	241	2	Q98TG9	Q98TG9	rattus norv	676	207.5	5.3	278	2	Q7OHS0	Q7OHS0	anopheles g
604	213.5	5.4	241	2	Q98TG9	Q98TG9	engrullia j	677	207.5	5.3	298	2	Q9NHO6	Q9NHO6	heliothis 2
605	213.5	5.4	248	2	Q9VQ98	Q9VQ98	drosoophila	678	207.5	5.3	900	2	Q6AX42	Q6AX42	anopheles lae
606	213.5	5.4	423	2	Q8BM10	Q8BM10	mus musculus	679	207.5	5.3	1282	2	Q8IER0	Q8IER0	homo sapien
607	213.5	5.4	562	2	Q7PN85	Q7PN85	anopheles g	680	207	5.2	238	1	TRYS_ASDAB	P29787	aeedes aegyp
608	213.5	5.4	2352	2	Q61240	Q61240	halocynthia	681	207	5.2	240	2	Q7SYO8	Q7SYO8	anopheles lae
609	213	5.4	355	2	Q7PFPS	Q7PFPS	anopheles g	682	207	5.2	260	1	NRPN_RAT	Q88780	rattus norv
610	213	5.4	355	2	Q9NFU1	Q9NFU1	anopheles g	683	207	5.2	329	2	Q7OBS72	Q7OBS72	anopheles g
611	213	5.4	394	2	P91817	P91817	techypius	684	206.5	5.2	195	2	Q6SPC0	Q6SPC0	homo sapien
612	213	5.4	615	2	Q81Z25	Q81Z25	homo sapien	685	206.5	5.2	256	1	TRIV_MANSE	P35045	manduca sex
613	212.5	5.4	615	2	Q7POB3	Q7POB3	anopheles g	686	206.5	5.2	269	2	Q96QV5	Q96QV5	homo sapien
614	212.5	5.4	250	1	KLKB_HUMAN	Q9UBX7	homo sapien	687	206.5	5.2	269	2	Q6ICV2	Q6ICV2	homo sapien
615	212.5	5.4	260	2	Q7RTY3	Q7RTY3	homo sapien	688	206.5	5.2	269	2	Q9V929	Q9V929	drosoophila

689	206.5	5.2	270	2	Q27824	Q27824 uca pugilac	762	202.5	5.1	339	2	Q6BD48	Q6bd48 penaeus jap
690	206.5	5.2	280	2	Q6NKS	Q6nks canis famli	763	202.5	5.1	372	2	Q9WZC8	Q9wzC8 drosophila
691	206.5	5.2	284	2	Q6NF86	Q6nf86 homo sapien	764	202	5.1	190	2	Q9QXD5	Q9qx5 mus musculu
692	206.5	5.2	321	1	TRYG_HUMAN	Q9nrz2 homo sapien	765	202	5.1	241	1	TRX1_GADMO	P16049 gadus morhu
693	206.5	5.2	467	2	Q6MwK2	Q6mwx2 homo sapien	766	202	5.1	246	1	KLK_PIG	P00752 sus scrofa
694	206.5	5.2	573	2	Q9V516	Q9v516 drosophila	767	202	5.1	380	2	Q68D21	Q68d21 homo sapien
695	206.5	5.2	726	2	Q7QBP4	Q7qbp4 anopheles g	768	202	5.1	488	2	Q81UV8	Q81uv8 homo sapien
696	206.5	5.2	1065	2	Q810H2	Q810h2 mus musculu	769	202	5.1	743	2	Q9YCE7	Q9yge7 oncorhynch
697	206.5	5.2	1403	2	Q70E20	Q70e20 mus musculu	770	202	5.1	2321	1	NTC3_HUMAN	Q9um7 homo sapien
698	206.5	5.2	263	2	Q9NB92	Q9nb92 agrotis ips	771	201.5	5.1	195	2	Q8J007	Q8j007 homo sapien
699	206.5	5.2	269	2	Q6AZF9	Q6azf9 xenopus lae	772	201.5	5.1	195	2	Q8J008	Q8j008 homo sapien
700	206.5	5.2	318	2	Q7Q9W4	Q7q9w4 anopheles g	773	201.5	5.1	246	1	TRX2_MOUSE	P07146 mus musculu
701	206.5	5.2	424	2	Q6R559	Q6r559 oestinia nu	774	201.5	5.1	255	2	Q6IS10	Q6is10 homo sapien
702	206.5	5.2	492	2	Q7Z155	Q7z155 chironomus	775	201.5	5.1	256	1	KLKX_HUMAN	Q9h25 homo sapien
703	206.5	5.2	4548	1	AP0A_HUMAN	P08519 homo sapien	776	201.5	5.1	320	2	Q7T0X2	Q7t0x2 xenopus lae
704	205.5	5.2	269	1	TRYM_CANPA	P19236 canis famli	777	201.5	5.1	334	2	Q640F8	Q640f8 xenopus lae
705	205.5	5.2	269	2	Q6ISM5	Q6ism5 homo sapien	778	201.5	5.1	394	2	Q7PQ76	Q7pq76 anopheles g
706	205.5	5.2	269	2	Q6ISP9	Q6isp9 homo sapien	779	201.5	5.1	438	2	Q6ZWK6	Q6zwk6 homo sapien
707	205.5	5.2	347	1	HPT_RAT	P08866 ratu	780	201	5.1	247	2	Q42608	Q42608 petromyzon
708	205.5	5.2	374	2	Q80YD5	Q80yd5 mus musculu	781	201	5.1	248	2	Q66105	Q66105 xenopus lae
709	205.5	5.2	416	2	Q8B213	Q8bz13 mus musculu	782	201	5.1	260	2	Q81W69	Q81w69 homo sapien
710	205.5	5.2	416	2	Q8B230	Q8bz30 mus musculu	783	201	5.1	275	2	Q66UD0	Q66ud0 culicoides
711	205.5	5.2	492	1	TMS2_HUMAN	P15588 hypoderm	784	201	5.1	333	2	Q705Z6	Q7q5z6 anopheles g
712	205	5.2	256	1	HYPB_HYPLI	P35588 hypoderm	785	201	5.1	351	2	Q816K0	Q816k0 holotrichia
713	205	5.2	264	2	Q02559	Q02559 culex quinq	786	201	5.1	175	2	Q9UWZ3	Q9umz3 drosophila
714	205	5.2	492	2	Q61T73	Q61t73 homo sapien	787	200.5	5.1	175	2	Q9UWV3	Q9umv3 homo sapien
715	205	5.2	870	2	Q81Q66	Q81q66 drosophila	788	200.5	5.1	231	1	TRYP_PIG	P00761 sus scrofa
716	204.5	5.2	216	2	Q9QX83	Q9qx83 ratu	789	200.5	5.1	241	2	Q7PEF7	Q7pf7 anopheles g
717	204.5	5.2	246	1	TRV2_RAT	P00763 ratu	790	200.5	5.1	246	2	Q792Z1	Q792z1 mus musculu
718	204.5	5.2	247	2	Q9CPN9	Q9cpn9 m mus	791	200.5	5.1	249	2	Q9WT01	Q9wt01 paralicthy
719	204.5	5.2	247	2	Q9D7Y7	Q9d7y7 mus musculu	792	200.5	5.1	281	2	Q6NSB4	Q6nrb4 homo sapien
720	204.5	5.2	256	1	TRVC_MANSE	P35047 manduca sex	793	200.5	5.1	358	2	Q57434	Q57434 fuga rubrip
721	204.5	5.2	381	2	Q46137	Q46137 lumbicus r	794	200.5	5.1	415	2	Q9UKZ9	Q9ukz9 homo sapien
722	204.5	5.2	267	2	Q70169	Q70169 mus musculu	795	200.5	5.1	752	1	CO2_HUMAN	P12545 macaca mula
723	204.5	5.2	449	2	Q95RA3	Q95ra3 drosophila	796	200.5	5.1	810	1	PLMN_MACMU	Q20176 caenorhabdi
724	204.5	5.2	470	2	Q661F4	Q661f4 xenopus tro	797	200.5	5.1	951	2	Q20176	Q20176 anopheles g
725	204.5	5.2	510	2	Q9H4V1	Q9h4v1 homo sapien	798	200	5.1	241	2	Q70310	Q70310 anopheles g
726	204.5	5.2	1497	1	CO2_PONPY	Q8eq75 pongo pygma	799	200	5.1	247	2	Q42158	Q42158 petromyzon
727	204.5	5.2	1972	2	Q8NBT9	Q8nbt9 homo sapien	800	200	5.1	385	1	TS50_HUMAN	Q9ui8 homo sapien
728	204.5	5.2	2470	1	KLK8_MOUSE	O3516 mus musculu	801	200	5.1	391	2	Q7PXJ5	Q7pxj5 anopheles g
729	204	5.2	260	1	KLK8_HUMAN	O60259 homo sapien	802	200	5.1	454	2	Q46506	Q46506 papio hamad
730	204	5.2	367	2	Q9QXJ2	Q9qxj2 mus musculu	803	200	5.1	504	2	Q9VFM0	Q9vfm0 drosophila
731	204	5.2	417	2	Q8VHJ4	Q8vhj4 ratu	804	200	5.1	564	2	Q7RTZ1	Q7rtz1 homo sapien
732	204	5.2	424	2	Q6R558	Q6r558 oestinia nu	805	199.5	5.1	223	2	Q9VB14	Q9vb14 drosophila
733	203.5	5.2	195	2	Q81XB4	Q81xb4 homo sapien	806	199.5	5.1	247	1	TRV3_RAT	P08426 ratu
734	203.5	5.2	247	1	TRV2_HUMAN	P07478 homo sapien	807	199.5	5.1	257	1	KLK1_MACFA	Q07246 macaca fasc
735	203.5	5.2	261	2	Q7Z5F3	Q7z5f3 homo sapien	808	199.5	5.1	258	2	Q28508	Q28508 macaca mula
736	203.5	5.2	263	1	CPAD_RAT	P33038 ratu	809	199.5	5.1	275	1	TRV3_ANOGA	P25037 anopheles g
737	203.5	5.2	285	1	F93_CAVPO	P18295 cavia porce	810	199.5	5.1	348	2	Q86W55	Q86w55 homo sapien
738	203.5	5.2	309	2	Q27083	Q27083 tachypneus	811	199.5	5.1	378	2	Q90WFO	Q90wfo tachemys b
739	203.5	5.2	335	2	Q8VIF2	Q8vif2 mus musculu	812	199.5	5.1	390	2	Q7PVQ3	Q7pvq3 anopheles g
740	203.5	5.2	404	2	Q7QF40	Q7qf40 anopheles g	813	199.5	5.1	1193	2	Q90819	Q90819 gallus gall
741	203.5	5.2	664	2	Q9IAT6	Q9iat6 brachydario	814	199.5	5.1	1275	2	Q99PW0	Q99pw0 ratu
742	203.5	5.2	734	2	Q69D12	Q69d12 sus scrofa	815	199.5	5.1	2556	1	NTC1_HUMAN	P46531 homo sapien
743	203.5	5.2	730	2	Q9W633	Q9w633 cyprinus ca	816	199.5	5.1	2653	2	Q25253	Q25253 lucilia cup
744	203.5	5.2	1323	2	Q7Z387	Q7z387 homo sapien	817	199	5.0	263	2	Q62562	Q62562 penaeus van
745	203.5	5.2	1432	2	Q99J86	Q99j86 ratu	818	199	5.0	264	2	Q8QGF6	Q8qgf6 xenopus lae
746	203.5	5.2	3494	2	Q7LCS3	Q7lcs3 homo sapien	819	199	5.0	264	2	Q6GPY5	Q6gpy5 xenopus lae
747	203.5	5.2	3623	2	Q60494	Q60494 homo sapien	820	199	5.0	401	2	Q6LH17	Q6lhi17 photobacter
748	203	5.1	177	2	Q9QX86	Q9qx86 ratu	821	199	5.0	441	2	Q9XXV0	Q9xxv0 bombyx mori
749	203	5.1	185	2	Q9QX88	Q9qx88 ratu	822	199	5.0	1303	2	Q66S84	Q66s84 okopoleura
750	203	5.1	185	2	Q9QX88	Q9qx88 ratu	823	198.5	5.0	181	2	Q9UUC7	Q9uuc7 homo sapien
751	203	5.1	186	2	Q9QX44	Q9qx44 mus musculu	824	198.5	5.0	237	2	Q17035	Q17035 anopheles g
752	203	5.1	289	2	Q7PBU1	Q7pbu1 anopheles g	825	198.5	5.0	243	1	TRV1_BOVIN	P00760 bos taurus
753	203	5.1	370	2	Q9V444	Q9v444 drosophila	826	198.5	5.0	260	2	Q7SZC3	Q7szc3 gallus gall
754	203	5.1	403	2	Q9KSQ6	Q9ksq6 vibrio chol	827	198.5	5.0	279	2	Q9QZ74	Q9qz74 ratu
755	203	5.1	537	2	Q9BYE1	Q9bye1 homo sapien	828	198.5	5.0	311	1	TRV3_MOUSE	Q9qul7 mus musculu
756	203	5.1	575	2	Q7Q9W3	Q7q9w3 anopheles g	829	198.5	5.0	364	2	Q9NWS9	Q9nas9 anopheles g
757	203	5.1	581	2	Q9BYE2	Q9bye2 homo sapien	830	198.5	5.0	365	2	Q7Q1D1	Q7q1d1 anopheles g
758	203	5.1	833	2	Q9VICS	Q9vics cyprinus ca	831	198.5	5.0	388	2	Q44330	Q44330 manduca sex
759	202.5	5.1	239	2	Q8N1C9	Q8nic9 homo sapien	832	198.5	5.0	461	2	Q8T4N2	Q8t4n2 rhipicephal
760	202.5	5.1	255	2	Q7U1G6	Q7u1g6 seguinus oe	833	198.5	5.0	752	2	Q86340	Q86340 gorilla gor
761	202.5	5.1	274	2	Q16133	Q16133 anopheles b	834	198.5	5.0	1214	2	Q90YD2	Q90yd2 xenopus lae

835	198	5.0	235	1	TRYP_HUMAN	Q9bzj3	homo sapien	508	194	4.9	806	1	PLMN_MACEU	O187g3	macropus eu
836	198	5.0	259	1	DEF3_DERPA	P49275	dermatophag	909	193.5	4.9	183	2	Q6PLJ7	O6p17	tenelopena
837	198	5.0	261	1	Q6QX60	Q6qx60	lepeophthei	910	193.5	4.9	245	2	Q792Y9	O792Y9	fennemusculu
838	198	5.0	293	2	Q7Q8F9	Q7q8f9	anopheles g	911	193.5	4.9	246	2	Q9QUK9	Q9quk9	mus musculu
839	198	5.0	427	2	Q6Y2X4	Q6y2x4	manduca sex	912	193.5	4.9	247	2	Q6T376	Q6t376	eisenia foe
840	198	5.0	760	1	CO2_MOUSE	P21180	mus musculu	913	193.5	4.9	247	2	Q9W705	Q9w705	paratichthy
841	198	5.0	1023	1	Q6UXD4	Q6uxd4	homo sapien	914	193.5	4.9	256	2	Q27540	Q27540	choristoneu
842	198	5.0	1024	1	S26L_HUMAN	Q9b4n1	homo sapien	915	193.5	4.9	263	2	Q9V5X7	Q9v5x7	drostoloneu
843	197.5	5.0	226	1	COGS_UCAPU	P00771	uca pugliat	916	193.5	4.9	271	2	Q7O820	Q7o820	anopheles g
844	197.5	5.0	242	1	Q6NTB8	Q6ntb8	homo sapien	917	193.5	4.9	282	2	Q7PVO2	Q7pvo2	anopheles g
845	197.5	5.0	245	2	Q6IE66	Q6ie66	rattus norv	918	193.5	4.9	317	2	Q9DGR3	Q9dgr3	xenopus lae
846	197.5	5.0	248	1	KLKC_HUMAN	Q9ukr0	homo sapien	919	193.5	4.9	327	2	Q7O530	Q7o530	anopheles g
847	197.5	5.0	253	1	Q96R00	Q96rq0	homo sapien	920	193.5	4.9	402	2	Q7O873	Q7o873	anopheles g
848	197.5	5.0	258	2	Q28805	Q28805	pan troglod	921	193.5	4.9	789	2	Q8N1E9	Q8n1e9	homo sapien
849	197.5	5.0	263	2	Q6H3J9	Q6h3j9	sus scrofa	922	193.5	4.9	1089	2	Q8T3A0	Q8t3a0	ciona intes
850	197.5	5.0	267	2	Q7Q4H6	Q7q4h6	anopheles g	923	193.5	4.9	1317	2	Q6IO50	Q6io50	homo sapien
851	197	5.0	222	2	Q9IWX0	Q9iwx0	rattus norv	924	193.5	4.9	2471	1	NTC2_RAT	NTC2	rattus norv
852	197	5.0	245	2	Q7Q2X3	Q7q2x3	anopheles g	925	193	4.9	253	1	CAC3_BOVIN	CAC3	bos taurus
853	197	5.0	250	2	Q7PWE3	Q7pwe3	anopheles g	926	193	4.9	258	2	Q867B0	Q867b0	canis fami1
854	197	5.0	261	2	Q9VXC7	Q9vxc7	dermatophila	927	193	4.9	269	2	Q9XV56	Q9xy56	ctenoccephal
855	197	5.0	338	1	PLMN_HORSE	P00010	equus cabal	928	193	4.9	299	2	Q9SKW7	Q9skw7	bos taurus
856	197	5.0	421	2	Q9SR56	Q9sr56	dermatophila	929	193	4.9	405	2	Q7OAC0	Q7oac0	anopheles g
857	197	5.0	585	2	Q9U082	Q9u082	tribolium c	930	193	4.9	423	2	Q57433	Q57433	fugu rubrip
858	197	5.0	745	2	Q91701	Q91701	xenopus lae	931	193	4.9	461	2	Q9H284	Q9h284	homo sapien
859	197	5.0	760	2	Q7O350	Q7o350	mus musculu	932	193	4.9	543	2	Q6PHN6	Q6phn6	mus musculu
860	196.5	5.0	219	2	Q91036	Q91036	gadus morhu	933	193	4.9	962	2	Q8CA20	Q8ca20	mus musculu
861	196.5	5.0	237	2	Q6GVY5	Q6gyv5	struthio ca	934	193	4.9	963	2	Q6PID5	Q6pid5	mus musculu
862	196.5	5.0	259	2	Q6GYU5	Q6gyu5	dermatophila	935	192.5	4.9	178	2	Q93594	Q93594	dicertrarch
863	196.5	5.0	269	1	ELB2B_HUMAN	P08218	homo sapien	936	192.5	4.9	222	2	Q94508	Q94508	dermatophag
864	196.5	5.0	298	2	Q8T4N4	Q8t4n4	hippicephal	937	192.5	4.9	246	2	Q9Z1R9	Q9z1r9	mus musculu
865	196.5	5.0	373	2	Q6LBY9	Q6lby9	homo sapien	938	192.5	4.9	249	2	Q8N9M4	Q8nm4	homo sapien
866	196.5	5.0	570	1	FBP3_STRPU	P49013	strongyloce	939	192.5	4.9	247	2	Q9QYH4	Q9qyh4	mus musculu
867	196.5	5.0	829	2	Q6NUL9	Q6nul9	homo sapien	940	192.5	4.9	250	2	Q632F2	Q632f2	rattus norv
868	196.5	5.0	2524	1	NOTC_XENLA	P21783	xenopus lae	941	192.5	4.9	256	1	TRYP_CHOFU	TRYP	christioneu
869	196	5.0	248	1	Q6GPX7	Q6gpx7	xenopus lae	942	192.5	4.9	276	2	Q9QYN3	Q9qyn3	m hipostas
870	196	5.0	270	1	ELB3B_HUMAN	P08861	homo sapien	943	192.5	4.9	361	2	Q8WQY4	Q8wqy4	dermatophila
871	196	5.0	275	2	Q66UC8	Q66uc8	homo sapien	944	192.5	4.9	438	2	Q9H804	Q9h804	homo sapien
872	196	5.0	347	2	Q7Q5V3	Q7q5v3	anopheles g	945	192.5	4.9	703	2	Q7O6S1	Q7o6s1	anopheles g
873	196	5.0	400	2	Q9GRS2	Q9grs2	tenebrio mo	946	192.5	4.9	754	2	P79816	P79816	oryzias lat
874	196	5.0	3623	2	Q7O244	Q7o244	rattus norv	947	192	4.9	244	2	Q42159	Q42159	petromyzon
875	195.5	5.0	257	1	GRAM_HUMAN	P51124	homo sapien	948	192	4.9	246	2	Q9BLI7	Q9bli7	lumbicus r
876	195.5	5.0	267	2	Q9GP27	Q9gp27	dermatophila	949	192	4.9	254	2	Q9XHY0	Q9xyh0	hyzopertha
877	195.5	5.0	271	1	FA9_PIG	P16293	sus scrofa	950	192	4.9	256	2	Q6WJY6	Q6wjy6	bdellovibri
878	195.5	5.0	274	2	Q17086	Q17086	anopheles s	951	192	4.9	376	2	Q7PRP7	Q7prp7	anopheles g
879	195.5	5.0	276	2	Q18443	Q18443	helicoverpa	952	192	4.9	380	2	Q9YIK5	Q9yik5	anopheles g
880	195.5	5.0	752	1	CO2_PANTR	Q8eq74	pan troglod	953	192	4.9	383	2	Q77102	Q77102	manduca sex
881	195.5	5.0	948	2	Q6IBX4	Q6ibx4	homo sapien	954	192	4.9	410	2	Q7QJ44	Q7qj44	anopheles g
882	195.5	5.0	2471	1	NTC2_HUMAN	Q04721	homo sapien	955	191.5	4.9	247	1	TRYP_HUMAN	TRYP	homo sapien
883	195	4.9	261	1	KLK6_MOUSE	P15947	mus musculu	956	191.5	4.9	247	2	Q17039	Q17039	anopheles g
884	195	4.9	262	2	Q720G3	Q720g3	phlebotomus	957	191.5	4.9	265	2	Q6O6I1	Q6o6i1	lepeophthei
885	195	4.9	276	2	Q9BRH3	Q9brh3	homo sapien	958	191.5	4.9	281	2	Q76898	Q76898	dermatophila
886	195	4.9	320	2	Q7PEV6	Q7pev6	anopheles g	959	191.5	4.9	284	2	Q8IRX5	Q8irx5	dermatophila
887	195	4.9	432	1	UKOK_RAT	P29598	rattus norv	960	191.5	4.9	360	2	Q8SKX4	Q8skx4	dermatophila
888	194.5	4.9	246	2	TRYP1_RAT	P00762	rattus norv	961	191.5	4.9	385	2	Q8SXE1	Q8sxe1	dermatophila
889	194.5	4.9	246	2	Q9R0T7	Q9r0t7	m pancrcreat	962	191.5	4.9	480	2	Q66IT1	Q66it1	xenopus lae
890	194.5	4.9	261	2	Q7Z5F4	Q7z5f4	homo sapien	963	191.5	4.9	579	2	Q9PD09	Q9pd09	homo sapien
891	194.5	4.9	283	2	Q9SV22	Q9sv22	lumbicus b	964	191.5	4.9	713	2	Q80RPO	Q80rpo	mus musculu
892	194.5	4.9	343	1	PLMN_SHEEP	P51286	ovis aries	965	191.5	4.9	830	1	LEH3_HUMAN	LEH3	homo sapien
893	194.5	4.9	1374	2	Q9VSU0	Q9vsu0	dermatophila	966	191.5	4.9	2468	2	Q800E4	Q800e4	brachydantio
894	194.5	4.9	1449	2	Q9U1I2	Q9u1i2	dermatophila	967	191.5	4.9	3336	2	Q9VW55	Q9vw55	dermatophila
895	194.5	4.9	1450	2	Q8I0B8	Q8i0b8	dermatophila	968	191	4.8	228	2	Q6PEJ8	Q6pej8	homo sapien
896	194.5	4.9	1462	2	Q9U1I3	Q9u1i3	dermatophila	969	191	4.8	254	1	KLK4_HUMAN	KLK4	homo sapien
897	194.5	4.9	2382	2	Q9B1I9	Q9b1i9	dermatophila	970	191	4.8	255	2	Q25277	Q25277	lucilia cup
898	194.5	4.9	2409	2	Q960G6	Q960g6	dermatophila	971	191	4.8	256	2	Q8IBES	Q8ibes	ochlerotatu
899	194.5	4.9	2428	2	Q8I6X6	Q8i6x6	boophilus m	972	191	4.8	277	2	Q8I0I0	Q8i0i0	dermatophila
900	194.5	4.9	2786	2	Q9VSU2	Q9vsu2	dermatophila	973	191	4.8	317	2	Q8K4D1	Q8k4d1	mus musculu
901	194	4.9	245	2	Q42160	Q42160	petromyzon	974	191	4.8	317	2	Q8K4I7	Q8k4i7	mus musculu
902	194	4.9	247	2	Q7O7T4	Q7o7t4	equus cabal	975	191	4.8	415	2	Q9GRW0	Q9grw0	holotrichia
903	194	4.9	253	2	Q9VAG3	Q9vag3	dermatophila	976	191	4.8	646	2	Q29097	Q29097	sus scrofa
904	194	4.9	253	1	CPAD_PIG	P51779	dermatophila	977	191	4.8	788	2	Q6K673	Q6k673	rattus norv
905	194	4.9	267	1	TRYP1_ANOGA	P35041	anopheles g	978	190.5	4.8	246	2	Q79220	Q79220	mus musculu
906	194	4.9	556	2	Q803D5	Q803d5	brachydantio	979	190.5	4.8	257	2	Q8IBE3	Q8ibe3	aedes polyn
907	194	4.9	593	2	Q6PJN5	Q6pjn5	homo sapien	980	190.5	4.8	270	2	Q7QON6	Q7qon6	anopheles g

981	190.5	4.8	329	2	Q7PEV8	Q7PEV8 anopheles g	1054	187	4.7	246	1	TRVA_RAT	P32821 rattus norv
982	190.5	4.8	579	2	Q9BY79	Q9BY79 homo sapien	1055	187	4.7	256	2	O18439	O18439 helicoverpa
983	190.5	4.8	762	2	O9YIC6	O9YIC6 cypirinus ca	1056	187	4.7	261	2	Q29474	Q29474 canis famli
984	190.5	4.8	768	1	LEM3_MOUSE	P01102 mus musculu	1057	187	4.7	271	1	CTRI_PENVA	Q00871 penaeus sex
985	190.5	4.8	1064	1	PBPI_STRPU	P10079 mus musculu	1058	187	4.7	291	2	Q25510	Q25510 manduca sex
986	190.5	4.8	2037	2	Q7OF52	Q7OF52 strongyloce	1059	187	4.7	890	2	Q7QJ41	Q7QJ41 anopheles g
987	190	4.8	243	2	Q6BVJ5	Q6BVJ5 anopheles g	1060	186.5	4.7	235	2	O9CTK7	O9CTK7 aedes albop
988	190	4.8	245	2	Q6DKQ3	Q6DKQ3 elsenla foe	1061	186.5	4.7	250	2	O9J365	O9J365 pseudopleur
989	190	4.8	253	2	Q8WZB4	Q8WZB4 homo sapien	1062	186.5	4.7	257	2	Q81BE2	Q81BE2 aedes trise
990	190	4.8	277	2	Q8SQ44	Q8SQ44 sus scrofa	1063	186.5	4.7	287	2	Q9VTV2	Q9VTV2 drosophila
991	190	4.8	282	2	Q25395	Q25395 lumbricus r	1064	186.5	4.7	397	2	Q9WJ14	Q9WJ14 drosophila
992	190	4.8	299	2	Q7Q9S0	Q7Q9S0 anopheles r	1065	186.5	4.7	3523	2	Q7QCP4	Q7QCP4 anopheles g
993	190	4.8	334	2	Q6S07	Q6S07 papio hamad	1066	186	4.7	181	2	O9GSN1	O9GSN1 chrysomya b
994	190	4.8	378	2	Q8SY50	Q8SY50 drosophila	1067	186	4.7	249	2	Q92046	Q92046 diisocotichu
995	190	4.8	414	2	Q8R4W6	Q8R4W6 mus musculu	1068	186	4.7	280	2	Q7Q494	Q7Q494 anopheles g
996	189.5	4.8	241	2	Q9Z135	Q9Z135 rattus norv	1069	186	4.7	334	2	Q6BD05	Q6BD05 drosophila
997	189.5	4.8	246	2	Q7M754	Q7M754 mus musculu	1070	186	4.7	449	2	Q9VDU8	Q9VDU8 drosophila
998	189.5	4.8	255	2	Q9Y7A9	Q9Y7A9 metarhizium	1071	186	4.7	1176	2	Q6ZW16	Q6ZW16 homo sapien
999	189.5	4.8	257	2	Q77440	Q77440 aedes aegypt	1072	186	4.7	1594	2	O9S218	O9S218 ocyrtolagus
1000	189.5	4.8	258	2	Q28804	Q28804 pan troglod	1073	185.5	4.7	211	2	O8U009	O8U009 homo sapien
1001	189.5	4.8	263	2	Q02570	Q02570 cullex quinq	1074	185.5	4.7	256	2	Q9XY51	Q9XY51 ctenocephal
1002	189.5	4.8	263	2	Q9TY16	Q9TY16 penaeus van	1075	185.5	4.7	261	1	DER3_DERPT	P39675 dermatophag
1003	189.5	4.8	266	2	Q27761	Q27761 penaeus van	1076	185.5	4.7	292	2	O18438	O18438 helicoverpa
1004	189.5	4.8	271	2	Q9YR56	Q9YR56 drosophila	1077	185.5	4.7	292	2	Q7PMW9	Q7PMW9 anopheles g
1005	189.5	4.8	281	2	Q8SY85	Q8SY85 drosophila	1078	185.5	4.7	310	1	DISP_MOUSE	Q9QY29 mus musculu
1006	189.5	4.8	369	2	Q7Q928	Q7Q928 anopheles g	1079	185.5	4.7	439	2	O8BH09	Q8BH09 m mus muscu
1007	189.5	4.8	381	2	Q9VB66	Q9VB66 drosophila	1080	185.5	4.7	542	2	Q7MK56	Q7MK56 vibrio vuln
1008	189.5	4.8	385	2	Q90WS2	Q90WS2 elaphe sp.	1081	185.5	4.7	711	1	HGFL_HUMAN	P26927 homo sapien
1009	189.5	4.8	470	2	O8T3A1	O8T3A1 clona intes	1082	185.5	4.7	928	1	NRPL_XENTLA	P28824 xenopus lae
1010	189.5	4.8	572	2	Q8BTK6	Q8BTK6 mus musculu	1083	185.5	4.7	1115	2	Q7OB67	Q7OB67 anopheles g
1011	189.5	4.8	649	2	Q28657	Q28657 ocyrtolagus	1084	185.5	4.7	1254	2	Q90Y56	Q90Y56 brachydantio
1012	189.5	4.8	2386	1	EFL4_HUMAN	Q727m0 homo sapien	1085	185.5	4.7	1254	2	Q9YH02	Q9YH02 brachydantio
1013	189	4.8	181	2	Q9GSM5	Q9GSM5 chrysomya b	1086	185	4.7	230	2	Q7P550	Q7P550 anopheles g
1014	189	4.8	245	1	Q9BLI8	Q9BLI8 lumbricus r	1087	185	4.7	256	1	KLK4_MOUSE	P00757 mus musculu
1015	189	4.8	246	1	TRYB_RAT	P32822 rattus norv	1088	185	4.7	258	2	Q9NH10	Q28773 papio hamad
1016	189	4.8	246	2	Q7TT42	P32822 mus musculu	1089	185	4.7	287	2	Q9NH10	Q9NH10 agrotis ips
1017	189	4.8	247	1	TRY4_RAT	P12788 rattus norv	1090	185	4.7	320	2	Q7OKL3	Q7OKL3 anopheles g
1018	189	4.8	253	1	KLK7_HUMAN	P49862 homo sapien	1091	185	4.7	708	2	Q8DA23	Q8DA23 vibrio vuln
1019	189	4.8	414	2	Q9CX06	Q9CX06 m mus muscu	1092	185	4.7	509	2	Q7ZTN9	Q7ZTN9 xenopus lae
1020	189	4.8	646	1	LEM3_BOVIN	P42201 bos taurus	1093	184.5	4.7	247	2	O66P09	O66P09 tugu rubrip
1021	189	4.8	758	2	O8CIP8	O8CIP8 rattus norv	1094	184.5	4.7	295	2	O18445	O18445 helicoverpa
1022	188.5	4.8	182	2	O6PLJ5	O6PLJ5 neocaridina	1095	184.5	4.7	321	2	O6GNK3	O6GNK3 xenopus lae
1023	188.5	4.8	239	2	O6LCU4	O6LCU4 lumbricus r	1096	184.5	4.7	427	2	O8BQH6	O8BQH6 mus musculu
1024	188.5	4.8	246	2	Q792Y8	Q792Y8 mus musculu	1097	184.5	4.7	923	2	O6PAR3	O6PAR3 mus musculu
1025	188.5	4.8	266	2	O6AZC0	O6AZC0 brachydantio	1098	184.5	4.7	923	2	O6PAR3	Q7qh41 anopheles g
1026	188.5	4.8	282	1	PA9_RAT	P16296 rattus norv	1099	184.5	4.7	1203	2	Q7OH41	Q90Y54 brachydantio
1027	188.5	4.8	290	1	PR27_HUMAN	O9BP43 homo sapien	1100	184.5	4.7	1213	1	JAG3_BRARE	Q7pn18 anopheles g
1028	188.5	4.8	330	2	O6TE62	O6TE62 rattus norv	1101	184.5	4.7	1582	2	Q7PNI8	Q7PNI8 anopheles g
1029	188.5	4.8	382	2	Q9OWT4	Q9OWT4 crocodylus	1102	184	4.7	246	2	O817P0	O817P0 lumbricus b
1030	188.5	4.8	713	1	Q962W9	Q962W9 podocoryne	1103	184	4.7	246	2	Q6DKQ2	Q6DKQ2 elsenla foe
1031	188.5	4.8	714	1	DL11_RAT	P97677 rattus norv	1104	184	4.7	314	1	TEST_HUMAN	Q9y6m0 homo sapien
1032	188.5	4.8	2330	1	EFL4_MOUSE	P60882 mus musculu	1105	184	4.7	350	2	Q7OKT0	Q7OKT0 anopheles g
1033	188	4.8	228	2	O6FHM3	O6FHM3 homo sapien	1106	184	4.7	381	2	Q7TP23	Q7TP23 rattus norv
1034	188	4.8	235	2	O8N4E0	Q8N4E0 homo sapien	1107	184	4.7	395	2	Q7KX51	Q7KX51 drosophila
1035	188	4.8	253	1	CPND_HUMAN	P00746 homo sapien	1108	184	4.7	405	2	O8SZ60	O8SZ60 drosophila
1036	188	4.8	253	1	O8NSN9	Q8NSN9 homo sapien	1109	184	4.7	745	2	O9OWP9	O9OWP9 triaklis bcy
1037	188	4.8	263	1	KLKR_PRANA	P32824 praomys nat	1110	184	4.7	988	2	O81WY4	O81WY4 homo sapien
1038	188	4.8	265	2	O6P3Z6	O6P3Z6 xenopus tro	1111	183.5	4.7	229	2	Q7PKD3	Q7PKD3 anopheles g
1039	188	4.8	266	2	O8WR10	O8WR10 paraltihode	1112	183.5	4.7	245	2	O6R670	O6R670 oreochromis
1040	188	4.8	271	2	O18487	O18487 penaeus van	1113	183.5	4.7	245	2	O6R671	O6R671 oreochromis
1041	188	4.8	276	2	Q9VXP8	Q9VXP8 drosophila	1114	183.5	4.7	247	2	Q9CPV7	Q9CPV7 mus musculu
1042	188	4.8	278	2	O66FNG	O66FNG brachydantio	1115	183.5	4.7	257	2	O86PV8	Q86PV8 aedes aegypt
1043	188	4.8	282	2	Q7K2R3	Q7K2R3 drosophila	1116	183.5	4.7	305	2	Q7Q654	Q7Q654 anopheles g
1044	188	4.8	333	1	PLMN_CANPA	P80009 canis famli	1117	183.5	4.7	326	2	Q7PZB8	Q7PZB8 anopheles g
1045	188	4.8	404	2	O64ID3	O64ID3 anthomomus	1118	183.5	4.7	329	2	Q42272	Q42272 xenopus lae
1046	188	4.8	505	2	Q7QCJ2	Q7QCJ2 anopheles g	1119	183.5	4.7	387	2	Q7PZP9	Q7PZP9 anopheles g
1047	187.5	4.8	250	2	O17036	Q17036 anopheles g	1120	183.5	4.7	431	2	Q7PV05	Q7PV05 anopheles g
1048	187.5	4.8	251	2	O8N2U3	Q8N2U3 homo sapien	1121	183.5	4.7	1372	2	P91526	P91526 caenorhabdi
1049	187.5	4.8	257	2	O9NB49	O9NB49 aedes aegypt	1122	183	4.6	161	1	PRTC_MACMU	Q28506 macaca mula
1050	187.5	4.8	283	2	Q25394	Q25394 lumbricus r	1123	183	4.6	257	2	O19023	O19023 macaca mula
1051	187.5	4.8	283	1	O8RTU7	O8RTU7 lumbricus r	1124	183	4.6	261	1	KLK1_RAT	P00758 rattus norv
1052	187.5	4.8	304	1	TRJ3_HUMAN	P35030 homo sapien	1125	183	4.6	265	2	Q68G17	Q68G17 rattus norv
1053	187.5	4.8	1216	2	Q90Y55	Q90Y55 brachydantio	1126	183	4.6	266	2	Q7Z0B3	Q7Z0B3 stomoxys ca

1127	183	4.6	267	2	Q9MZ6	Q9MZ6 macaca fasc	1200	180.5	4.6	264	2	062561	062561 penaeus van
1128	183	4.6	272	2	Q9V5X6	Q9V5X6 dirosophila	1201	180.5	4.6	266	2	Q81916	Q81916 biotoma trop
1129	183	4.6	309	2	Q6DHH4	Q6DHH4 brachydanio	1202	180.5	4.6	275	1	FA9_RABIT	FA9_RABIT
1130	183	4.6	322	2	Q9VZ15	Q9VZ15 dirosophila	1203	180.5	4.6	293	2	Q7Z5A4	Q7Z5A4 mus sapien
1131	183	4.6	387	2	Q7RTY4	Q7RTY4 homo sapien	1204	180.5	4.6	390	2	Q8MP08	Q8MP08 bombyx mori
1132	183	4.6	392	1	EAST_DROME	P13582 dirosophila	1205	180.5	4.6	436	1	ACRO_MOUSE	P23578 mus musculu
1133	183	4.6	417	2	Q6JES0	Q6JES0 homo sapien	1206	180.5	4.6	520	2	Q8S793	Q8S793 dirosophila
1134	183	4.6	752	2	Q42374	Q42374 brachydanio	1207	180.5	4.6	717	2	P70006	P70006 xenopus lae
1135	182.5	4.6	157	2	Q6ZMJ3	Q6ZMJ3 homo sapien	1208	180	4.6	157	1	PRTC_HORSE	Q28380 equus cabal
1136	182.5	4.6	248	1	TRY1_CHICK	Q90627 gallus gall	1209	180	4.6	203	2	Q9NE77	Q9NE77 heliothis z
1137	182.5	4.6	257	2	Q8IS83	Q8IS83 aedes albop	1210	180	4.6	234	2	Q9CV76	Q9CV76 mus musculu
1138	182.5	4.6	259	2	Q7QK17	Q7QK17 anopheles g	1211	180	4.6	234	2	Q01136	Q01136 metathizium
1139	182.5	4.6	274	2	Q9VRS7	Q9VRS7 anopheles g	1212	180	4.6	256	2	Q9Y842	Q9Y842 metathizium
1140	182.5	4.6	295	2	Q9M6C6	Q9M6C6 heliothis z	1213	180	4.6	261	1	KLKB_MOUSE	P15946 mus musculu
1141	182.5	4.6	297	2	Q86M89	Q86M89 spodoptera	1214	180	4.6	274	2	Q6DHC9	Q6DHC9 brachydanio
1142	182.5	4.6	327	2	Q8MS77	Q8MS77 dirosophila	1215	180	4.6	275	1	TRY4_ANOGA	P35078 anopheles g
1143	182.5	4.6	330	2	Q6NVP7	Q6NVP7 xenopus tro	1216	180	4.6	292	2	Q7PV05	Q7PV05 anopheles g
1144	182.5	4.6	371	2	Q8MRJ3	Q8MRJ3 dirosophila	1217	180	4.6	324	2	Q6BD16	Q6BD16 dirosophila
1145	182.5	4.6	395	2	Q7PWE2	Q7PWE2 anopheles g	1218	180	4.6	472	2	Q6IGB2	Q6IGB2 dirosophila
1146	182.5	4.6	468	1	PCOI_RAT	Q08628 rattus norv	1219	180	4.6	511	2	Q9VZ15	Q9VZ15 dirosophila
1147	182.5	4.6	470	2	Q7O1S5	Q7O1S5 anopheles g	1220	180	4.6	546	2	Q8SXG6	Q8SXG6 dirosophila
1148	182.5	4.6	482	2	Q28982	Q28982 sus scrofa	1221	180	4.6	1823	2	Q7PRP5	Q7PRP5 anopheles g
1149	182.5	4.6	484	1	LEM2_PIG	P88110 sus scrofa	1222	179.5	4.6	243	1	TRY1_XENLA	P19799 xenopus lae
1150	182.5	4.6	520	2	Q8ING0	Q8ING0 dirosophila	1223	179.5	4.6	250	1	KLK9_HUMAN	Q9UK49 homo sapien
1151	182.5	4.6	722	1	DL11_MOUSE	Q61483 mus musculu	1224	179.5	4.6	258	1	TRY1_DROER	P54629 dirosophila
1152	182.5	4.6	722	1	Q6PFV7	Q6PFV7 mus musculu	1225	179.5	4.6	259	1	CFAD_MOUSE	P03953 mus musculu
1153	182.5	4.6	1551	2	Q9NGV4	Q9NGV4 dirosophila	1226	179.5	4.6	274	1	FA9_SHEEP	P16291 ovis aries
1154	182.5	4.6	2531	2	Q16004	Q16004 lytechinus	1227	179.5	4.6	277	2	Q7Q1D2	Q7Q1D2 anopheles g
1155	182	4.6	240	2	Q9GQ03	Q9GQ03 biophthalari	1228	179.5	4.6	334	2	Q9UE11	Q9UE11 dirosophila
1156	182	4.6	241	2	Q917L2	Q917L2 dirosophila	1229	179.5	4.6	416	2	Q6D3J2	Q6D3J2 xenopus tro
1157	182	4.6	254	2	Q184J4	Q184J4 helioverpa	1230	179.5	4.6	581	2	Q96015	Q96015 dirosophila
1158	182	4.6	261	1	KLK5_MOUSE	P15945 mus musculu	1231	179.5	4.6	728	2	Q90656	Q90656 gallus gall
1159	182	4.6	262	1	TRY1_DROER	P54628 dirosophila	1232	179.5	4.6	1047	2	Q24019	Q24019 dirosophila
1160	182	4.6	278	2	Q7PNE6	Q7PNE6 anopheles g	1233	179.5	4.6	1047	2	Q9VZH2	Q9VZH2 dirosophila
1161	182	4.6	280	2	Q9V5X8	Q9V5X8 dirosophila	1234	179	4.5	253	1	TRYB_DROER	P54625 dirosophila
1162	182	4.6	391	2	Q9V322	Q9V322 dirosophila	1235	179	4.5	266	1	EL1_PIG	P00772 sus scrofa
1163	182	4.6	421	2	Q6ZMR5	Q6ZMR5 homo sapien	1236	179	4.5	270	2	Q8MR11	Q8MR11 parathiodo
1164	182	4.6	726	2	Q8AM87	Q8AM87 cyrops pyrr	1237	179	4.5	280	1	TRY2_DROME	P42280 dirosophila
1165	182	4.6	1238	1	JAG2_HUMAN	Q9Y219 homo sapien	1238	179	4.5	282	2	Q18655	Q18655 plodia inte
1166	181.5	4.6	227	2	Q7R0J1	Q7R0J1 anopheles g	1239	179	4.5	282	2	Q76B45	Q76B45 blarina bre
1167	181.5	4.6	229	2	Q7PHP2	Q7PHP2 anopheles g	1240	179	4.5	283	2	Q7PVP9	Q7PVP9 anopheles g
1168	181.5	4.6	247	1	GRAB_MOUSE	P04187 mus musculu	1241	179	4.5	290	2	Q6UDQ6	Q6UDQ6 penaeus mon
1169	181.5	4.6	258	1	GRAM_RAT	Q03238 rattus norv	1242	179	4.5	384	2	Q9XY63	Q9XY63 ctenocephal
1170	181.5	4.6	269	2	Q7O656	Q7O656 anopheles g	1243	179	4.5	440	2	Q8MR66	Q8MR66 dirosophila
1171	181.5	4.6	284	2	Q96089	Q96089 haemaphysal	1244	179	4.5	474	2	Q6ABE1	Q6ABE1 mus musculu
1172	181.5	4.6	284	2	Q7Q493	Q7Q493 anopheles g	1245	179	4.5	549	1	Q6ABE1	Q6ABE1 mus musculu
1173	181.5	4.6	295	2	Q9NH07	Q9NH07 heliothis z	1246	179	4.5	606	2	P70412	P70412 mus musculu
1174	181.5	4.6	437	1	ACRO_RAT	P29293 rattus norv	1247	179	4.5	612	1	Q7M761	Q7M761 mus musculu
1175	181.5	4.6	450	2	Q7SY99	Q7SY99 xenopus lae	1248	179	4.5	609	2	LEM2_MOUSE	Q00690 mus musculu
1176	181.5	4.6	487	2	Q7ZWR8	Q7ZWR8 xenopus lae	1249	179	4.5	675	2	Q9W6J8	Q9W6J8 dirosophila
1177	181.5	4.6	754	2	Q98UR6	Q98UR6 cyrtinus ca	1250	179	4.5	905	2	Q800L4	Q800L4 gallus gall
1178	181	4.6	249	2	Q788V0	Q788V0 dirosophila	1251	179	4.5	919	2	Q8UVR0	Q8UVR0 gallus gall
1179	181	4.6	254	2	Q184J6	Q184J6 helioverpa	1252	179	4.5	936	2	Q8UVO9	Q8UVO9 gallus gall
1180	181	4.6	254	2	Q76954	Q76954 lacanobia o	1253	179	4.5	2898	2	Q9VLT6	Q9VLT6 dirosophila
1181	181	4.6	255	2	Q34289	Q34289 salvelinus	1254	178.5	4.5	201	2	Q7OAX3	Q7OAX3 anopheles g
1182	181	4.6	255	2	Q63ZFR4	Q63ZFR4 rattus norv	1255	178.5	4.5	243	2	Q7S206	Q7S206 xenopus lae
1183	181	4.6	261	1	KLK3_MOUSE	P00756 mus musculu	1256	178.5	4.5	255	1	TRY4_LUCU	P35044 lucilia cup
1184	181	4.6	261	2	Q7PXE5	Q7PXE5 anopheles g	1257	178.5	4.5	256	2	Q6R561	Q6R561 ostrinia nu
1185	181	4.6	270	2	Q819P2	Q819P2 aplysiina fi	1258	178.5	4.5	262	2	Q7PRT3	Q7PRT3 anopheles g
1186	181	4.6	318	2	Q7QC37	Q7QC37 anopheles g	1259	178.5	4.5	292	2	Q18444	Q18444 agrotis ips
1187	181	4.6	370	2	Q6GQ03	Q6GQ03 rattus norv	1260	178.5	4.5	300	2	Q9NH08	Q9NH08 agrotis ips
1188	181	4.6	405	2	Q8MOS8	Q8MOS8 apis mellif	1261	178.5	4.5	346	2	Q7P243	Q7P243 anopheles g
1189	181	4.6	412	2	Q7SYT3	Q7SYT3 xenopus lae	1262	178.5	4.5	400	2	Q9VCU8	Q9VCU8 dirosophila
1190	181	4.6	494	2	Q9VUD7	Q9VUD7 dirosophila	1263	178.5	4.5	468	1	PCOI_MOUSE	Q61338 mus musculu
1191	181	4.6	674	2	Q7QFW7	Q7QFW7 anopheles g	1264	178.5	4.5	922	1	NRPI_RAT	Q9QW33 rattus norv
1192	181	4.6	840	2	Q9UJ45	Q9UJ45 homo sapien	1265	178.5	4.5	933	1	NRPI_MOUSE	Q09020 rattus norv
1193	181	4.6	910	2	Q6UXD5	Q6UXD5 homo sapien	1266	178	4.5	212	2	Q09020	Q09020 rattus norv
1194	181	4.6	1271	1	YC81_CABEL	Q19981 caenorhabdi	1267	178	4.5	253	1	TRYD_DROER	P54656 dirosophila
1195	181	4.6	1329	2	Q9BME0	Q9BME0 caenorhabdi	1268	178	4.5	256	2	Q18559	Q18559 dirosophila
1196	180.5	4.6	182	2	Q6PLU6	Q6PLU6 penaeus jap	1269	178	4.5	259	2	Q63ZF5	Q63ZF5 rattus norv
1197	180.5	4.6	248	1	TRY2_CHICK	Q90628 gallus gall	1270	178	4.5	289	2	Q8MR67	Q8MR67 dirosophila
1198	180.5	4.6	261	1	EUM3_EURMA	Q97370 euroglyphus	1271	178	4.5	290	2	Q9VRT2	Q9VRT2 dirosophila
1199	180.5	4.6	263	2	Q7Q258	Q7Q258 anopheles g	1272	178	4.5	292	2	Q7QK16	Q7QK16 anopheles g

1273	178	4.5	313	2	Q7Q6S3	Q7q6s3 anopheles g	1346	175	4.4	555	2	Q9H2E2	Q9h2e2 homo sapien
1274	178	4.5	434	2	Q9V7S7	Q9v7s7 drosophila	1347	175	4.4	901	2	Q9H2D5	Q9h2d5 homo sapien
1275	178	4.5	528	1	GD_DROME	GD2589 drosophila	1348	175	4.4	901	2	Q9H2E4	Q9h2e4 homo sapien
1276	178	4.5	996	2	O8TD25	O8td25 homo sapien	1349	175	4.4	906	2	Q9H2D4	Q9h2d4 homo sapien
1277	178	4.5	1212	2	O42347	O42347 gallus gall	1350	175	4.4	906	2	Q9H2E3	Q9h2e3 homo sapien
1278	177.5	4.5	248	1	NKPI_RAT	PI8291 rattus norv	1351	175	4.4	931	1	NRP2_HUMAN	OR6462 homo sapien
1279	177.5	4.5	261	2	Q00J34	Q00j34 ceciliobolu	1352	175	4.4	931	1	Q723T9	Q723t9 homo sapien
1280	177.5	4.5	261	2	Q00J34	Q00j34 ceciliobolu	1353	174.5	4.4	232	2	Q9TXE6	Q9txe6 bombyx mori
1280	177.5	4.5	267	2	Q00J34	Q00j34 ceciliobolu	1354	174.5	4.4	246	1	TRV1_CANFA	P06871 canis famli
1281	177.5	4.5	328	2	O6IR44	O6ire4 xenopus lae	1355	174.5	4.4	371	1	Q7P2P6	Q7p2p6 anopheles g
1282	177.5	4.5	556	2	O6DEK7	O6dek7 brachydantio	1356	174.5	4.4	1676	2	O8IMW2	O8imw2 drosophila
1283	177.5	4.5	691	2	O7PKC4	O7pkc4 anopheles g	1357	174.5	4.4	250	2	O8T4P4	O8t4p4 lepeophthet
1284	177.5	4.5	1964	1	NTC4_MOUSE	PI1695 mus musculu	1357	174	4.4	257	2	Q7Q2X4	Q7q2x4 anopheles g
1285	177.5	4.5	2524	2	O9GPA5	O9gpa5 branchiocto	1358	174	4.4	258	1	EL1_HUMAN	O9un11 homo sapien
1286	177.5	4.5	2811	2	Q7Q434	Q7q434 anopheles g	1359	174	4.4	259	1	KLKM_MOUSE	PI5948 mus musculu
1287	177.5	4.5	233	2	Q7P2R7	Q7p2r7 homo sapien	1360	174	4.4	259	1	KLKI_MOUSE	P00755 mus musculu
1288	177	4.5	257	2	O6IE61	O6ie61 rattus norv	1361	174	4.4	261	1	Q9NIQ1	Q9niq1 saguinus oe
1289	177	4.5	258	2	O9M5U8	O9m5u8 drosophila	1362	174	4.4	262	2	O8T4P7	O8t4p7 lepeophthet
1290	177	4.5	271	1	CTR2_PENVA	PI6178 penaeus van	1363	174	4.4	263	1	KLKO_MOUSE	O61754 mus musculu
1291	177	4.5	328	2	O8BUT6	O8bvt6 mus musculu	1364	174	4.4	266	1	EL1_BOVIN	Q28153 bos taurus
1292	177	4.5	385	2	O251O1	O251o1 hermania m	1365	174	4.4	266	1	EL1_BOVIN	Q28153 bos taurus
1292	177	4.5	385	2	O251O1	O251o1 hermania m	1366	174	4.4	280	2	Q7QNE3	Q7qne3 anopheles g
1293	177	4.5	425	2	Q9MIQ9	O9miq9 anopheles g	1367	174	4.4	439	2	O8BLH5	O8blh5 mus musculu
1294	177	4.5	452	2	O7PZ86	O7p286 anopheles g	1368	174	4.4	923	2	O8ET59	O8et59 homo sapien
1295	177	4.5	473	1	FP2_MYTGA	O25464 mytilus gal	1369	174	4.4	1295	1	GLP1_CABEL	PI3508 caenorhabdi
1296	177	4.5	536	2	Q7PX72	O7px72 anopheles g	1370	174	4.4	1961	2	O6MGB9	O6mg99 rattus norv
1297	177	4.5	737	2	Q9Q422	Q9q422 brachydantio	1371	173.5	4.4	205	2	O9GUB0	O9gub0 homo sapien
1298	177	4.5	747	2	Q91900	O91900 xenopus lae	1372	173.5	4.4	205	2	O9GUB2	O9gub2 homo sapien
1299	177	4.5	927	2	O69DB6	O69db6 brachydantio	1373	173.5	4.4	236	2	Q7S1G3	Q7s1g3 salmo salar
1300	176.5	4.5	182	2	O6PLJ8	O6plj8 procambarus	1374	173.5	4.4	260	1	COGS_HYPLI	P08897 hypodermis 1
1301	176.5	4.5	267	2	O9VRU0	O9vru0 drosophila	1375	173.5	4.4	260	2	O9BPQ4	O9bpq4 hydropoderm 1
1302	176.5	4.5	269	2	O7PM17	O7pm17 anopheles g	1376	173.5	4.4	262	2	O9BN91	O9bn91 agrotis ips
1303	176.5	4.5	413	2	Q7SY25	O7sy25 brachydantio	1377	173.5	4.4	279	2	O6NNB3	O6nnb3 drosophila
1304	176.5	4.5	716	2	Q91691	O91691 xenopus lae	1378	173.5	4.4	319	2	O7PMW4	O7pmw4 anopheles g
1305	176.5	4.5	925	1	NRP2_RAT	O8qzy7 mus musculu	1379	173.5	4.4	369	2	O6Q6S3	Q6q6s3 callinectes g
1306	176.5	4.5	926	2	O8QZV7	O8qzy7 mus musculu	1380	173.5	4.4	548	2	O9XKJ1	O9xkj1 vibrio chol
1307	176.5	4.5	933	1	NRP4_MOUSE	O94466 homo sapien	1381	173.5	4.4	607	2	O35360	O35360 rattus norv
1308	176.5	4.5	2003	1	NTC4_HUMAN	O8av83 brachydantio	1382	173.5	4.4	607	2	O9QZT0	O9qzt0 rattus norv
1309	176	4.5	243	2	O8AV83	O8av83 brachydantio	1383	173.5	4.4	684	2	O8I498	O8i498 cupiennius
1310	176	4.5	260	2	O8T4P5	O8t4p5 lepeophthet	1384	173.5	4.4	717	2	P87357	P87357 brachydantio
1311	176	4.5	261	1	KLK7_RAT	P36373 rattus norv	1385	173.5	4.4	720	2	O8UW44	O8uw44 brachydantio
1312	176	4.5	261	1	KLK9_MOUSE	PI5949 mus musculu	1386	173.5	4.4	809	2	O9BW82	O9bw82 homo sapien
1313	176	4.5	264	1	VDP_BOMMO	O07943 bombyx mori	1387	173.5	4.4	853	2	O9U477	O9u477 homo sapien
1314	176	4.5	265	2	O6GNCO	O6ngco xenopus lae	1388	173.5	4.4	914	1	NRP1_CHICK	P79795 gallus galli
1315	176	4.5	270	1	EL3A_HUMAN	P03093 homo sapien	1389	173.5	4.4	927	2	O6T868	O6t868 brachydantio
1316	176	4.5	270	2	O96QJ8	O96qj8 homo sapien	1390	173.5	4.4	159	2	O282B6	O282b6 canis famli
1317	176	4.5	282	2	O7QCX2	O7qcx2 anopheles g	1391	173	4.4	229	1	TRYP_SQUAC	P00764 equalus aca
1318	176	4.5	297	2	O9W174	O9w174 drosophila	1392	173	4.4	246	2	O6P3E0	O6p3e0 mus musculu
1319	176	4.5	389	2	O9V517	O9v517 drosophila	1393	173	4.4	248	1	MCTR_RAT	P97594 rattus norv
1320	176	4.5	575	2	O22328	O22328 caenorhabdi	1394	173	4.4	250	2	O8HTV6	O8htv6 cyrtocolagus
1321	176	4.5	584	2	O8K480	O8k480 mus musculu	1395	173	4.4	253	2	O9NGV5	O9ngv5 heliothis v
1322	176	4.5	891	2	O9V438	O9v438 drosophila	1396	173	4.4	276	2	P91894	P91894 arenicola m
1323	176	4.5	2318	1	NTC3_MOUSE	O61982 mus musculu	1397	173	4.4	276	2	O7QLD4	O7ql4d anopheles g
1324	176	4.5	2319	1	NTC3_MOUSE	O9i172 rattus norv	1398	173	4.4	287	2	O8CGR6	O8cgr6 mus musculu
1325	175.5	4.4	220	2	O7QMG1	O7qm61 anopheles g	1399	173	4.4	287	2	O67S50	O67s50 olkopleura
1326	175.5	4.4	257	2	O8I8E4	O8i8e4 ochlerotatu	1400	173	4.4	406	2	O250S9	O250s9 helioicidari
1327	175.5	4.4	257	2	O6RS60	O6rs60 oestrinia nu	1401	173	4.4	421	2	O6ICK2	O6ick2 homo sapien
1328	175.5	4.4	272	2	O9VRS3	O9vrs3 anopheles g	1402	173	4.4	438	2	O9VRL1	O9vrl1 drosophila
1329	175.5	4.4	274	1	TRY5_ANOGA	P35039 anopheles g	1403	173	4.4	444	2	O8I6J9	O8i6j9 tenebrio mo
1330	175.5	4.4	459	2	O9V4W7	O9v4w7 drosophila	1404	173	4.4	504	2	O28908	O28908 bos taurus
1331	175.5	4.4	522	2	O8WQW9	O8wqm9 drosophila	1405	173	4.4	578	2	O8BPP4	O8bppy4 mus musculu
1332	175.5	4.4	617	2	O8JIS1	O8jis1 triakis scy	1406	173	4.4	768	1	LEW3_RAT	P88106 rattus norv
1333	175.5	4.4	677	2	O9VTC7	O9vyc7 drosophila	1407	173	4.4	2656	2	O9GNJ3	O9gnj3 paracentroc
1334	175.5	4.4	921	2	O9QX38	O9qx38 rattus norv	1408	173	4.4	249	1	GRAC_MOUSE	O9lve3 m thymopsin
1335	175.5	4.4	1316	2	O96XJ7	O96xj7 homo sapien	1409	172.5	4.4	249	1	O91VE3	O91ve3 mus musculu
1336	175	4.4	249	2	O6QX62	O6qx62 lepeophthet	1410	172.5	4.4	274	2	O7Q9Z7	O7q9z7 anopheles g
1337	175	4.4	260	2	O8T4P6	O8t4p6 lepeophthet	1411	172.5	4.4	274	2	TRY2_ANOGA	O7g927 anopheles g
1338	175	4.4	261	2	O6Z598	O6z598 plodia inte	1412	172.5	4.4	278	1	P91893	P91893 arenicola m
1339	175	4.4	263	2	O7ZIDS	O7zids lepeophthet	1413	172.5	4.4	306	2	O7Q9Z9	O7q9z9 anopheles g
1340	175	4.4	264	2	O8IPY7	O8ipy7 drosophila	1414	172.5	4.4	335	2	O9VJZ8	O9vjz8 drosophila
1341	175	4.4	264	2	O7YSS9	O46644 macaca fasc	1415	172.5	4.4	431	1	ACRO_RABIT	P48038 oryctolagus
1342	175	4.4	266	2	O46644	O46644 macaca fasc	1416	172.5	4.4	433	2	O8T3A2	O8t3a2 clona inces
1343	175	4.4	301	2	O6U8A8	O6u8a8 crithodoro	1417	172.5	4.4	439	2	O9Y122	O9y122 drosophila
1344	175	4.4	340	2	O9W6J9	O9w6j9 diisostichu	1418	172.5	4.4				
1345	175	4.4	421	1	ACRO_HUMAN	PI0323 homo sapien							

1419	172.5	4.4	449	1	PCOI_HUMAN	Q15113	homo sapien
1420	172.5	4.4	863	2	O6AXF9	Q6AXF9	mus musculus
1421	172.5	4.4	923	2	O91X64	Q91X64	mus musculus
1422	172.5	4.4	1202	1	JAG2_RAT	P97607	rattus norv
1423	172	4.4	157	1	PRTC_CAPI	Q28315	capra hircu
1424	172	4.4	235	2	O66P58	Q66P58	fugu rubrip
1425	172	4.4	242	1	F1BC_LUMRU	P81258	lumbicus b
1426	172	4.4	242	2	O96687	Q96687	lumbicus b
1427	172	4.4	249	2	O7KR00	Q7KR00	dirosophila
1428	172	4.4	249	2	O9W6K0	Q9W6K0	notochenta
1429	172	4.4	254	1	TRYP_SABU	P51568	sarcophaga
1430	172	4.4	254	1	O765Z0	Q765Z0	stomoxys ca
1431	172	4.4	260	1	ESTA_CANFA	P09562	canis fami
1432	172	4.4	260	2	O9V7G4	Q9V7G4	dirosophila
1433	172	4.4	261	1	KLK8_MOUSE	P07628	mus musculus
1434	172	4.4	261	2	O6H3Z0	Q6H3Z0	bos taurus
1435	172	4.4	262	2	TRYP_DROME	P42278	dirosophila
1436	172	4.4	262	1	O8S2Q7	Q8S2Q7	dirosophila
1437	172	4.4	262	2	O9V5Y0	Q9V5Y0	dirosophila
1438	172	4.4	390	2	O819Z7	Q819Z7	hyphantria
1439	172	4.4	415	1	ACRO_PIG	P08001	sus scrofa
1440	172	4.4	415	2	O290T5	Q290T5	sus sp. pre
1441	172	4.4	441	2	O81917	Q81917	manduca gex
1442	172	4.4	581	2	O819Z5	Q819Z5	hyphantria
1443	172	4.4	655	2	O7KR00	Q7KR00	dirosophila
1444	172	4.4	721	2	O95YGO	Q95YGO	clona saavig
1445	172	4.4	721	2	O91902	Q91902	xenopus lae
1446	172	4.4	1208	1	O80YA8	Q80YA8	mus musculus
1447	172	4.4	1247	1	JAG2_MOUSE	Q9QY65	mus musculus
1448	171.5	4.3	241	2	O9GQ02	Q9GQ02	biomphalari
1449	171.5	4.3	248	2	O81RE2	Q81RE2	dirosophila
1450	171.5	4.3	261	2	O6H3Z2	Q6H3Z2	equus caball
1451	171.5	4.3	262	1	KLK1_HUMAN	P06870	homo sapien
1452	171.5	4.3	262	2	O7PX38	Q7PX38	anopheles g
1453	171.5	4.3	277	2	O9VPM8	Q9VPM8	dirosophila
1454	171.5	4.3	278	2	O8MQQ2	Q8MQQ2	dirosophila
1455	171.5	4.3	292	2	O9NGY4	Q9NGY4	heliothis v
1456	171.5	4.3	321	2	O61E60	Q61E60	rattus norv
1457	171.5	4.3	373	2	O7PVU0	Q7PVU0	anopheles g
1458	171.5	4.3	1785	2	O9Y211	Q9Y211	homo sapien
1459	171.5	4.3	1785	2	O9Y4V9	Q9Y4V9	homo sapien
1460	171.5	4.3	2403	2	O9UGM2	Q9UGM2	homo sapien
1461	171.5	4.3	2413	2	O96DU4	Q96DU4	homo sapien
1462	171.5	4.3	2413	2	O9UK44	Q9UK44	homo sapien
1463	171.5	4.3	2426	2	O9UGM3	Q9UGM3	homo sapien
1464	171	4.3	175	2	O6PLJ9	Q6PLJ9	equilla ora
1465	171	4.3	245	2	O17439	Q17439	bolitena vi
1466	171	4.3	248	2	O8TAP2	Q8TAP2	lepeophthei
1467	171	4.3	258	2	O61SM6	Q61SM6	homo sapien
1468	171	4.3	260	1	GRAA_MOUSE	P11032	mus musculus
1469	171	4.3	262	2	O7Z1D6	Q7Z1D6	lepeophthei
1470	171	4.3	266	1	EL1_RAT	P00773	rattus norv
1471	171	4.3	273	1	TRV6_ANOGA	P35040	anopheles g
1472	171	4.3	277	1	KLK1_HUMAN	Q9UK43	homo sapien
1473	171	4.3	319	2	O9VAD4	Q9VAD4	homo sapien
1474	171	4.3	358	2	O450Z9	Q450Z9	dirosophila
1475	171	4.3	426	2	O8CFR9	Q8CFR9	mus musculus
1476	171	4.3	454	2	O8TBA2	Q8TBA2	homo sapien
1477	171	4.3	609	2	O9GLF0	Q9GLF0	canis fami
1478	171	4.3	611	1	LEM2_CANFA	P33730	canis fami
1479	171	4.3	737	2	O81YF0	Q81YF0	homo sapien
1480	171	4.3	737	2	O8NFT8	Q8NFT8	homo sapien
1481	171	4.3	737	2	O9JTB4	Q9JTB4	mus musculus
1482	171	4.3	2139	1	CRB_DROME	P10040	dirosophila
1483	171	4.3	2146	2	O9VC57	Q9VC57	dirosophila
1484	171	4.3	2259	2	O9U5J7	Q9U5J7	homo sapien
1485	170.5	4.3	273	2	O45048	Q45048	anopheles g
1486	170.5	4.3	282	2	O57659	Q57659	gallus gall
1487	170.5	4.3	282	2	O7PVP7	Q7PVP7	anopheles g
1488	170.5	4.3	328	2	O6BEA2	Q6BEA2	rattus norv
1489	170.5	4.3	350	2	O9V553	Q9V553	dirosophila
1490	170.5	4.3	377	2	O9V868	Q9V868	dirosophila
1491	170.5	4.3	390	2	O9Y157	Q9Y157	dirosophila

1492	170.5	4.3	408	2	O8MR95	Q8MR95	dirosophila
1493	170.5	4.3	473	2	O7PV63	Q7PV63	anopheles g
1494	170.5	4.3	669	2	Q922H0	Q922H0	mus muscul
1495	170.5	4.3	705	2	O6MZN4	Q6MZN4	homo sapie
1496	170.5	4.3	772	2	O6DI48	Q6DI48	brachydanio
1497	170.5	4.3	802	2	O57462	Q57462	brachydanio
1498	170	4.3	239	2	O8TAP3	Q8TAP3	lepeophthe
1499	170	4.3	239	2	O63Z75	Q63Z75	rattus norv
1500	170	4.3	245	1	MCT1_SHEEP	P80931	ovis aries
ALIGNMENTS							
RESULT 1							
06UXH9	PRELIMINARY;	PRT;	720 AA.				
AC	O6UXH9;						
DT	05-JUL-2004 (TrEMBLrel. 27, Created)						
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)						
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)						
DE	ELGCG699.						
GN	ORFNames=UNO699;						
OS	Homo sapiens (Human).						
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.						
OX	NCBI_TaxID=9606;						
RN	[1]						
RP	SEQUENCE FROM N.A.						
RX	MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;						
RA	Chen H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Bush J.,						
RA	Claik J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,						
RA	Baton D., Foster J., Grimaldi C., Gu O., Hase P.E., Heidens S.,						
RA	Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,						
RA	Lewis L., Liao D., Mark W., Robbie E., Sanchez C., Schonfeld J.,						
RA	Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,						
RA	Vandenberg R., Watanabe C., Wieda D., Woods K., Xie M.H., Yansura D.,						
RA	Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,						
RA	Godowski P.;						
RT	"The secreted protein discovery initiative (SPDI), a large-scale						
RT	effort to identify novel human secreted and transmembrane proteins: a						
RT	bioinformatics assessment."						
RL	Genome Res. 13:2265-2270(2003).						
CC	-1- SIMILARITY: Belongs to peptidase family S1.						
CC	-1- SIMILARITY: Contains 1 EGF-like domain.						
DR	EMBL; AY558346; AAC8712.1; -.						
DR	HSSP: P00734; IBB0.						
DR	GO; GO:0005509; F:calcium ion binding; IEA.						
DR	GO; GO:0004263; F:chymotrypsin activity; IEA.						
DR	GO; GO:0008233; F:peptidase activity; IEA.						
DR	GO; GO:0004295; F:trypsin activity; IEA.						
DR	GO; GO:0006508; P:proteolysis and peptidolysis; IEA.						
DR	InterPro; IPR000859; CUB.						
DR	InterPro; IPR000742; EGF_2.						
DR	InterPro; IPR001881; EGF_Ca.						
DR	InterPro; IPR006209; EGF-like.						
DR	InterPro; IPR006210; IEGF.						
DR	InterPro; IPR001254; Peptidase_S1.						
DR	InterPro; IPR001314; Peptidase_S1A.						
DR	InterPro; IPR009003; Pept_Ser_Cys.						
DR	InterPro; IPR000436; Sushi_SCR_CCP.						
DR	Pfam; PF00433; CUB; 1.						
DR	Pfam; PF00031; EGF; 1.						
DR	Pfam; PF00084; Sushi; 1.						
DR	PRINTS; PR00722; CHYMOTRYPSIN.						
DR	SMART; SM00032; CCP; 2.						
DR	SMART; SM00042; CUB; 1.						
DR	SMART; SM00181; EGF; 2.						
DR	SMART; SM00179; EGF_CA; 1.						
DR	SMART; SM00020; TYP_SPC; 1.						
DR	PROSITE; PS01180; CUB; 1.						
DR	PROSITE; PS00022; EGF_1; 1.						
DR	PROSITE; PS01186; EGF_2; 1.						

DR PROSITE; PS50026; EGF_3; 1.
 DR PROSITE; PS50923; SUSH1; 2.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR EGF-like domain; Hydrolase; Protease; Serine protease.
 SQ SEQUENCE 720 AA; 80198 MW; DC98B8C7241289D3 CRC64;

Query Match 100.0%; Score 3945; DB 2; Length 720;
 Best Local Similarity 100.0%; Pred. No. 1,6e-287;
 Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MELGCMTQLGTLFTQLLLISLTPREYVINEACPGAEWNIMCRCECEYDQIECVCPKRE 60
 DB 1 MELGCMTQLGTLFTQLLLISLTPREYVINEACPGAEWNIMCRCECEYDQIECVCPKRE 60
 OY 61 VVGITIPCCRNENECDSCLIHPGCTIFENCKSCRNCSWGTLDDFYVKGFCACRAGW 120
 DB 61 VVGITIPCCRNENECDSCLIHPGCTIFENCKSCRNCSWGTLDDFYVKGFCACRAGW 120
 OY 121 YGDCMRCGOVLRAPKQIILLESYPLNHCMTIHAKEGYIQLRFVWLSEFPYMCQYD 180
 DB 121 YGDCMRCGOVLRAPKQIILLESYPLNHCMTIHAKEGYIQLRFVWLSEFPYMCQYD 180
 OY 121 YGDCMRCGOVLRAPKQIILLESYPLNHCMTIHAKEGYIQLRFVWLSEFPYMCQYD 180
 DB 121 YGDCMRCGOVLRAPKQIILLESYPLNHCMTIHAKEGYIQLRFVWLSEFPYMCQYD 180
 OY 181 YVEVRDGNRDGOILKRVCGNERPAPIQSISSLHLVLFHSDGSKNPFDFHAIYEITRACS 240
 DB 181 YVEVRDGNRDGOILKRVCGNERPAPIQSISSLHLVLFHSDGSKNPFDFHAIYEITRACS 240
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 DB 181 YVEVRDGNRDGOILKRVCGNERPAPIQSISSLHLVLFHSDGSKNPFDFHAIYEITRACS 240
 OY 241 SSPCFHDTGTLVDKAGSYKACLAGYTGRCENLLEERNCSDPGGPVNGYOKITGGPGLI 300
 DB 241 SSPCFHDTGTLVDKAGSYKACLAGYTGRCENLLEERNCSDPGGPVNGYOKITGGPGLI 300
 OY 241 SSPCFHDTGTLVDKAGSYKACLAGYTGRCENLLEERNCSDPGGPVNGYOKITGGPGLI 300
 DB 241 SSPCFHDTGTLVDKAGSYKACLAGYTGRCENLLEERNCSDPGGPVNGYOKITGGPGLI 300
 OY 301 NGRHAKIGTVVSFFCNNSYVLSGNEKRTCOONGESGKOPICIAACREPKISDLVRRRVL 360
 DB 301 NGRHAKIGTVVSFFCNNSYVLSGNEKRTCOONGESGKOPICIAACREPKISDLVRRRVL 360
 OY 301 NGRHAKIGTVVSFFCNNSYVLSGNEKRTCOONGESGKOPICIAACREPKISDLVRRRVL 360
 DB 301 NGRHAKIGTVVSFFCNNSYVLSGNEKRTCOONGESGKOPICIAACREPKISDLVRRRVL 360
 OY 361 PMOVSRRTPLHOLYSAFSGKOKLOSAPTCKPALPFGLPMGYOHLHTQLOYECISPPYR 420
 DB 361 PMOVSRRTPLHOLYSAFSGKOKLOSAPTCKPALPFGLPMGYOHLHTQLOYECISPPYR 420
 OY 421 RLGSRRRTCLRTGKSGRAPSCIPICGKIENITAKTGGLMPPMAIYRRTSGVHDSGL 480
 DB 421 RLGSRRRTCLRTGKSGRAPSCIPICGKIENITAKTGGLMPPMAIYRRTSGVHDSGL 480
 OY 421 RLGSRRRTCLRTGKSGRAPSCIPICGKIENITAKTGGLMPPMAIYRRTSGVHDSGL 480
 DB 421 RLGSRRRTCLRTGKSGRAPSCIPICGKIENITAKTGGLMPPMAIYRRTSGVHDSGL 480
 OY 481 HKGAMFLVCSGALNERTVYVAACVTDLGKTYMKTADLVYLGKFRDDDBDEKTIQS 540
 DB 481 HKGAMFLVCSGALNERTVYVAACVTDLGKTYMKTADLVYLGKFRDDDBDEKTIQS 540
 OY 541 LOISAIILHPNVDPILLDADAILKLDKARISTRVOPICLAASRDLSTFOESHITVAG 600
 DB 541 LOISAIILHPNVDPILLDADAILKLDKARISTRVOPICLAASRDLSTFOESHITVAG 600
 OY 601 MNVLADVSPGFKNDTLRSQVSVVDLLCEQHEHDGIPVSVTDNMECASMEPTAPSDI 660
 DB 601 MNVLADVSPGFKNDTLRSQVSVVDLLCEQHEHDGIPVSVTDNMECASMEPTAPSDI 660
 OY 661 CTAEFGGIAAIVSFFGRASBPFRMHLMGLVSMYDKTCSHRISTATTKVLFPKDIATERMK 720
 DB 661 CTAEFGGIAAIVSFFGRASBPFRMHLMGLVSMYDKTCSHRISTATTKVLFPKDIATERMK 720
 OY 661 CTAEFGGIAAIVSFFGRASBPFRMHLMGLVSMYDKTCSHRISTATTKVLFPKDIATERMK 720
 DB 661 CTAEFGGIAAIVSFFGRASBPFRMHLMGLVSMYDKTCSHRISTATTKVLFPKDIATERMK 720

RESULT 2

Q6N062 PRELIMINARY; PRT; 720 AA.
 ID Q6N062;
 AC Q6N062;
 DT 05-JUL-2004 (Tremblrel. 27, Created)
 DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
 DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
 DE Hypothetical protein DKFZp66N24154.
 GN Name=DKFZp66N24154;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euteria; Primates; Catarrhini; Hominoidea; Homo.
 OK NCBI_taxonomy9606;
 RN [1]

RP SEQUENCE FROM N.A.
 RC TISSUE=Colon endothel;
 RG The German CDNA Consortium;
 RA Koehler K., Beyer A., Mewes H.W., Weil B., Amlid C., Osanger A.,
 RA Pobo G., Han M., Wiemann S.,
 RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to peptidase family S1.
 CC -1- SIMILARITY: Contains 1 EGF-like domain.

DR EMBL; BX640676; CAE5808.1; -.
 DR HSSP; P00734; 1BB0.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0004295; F:trypsin activity; IEA.
 DR GO; GO:0006508; F:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR000859; CUB.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF_Like.
 DR InterPro; IPR006210; IEGF.
 DR InterPro; IPR001254; Peptidase_S1.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR InterPro; IPR009003; Pept_Ser_Cys.
 DR InterPro; IPR000436; Sush1_SCF_CCP.
 DR Pfam; PF00431; CUB; 1.
 DR Pfam; PF00008; EGF_1.
 DR Pfam; PF00084; Sush1; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00032; CCP; 2.
 DR SMART; SM00042; CUB; 1.
 DR SMART; SM00181; EGF; 2.
 DR SMART; SM00179; EGF_Ca; 1.
 DR SMART; SM00020; Tryp_Spc; 1.
 DR PROSITE; PS01180; CUB; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS50026; EGF_3; 1.
 DR PROSITE; PS50923; SUSH1; 2.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR EGF-like domain; Hydrolase; Hypothetical protein; Protease;
 KW Serine protease.
 SQ SEQUENCE 720 AA; 80196 MW; E98A9F9948EE777D CRC64;

Query Match 99.8%; Score 3936; DB 2; Length 720;
 Best Local Similarity 99.7%; Pred. No. 7,5e-287;
 Matches 718; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 MELGCMTQLGTLFTQLLLISLTPREYVINEACPGAEWNIMCRCECEYDQIECVCPKRE 60
 DB 1 MELGCMTQLGTLFTQLLLISLTPREYVINEACPGAEWNIMCRCECEYDQIECVCPKRE 60
 OY 61 VVGITIPCCRNENECDSCLIHPGCTIFENCKSCRNCSWGTLDDFYVKGFCACRAGW 120
 DB 61 VVGITIPCCRNENECDSCLIHPGCTIFENCKSCRNCSWGTLDDFYVKGFCACRAGW 120
 OY 121 YGDCMRCGOVLRAPKQIILLESYPLNHCMTIHAKEGYIQLRFVWLSEFPYMCQYD 180
 DB 121 YGDCMRCGOVLRAPKQIILLESYPLNHCMTIHAKEGYIQLRFVWLSEFPYMCQYD 180
 OY 121 YGDCMRCGOVLRAPKQIILLESYPLNHCMTIHAKEGYIQLRFVWLSEFPYMCQYD 180
 DB 121 YGDCMRCGOVLRAPKQIILLESYPLNHCMTIHAKEGYIQLRFVWLSEFPYMCQYD 180
 OY 181 YVEVRDGNRDGOILKRVCGNERPAPIQSISSLHLVLFHSDGSKNPFDFHAIYEITRACS 240
 DB 181 YVEVRDGNRDGOILKRVCGNERPAPIQSISSLHLVLFHSDGSKNPFDFHAIYEITRACS 240
 OY 181 YVEVRDGNRDGOILKRVCGNERPAPIQSISSLHLVLFHSDGSKNPFDFHAIYEITRACS 240
 DB 181 YVEVRDGNRDGOILKRVCGNERPAPIQSISSLHLVLFHSDGSKNPFDFHAIYEITRACS 240
 OY 241 SSPCFHDTGTLVDKAGSYKACLAGYTGRCENLLEERNCSDPGGPVNGYOKITGGPGLI 300
 DB 241 SSPCFHDTGTLVDKAGSYKACLAGYTGRCENLLEERNCSDPGGPVNGYOKITGGPGLI 300
 OY 241 SSPCFHDTGTLVDKAGSYKACLAGYTGRCENLLEERNCSDPGGPVNGYOKITGGPGLI 300
 DB 241 SSPCFHDTGTLVDKAGSYKACLAGYTGRCENLLEERNCSDPGGPVNGYOKITGGPGLI 300
 OY 301 NGRHAKIGTVVSFFCNNSYVLSGNEKRTCOONGESGKOPICIAACREPKISDLVRRRVL 360
 DB 301 NGRHAKIGTVVSFFCNNSYVLSGNEKRTCOONGESGKOPICIAACREPKISDLVRRRVL 360
 OY 361 PMOVSRRTPLHOLYSAFSGKOKLOSAPTCKPALPFGLPMGYOHLHTQLOYECISPPYR 420
 DB 361 PMOVSRRTPLHOLYSAFSGKOKLOSAPTCKPALPFGLPMGYOHLHTQLOYECISPPYR 420

Db 361 PMVQSFETLHQLYSAFSSKQKLSAPTKKPLPFEDLPMGVQHLHTQLQYECISPFYR 420
 QY 421 RLGSRRRTCLRTGWSGRAPSCIPICGKINENTAPKTQGLRWPQOAIYRTSGVHDGSL 480
 Db 421 RLGSRRRTCLRTGWSGRAPSCIPICGKINENTAPKTQGLRWPQOAIYRTSGVHDGSL 480
 QY 481 HKAMFLVSGALVNEFTVVAHCVTDLKGVTMIKTADLKVYLGKRYRDDDEKTIQS 540
 Db 481 HKAMFLVSGALVNEFTVVAHCVTDLKGVTMIKTADLKVYLGKRYRDDDEKTIQS 540
 QY 541 LQISATILHNPYPIILDADIALIKLIDKARISRRVNPICLASRDISTFQESHITVAG 600
 Db 541 LQISATILHNPYPIILDADIALIKLIDKARISRRVNPICLASRDISTFQESHITVAG 600
 QY 601 MWVLADVRSPGPKNDTLRSGVSVSDSLCEQEHEDHGIPIVSYTDNMFCSWEPAPSIDI 660
 Db 601 MWVLADVRSPGPKNDTLRSGVSVSDSLCEQEHEDHGIPIVSYTDNMFCSWEPAPSIDI 660
 QY 661 CTAAETGIAVSPFGRASPEPRHMLMGLVSWSYDKTCSHRLSTAFYKVLPEPKMIEERNMK 720
 Db 661 CTAAETGIAVSPFGRASPEPRHMLMGLVSWSYDKTCSHRLSTAFYKVLPEPKMIEERNMK 720
 RESULT 3
 Q96JW2 PRELIMINARY; PRT; 737 AA.
 AC Q96JW2;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein FLJ14935.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NX NCBI_TaxID=9606;
 RX NCBI_TaxID=9606;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX PubMed=1702039; DOI=10.1038/ng1285;
 RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
 Makametu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
 Sekine M., Ohyashiki M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
 Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahara K.,
 Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
 Sudo H., Hoshiro T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
 Takahashi H., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
 Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
 Nishimura K., Iwihara T., Yamashita H., Murakawa K., Fujimori K.,
 Tanai H., Kimura M., Watanabe M., Hirakawa S., Chiba Y., Ishida S.,
 Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
 Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,
 Togliya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
 Nishisehri K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
 Yoshioka K., Matsunawa H., Ichihara T., Shiohara N., Sano S.,
 Moriya S., Momiya H., Satoh N., Takami S., Terashima Y., Suzuki O.,
 Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
 Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kakikami B.,
 Hleihgaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
 Fujimori Y., Komiyama M., Taehiro H., Tanigami A., Fujizawa T.,
 Oho T., Yamada K., Fujii Y., Ozaki K., Hiroo M., Ohmori Y.,
 Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
 Ohtsani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
 Matsunuma K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
 Togaishi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
 Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
 Okumura K., Nagase T., Nomura N., Kikuchi H., Maezono Y., Yamashita R.,
 Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
 RT "Complete sequencing and characterization of 21,243 full-length human
 cDNAs";
 RL Nac. Genet. 36:40-45(2004).
 CC -1- SIMILARITY: Belongs to peptidase family S1.
 CC -1- SIMILARITY: Contains 1 EGF-like domain.
 DR EMBL, AK027841; BAB55404.1; -.

DR HSP, P00736, 1GPZ.
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0004295; F:trypsin activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro: IPR000859; CUB.
 DR InterPro: IPR000742; EGF_2.
 DR InterPro: IPR006209; EGF-like.
 DR InterPro: IPR006210; IEGF.
 DR InterPro: IPR001254; Peptidase_S1.
 DR InterPro: IPR001314; Peptidase_S1A.
 DR InterPro: IPR009003; Pept_Set_Cys.
 DR InterPro: IPR000436; Sushi_SCR_CCP.
 DR Pfam: PF000431; CUB; 1.
 DR Pfam: PF00008; EGF; 1.
 DR Pfam: PF00084; Sushi; 1.
 DR Pfam: PF00089; Sushi_SCR_CCP.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR SMART: SM00032; CCP; 2.
 DR SMART: SM00042; CUB; 1.
 DR SMART: SM00181; EGF; 2.
 DR SMART: SM00020; TRYPSIN; 1.
 DR PROSITE: PS01180; CUB; 1.
 DR PROSITE: PS00022; EGF_1; 1.
 DR PROSITE: PS01186; EGF_2; 1.
 DR PROSITE: PS50026; EGF_3; 1.
 DR PROSITE: PS50923; Sushi; 2.
 DR PROSITE: PS50240; TRYPSIN_DOM; 1.
 DR EGF-like domain; Hydroxylase; Protease; Serine protease.
 KW EGF-like domain; Hydroxylase; Protease; Serine protease.
 SQ SEQUENCE 737 AA; 81952 MW; 4f51689c5eb32b44 CRC64;

Query Match 99.4%; Score 3921.5; DB 2; Length 737;
 Best local Similarity 97.6%; Pred. No. 9.5e-286;
 Matches 719; Conservative 0; Mismatches 1; Indels 17; Gaps 1;

QY 1 MELGCTWQLGLTFLQLLLISLPRBYTVINEACPGAEMWIMCECEYDQIECVCPGKRE 60
 Db 1 MELGCTWQLGLTFLQLLLISLPRBYTVINEACPGAEMWIMCECEYDQIECVCPGKRE 60
 QY 61 VNGYTTPCCNENENEDSCLIHRCCTIFENCKSCRGSGCTLDDPYVVGFCABRAGW 120
 Db 61 VNGYTTPCCNENENEDSCLIHRCCTIFENCKSCRGSGCTLDDPYVVGFCABRAGW 120
 QY 121 YGSDCKRCGCVLAPAPGQILLESYPLNAHCWTHAKPGVQLRVMLSLEPDYMCQYD 180
 Db 121 YGSDCKRCGCVLAPAPGQILLESYPLNAHCWTHAKPGVQLRVMLSLEPDYMCQYD 180
 QY 181 YVEVRDGDNRDQIIRKVCGERPADIQISGLHVLPHSDGSKNFDGPHAIYEEITACS 240
 Db 181 YVEVRDGDNRDQIIRKVCGERPADIQISGLHVLPHSDGSKNFDGPHAIYEEITACS 240
 QY 241 SSGCFHDGTCVLDKASYSKACLAGYTGQRCENL-----LEERRNSDP 283
 Db 241 SSGCFHDGTCVLDKAPYKCACTAGYTGQRCENLLEARRNSDP 300
 QY 284 GGPVNGYOKITGGPGGLNGHAKIGTVSPFCNSVYLSGNERKTCQONGSGKQPICI 343
 Db 301 GGPVNGYOKITGGPGGLNGHAKIGTVSPFCNSVYLSGNERKTCQONGSGKQPICI 360
 QY 344 KACREPKISDLYARRVLPVQVQRETPPLQLVSAFSSKQKLSAPTKKPLPFEDLPMGY 403
 Db 361 KACREPKISDLYARRVLPVQVQRETPPLQLVSAFSSKQKLSAPTKKPLPFEDLPMGY 420
 QY 404 QHLHTQLQYECISPPFRRLASSRRTCLRTGWSGRAPSCIPICGKINENTAPKTQGLRWP 463
 Db 421 QHLHTQLQYECISPPFRRLASSRRTCLRTGWSGRAPSCIPICGKINENTAPKTQGLRWP 480
 QY 464 WQAIYRRTSGVVDGSLHKAMFLVSGALVNEFTVVAHCVTDLKGVTMIKTADLKVY 523
 Db 481 WQAIYRRTSGVVDGSLHKAMFLVSGALVNEFTVVAHCVTDLKGVTMIKTADLKVY 540
 QY 524 LKGYRDDDEKTIQSLQISATILHNPYPIILDADIALIKLIDKARISRRVNPICLAS 583

Db 541 LGKRYRDDDDREKTIQSIQISAIILHPNYDPIILDADIALIKLIDKARISTRVOPICLAA 600
Qy 584 SRDLSTSFQESHITVAGNNVLADVRSPGKNDTLRSQVSVVVDLCEQHEHDGIPVSV 643
Db 601 SRDLSTSFQESHITVAGNNVLADVRSPGKNDTLRSQVSVVVDLCEQHEHDGIPVSV 660
Qy 644 TDNNFCSAWEPTASDICTAETGCIAAVSFPGRASPEPRHMLMGLVMSYDTKTSRHLST 703
Db 661 TDNNFCSAWEPTASDICTAETGCIAAVSFPGRASPEPRHMLMGLVMSYDTKTSRHLST 720
Qy 704 AFTKVLPEPKDWIERNMK 720
Db 721 AFTKVLPEPKDWIERNMK 737
RESULT 4
Q8BU25 PRELIMINARY, PRT, 720 AA.
AC Q8BU25
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 26, Last annotation update)
DE Mus musculus 2 days neonate thymus thymic cells cDNA, RIKEN full-length enriched library, clone:EA30002G05 product:hypothetical EGF-like domain, CUB domain, Sushi domain / SCR repeat / CCP module and Serine protease, trypsin family domain containing protein, full insert sequence.
GN Name=EA30002G05Rik.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD; TISSUE=Thymus;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RL "High-efficiency full-length cDNA cloning";
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD; TISSUE=Thymus;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RL "Functional annotation of a full-length mouse cDNA collection";
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD; TISSUE=Thymus;
RA The FANTOM Consortium;
RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD; TISSUE=Thymus;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Komno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD; TISSUE=Thymus;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Komno H., Akiyama Y., Nishi K., Katsunai T., Teshiro H., Itoh M., Suni N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe K., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,

RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN Integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD; TISSUE=Thymus;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T., Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., Katoh H., Kawai J., Kojima Y., Kondo S., Komno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ono M., Ohnato N., Okazaki Y., Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M., Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T., Tomari A., Tota T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to peptidase family S1.
CC -1- SIMILARITY: Contains 1 EGF-like domain.
DR EMBL: AK088017; BAC40098.1; -.
DR HSSP: P00736; 1GPZ.
DR MGD: MGI:2445082; E430002G05Rik.
DR CO: CO:005615; C:extracellular space; TAs.
DR InterPro: IPR000859; CUB.
DR InterPro: IPR000742; EGF_2.
DR InterPro: IPR006209; EGF_1like.
DR InterPro: IPR06210; 1EGF.
DR InterPro: IPR001254; Peptidase_S1.
DR InterPro: IPR009303; Pept_Ser_Cys.
DR InterPro: IPR000436; Sushi_SCR_CCP.
DR Pfam: PF00431; CUB; 1.
DR Pfam: PF00008; EGF; 1.
DR Pfam: PF00084; Sushi; 1.
DR Pfam: PF00089; Trypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR SMART: SM00032; CCP; 2.
DR SMART: SM00042; CUB; 1.
DR SMART: SM00181; EGF; 2.
DR SMART: SM00020; TRYD_SPC; 1.
DR PROSITE: PS01180; CUB; 1.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS01186; EGF_2; 1.
DR PROSITE: PS50026; EGF_3; 1.
DR PROSITE: PS50923; SUSH1; 2.
DR PROSITE: PS50240; TRYPSIN_DOM; 1.
KW EGF-like domain; Hydrolase; Hypothetical protein; Protease;
KW Serine protease.
SQ SEQUENCE 720 AA; 80300 MW; C09BE076D903A5A0 CRC64;
Query Match 91.6%; Score 3612; DB 2; Length 720;
Best Local Similarity 90.1%; Pred. No. 1.6e-262;
Matches 649; Conservative 33; Mismatches 38; Indels 0; Gaps 0;
Qy 1 MEGACWTQLGLTFLQILLISLPREYTVINEACPGAEWNTMCRBCCEYDQIECVCPKRE 60
Db 1 MELDRWAQLGLVFLQILLISLPREYTVINEACPGAEWNTMCRBCCEYDQIECVCPKRE 60
Qy 61 VVGTTTCCNRENEECSCLIHQCTTFENCKSCRNSMGCTLDDFFVYKGFYCAECRAGW 120
Db 61 VVGTTTCCNRENEECSCLIHQCTTFENCKSCRNSMGCTLDDFFVYKGFYCAECRAGW 120
Qy 121 YGGDCMRGGVLRAPKQGIILLESYPLNAHCEWTHAKRGFVQLRFLYMSLEPDMCOYD 180
Db 121 YGGDCMRGGVLRAPKQGIILLESYPLNAHCEWTHAKRGFVQLRFLYMSLEPDMCOYD 180
Qy 181 YVEVRDNDNDGQIIRKVCNERPAPIQSIGSSLHVLFHSDGSKNPDGFPAIYEBITACS 240
Db 181 YVEVRDNDNDSPRIKRCNERPAPIRISGSSLHVLFHSDGSKNPDGFPAIYEBITACS 240
Qy 241 SSPCFHDGTCVLDKAGSYKCAICLAGTYGRCENLLEBRNCSDPGCPVNGYQKITGGGLI 300

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Db      241  SSBPCFHGTCGLDPTTGSFKACLAGYTGORCENLLEBRNCSDLGGPVGNGYKKTTEGGGL
Qy      301  NGRHAKIGTVSPFCNNSYVLSNGEKRTCOONGEMSGKOPICIKACREPKISDLVRRVL
Db      301  NEHHVAKIGTVSPFCNNSYVLSNGEKRTCOONGEMSGKOPICIKACREPKISDLVRRVL
Qy      361  PMOVOSRETPHLQLYSAFSGKQLQSAPTKKPALPFGLDPMGYOHLTOLQYECISPFYR
Db      361  SMOVOSRETPHLQLYSAFSGKQLQSAPTKKPALPFGLDPMGYOHLTOLQYECISPFYR
Qy      421  RLSSSRRTCLRTGWSGRABSCIPICGKIENITAPKTQGLRWPMQAIYRTSGVHDGSL
Db      421  RLSSSRRTCLRTGWSGRABSCIPICGKIENITAPKTQGLRWPMQAIYRTSGVHDGSL
Qy      481  HKGAMFLVCGALVNERVTVAHAHCVTLGKATMTKADLKVYLGRFYRDDDEKTIOS
Db      481  HKGAMFLVCGALVNERVTVAHAHCVTLGKATMTKADLKVYLGRFYRDDDEKTIOS
Qy      541  LQISAILHBNYDPIILDADIALIKLADKARISTRVOPICLAARDLSTFOSHSITVAG
Db      541  LQISAILHBNYDPIILDADIALIKLADKARISTRVOPICLAARDLSTFOSHSITVAG
Qy      601  WNLVADYRSPGKNDTLRSGVSVVDSLLCEBOHEDHGIPVSVTDNNFCASWEPTASDI
Db      601  WNLVADYRSPGKNDTLRSGVSVVDSLLCEBOHEDHGIPVSVTDNNFCASWEPTASDI
Qy      661  CTATETGIAVSPGRASPEPRMMLGMSVYKCTSHSLSTFTVULPFKMIERNMK
Db      661  CTATETGIAVSPGRASPEPRMMLGMSVYKCTSHSLSTFTVULPFKMIERNMK

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RESULT 5

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ID      08K2B8      PRELIMINARY;      PRT;      720 AA.
AC      08K2B8;
DT      01-OCT-2002 (TREMBLREL, 22, Created)
DT      01-OCT-2002 (TREMBLREL, 22, Last sequence update)
DT      25-OCT-2004 (TREMBLREL, 28, Last annotation update)
DE      Regeneration associated muscle protease.
GN      Name=B430002605Rik;
OS      Mus musculus (Mouse);
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxId=10099;
RN      [1]
RA      STRAIN=CZECH II, TISSUE=Mammary tumor;
RA      MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA      Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA      Kraemer R.D., Collins F.S., Wagner L., Shermen C.M., Schuler G.D.,
RA      Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhac N.K.,
RA      Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA      Datschenko L., Marulima K., Farmer A.A., Rubin G.M., Hong L.,
RA      Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA      Raha S.S., Loguolino N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA      Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA      Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.U., Hulyk S.W.,
RA      Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA      Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA      Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA      Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA      Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA      Krzyzanski M.I., Skelton U., Smallin D.E., Scheraga A., Schein J.E.,
RA      Jones S.J., Marra M.A.;
RT      "Generation and initial analysis of more than 15,000 full-length human
RT      and mouse cDNA sequences";
RL      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN      [2]
RA      STRAIN=CZECH II, TISSUE=Mammary tumor;
RA      Strauberg R.;

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RL      Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RN      [3]
RA      STRAIN=CZECH II, TISSUE=Mammary tumor;
RA      Strauberg R.;
RL      Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
CC      -1- SIMILARITY: Belongs to peptidase family S1.
DR      EMBL; BC031841; AAH31841.1; -
DR      EMBL; BC057685; AAH57685.1; -
DR      HSP; P00736; 1GPZ.
DR      MGI; MGI:2445082; E430002G05Rik.
DR      GO; GO:0005615; C:extracellular space; TAS.
DR      Interpro; IPR000859; CUB.
DR      Interpro; IPR000742; EGF_2.
DR      Interpro; IPR006209; EGF_like.
DR      Interpro; IPR001254; Peptidase_S1.
DR      Interpro; IPR001314; Peptidase_S1.
DR      Interpro; IPR009003; Pept_Ser_Cys.
DR      Interpro; IPR000436; Sushi_SCR_CCP.
DR      Pfam; PF00431; CUB; 1.
DR      Pfam; PF00008; EGF; 1.
DR      Pfam; PF00084; Sushi; 1.
DR      Pfam; PF00089; Trypsin; 1.
DR      PRINTS; PR00722; CHYMOTRYPSIN.
DR      PROSITE; PS01180; CUB; 1.
DR      PROSITE; PS00022; EGF_1; 1.
DR      PROSITE; PS01186; EGF_2; 1.
DR      PROSITE; PSS0026; EGF_3; 1.
DR      PROSITE; PSS0923; Sushi; 2.
DR      PROSITE; PSS0240; TRYPSIN_DOM; 1.
DR      Hydrolase; Protease; Serine protease.
SQ      SEQUENCE 720 AA; 80377 MW; 7172B7F1E690FD0E CRC64;

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Query Match 91.6%; Score 3612; DB 2; Length 720;

Best Local Similarity 90.1%; Pred. No. 1.6e-262; Index 0; Gaps 0;

Matches 649; Conservative 33; Mismatches 38; Indels 0;

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Qy      1  MEIGCWTOGLATFLOLLISLSPREYVINEACPAEAMIMCRECEYDIECVCPKRE 60
Db      1  MELDRNAQLGLVFLQLLISLSPREYVINEACPAEAMIMCRECEYDIECLCPKKE 60
Qy      61  VVGITPPCCNENBECDSLIHPGCTIFENCKSCRNGSGWGLTDDPFVKGFCYACRCAGW 120
Db      61  VVGITPPCCNENBECDSLIHPGCTIFENCKSCRNGSGWGLTDDPFVKGFCYECRCAGW 120
Qy      121  YGSDCRRCGVNAPAPGQILLESYPLNAHCEWTIHAHKGVIOLRFPMLSLEFDYMCQYD 180
Db      121  YGSDCRRCGVNAPAPGQILLESYPLNAHCEWTIHAHKGVIOLRFPMLSLEFDYMCQYD 180
Qy      181  YVEVRDQDNNDGQIIRKVCNERPAPIOSIGSSLHYLFHSDGSKNPFDAIYEETIACS 240
Db      181  YVEVRDQDNNDGQIIRKVCNERPAPIRSGSSLHYLFHSDGSKNPFDAIYEETIACS 240
Qy      241  SSBPCFHGTCGLDPTTGSFKACLAGYTGORCENLLEBRNCSDBGPNVGYOKITGGGLI 300
Db      241  SSBPCFHGTCGLDPTTGSFKACLAGYTGORCENLLEBRNCSDBGPNVGYOKITGGGLI 300
Qy      301  NGRHAKIGTVSPFCNNSYVLSNGEKRTCOONGEMSGKOPICIKACREPKISDLVRRVL 360
Db      301  NEHHVAKIGTVSPFCNNSYVLSNGEKRTCOONGEMSGKOPICIKACREPKISDLVRRVL 360
Qy      361  PMOVOSRETPHLQLYSAFSGKQLQSAPTKKPALPFGLDPMGYOHLTOLQYECISPFYR 420
Db      361  SMOVOSRETPHLQLYSAFSGKQLQSAPTKKPALPFGLDPMGYOHLTOLQYECISPFYR 420
Qy      421  RLSSSRRTCLRTGWSGRABSCIPICGKIENITAPKTQGLRWPMQAIYRTSGVHDGSL 480
Db      421  RLSSSRRTCLRTGWSGRABSCIPICGKIENITAPKTQGLRWPMQAIYRTSGVHDGSL 480
Qy      481  HKGAMFLVCGALVNERVTVAHAHCVTLGKATMTKADLKVYLGRFYRDDDEKTIOS 540
Db      481  HKGAMFLVCGALVNERVTVAHAHCVTLGKATMTKADLKVYLGRFYRDDDEKTIOS 540

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QY 541 LQSAIIILHPNYDPIILDADIAIKLIDKARISTRVOPICLAASRDLSFQESHITVAG 600
DQ 541 LRVSAIIILHPNYDPIILDADIAIKLIDKARISTRVOPICLATRDRISFQESHITVAG 600
QY 601 MNVLADVRSPGKNDTLRSQGVSVVSDSLCEQEHEDHGPVSVYDNMFCAWSMETAPSDI 660
DQ 601 MNVLADVRSPGKNDTLRSQGVSVVSDSLCEQEHEDHGPVSVYDNMFCAWSMETAPSDI 660
QY 661 CTAETGGAIVAFSPGRASPEPRMHLMGVSVSYKTCGSHRLSTAFTKVLPEKWIERNMK 720
DQ 661 CTAETGGAIVAFSPGRASPEPRMHLMGVSVSYKTCGSHRLSTAFTKVLPEKWIERNMK 720
RESULT 6
Q6DIVS PRELIMINARY; PRT; 722 AA.
AC Q6DIVS.
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE MGC89196 protein.
GN Name=MGC89196.
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8364;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=whole body;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Alauser R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Ditachenko L., Marzina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usadi T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
Villalón D.K., Muzny D.M., Sodergren E.O., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
Kryzhanovskii M.I., Skalska U., Smalov D.E., Scherch A., Schin J.E.,
Jones S.J., Maitra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=whole body;
RA Klein S., Gerhardt D.S.,
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 EGF-like domain.
EMBL: BC075430: AAH75430.1.
DR GO: GO:0005509; F:calcium ion binding; IEA.
DR GO: GO:0004295; F:trypsin activity; IEA.
DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro: IPR000859; CUB.
DR InterPro: IPR000742; EGF_2.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR006209; EGF_Like.
DR InterPro: IPR006210; IEGF.
DR InterPro: IPR001254; Peptidase_S1.
DR InterPro: IPR009003; Pept_Ser_Cys.
DR InterPro: IPR000436; Sushi_SCR_CCP.
DR Pfam: PF00431; CUB; 1.
DR Pfam: PF00008; EGF; 1.
DR Pfam: PF00084; Sushi; 2.
DR Pfam: PF00089; Trypsin; 1.

DR SMART; SM00032; CCP; 2.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00181; EGF; 2.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS01160; CUB; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS50026; EGF_3; 1.
DR PROSITE; PS50923; SUSHI; 2.
DR PROSITE; PS50240; TRYPsin_DOM; 1.
KW EGF-like domain; Hydrolyase; Protease; Serine protease.
SQ SEQUENCE 722 AA; 80366 MW; F17356320601A82 CRC64;

Query Match 71.6%; Score 2823; DB 2; Length 722;
Best Local Similarity 66.9%; Pred. No. 2,9e-203;
Matches 483; Conservative 110; Mismatches 127; Indels 2; Gaps 1;

QY 1 MEIGCWTLGLTLQLLLISLP--REYTYINACRGAEMNIMCRCECEYDOIECVPRGK 58
DQ 1 MALIVMSLVVASIHLGLTAAPRSKTYVINENCPGAEMNIMCRDCEYDOVECAAPDG 60
QY 59 REVVGVTIPCCRBENECDSCLHPGCTIPENCKSCNNGSGTLDPFYKGFCAECRA 118
DQ 61 NQKVGTIPCCRBENECDSCLHPGCTIPENCKSCNNGSGTLDPFYKGFCAECRA 120
QY 119 GWYGDGCMRGGOYLRAPKGQILLESYPLNACEMTHAKGFYIQLRFVNLSEFDYMQ 178
DQ 121 GWYGDGCMRGGOYLRAPKGQILLESYPLNACEMTHAKGFYIQLRFVNLSEFDYMQ 180
QY 179 YDVEVVDGNNRGQITIKRCGNERRAPIGSTSSLHVLFHSGSKRDPFHAIEYITA 238
DQ 181 YDVEVVDGNNRGQITIKRCGNERRAPIGSTSSLHVLFHSGSKRDPFHAIEYITA 240
QY 239 CSSSPCHDGTCLVDKXASYKACLAGYTGORCENLLEERNCSDPGPNVNGYQIKGAP 298
DQ 241 CSSSPCHDGTCLVDKXASYKACLAGYTGORCENLLEERNCSDPGPNVNGYQIKGAP 300
QY 299 LINGRHAQITGVSPFCNNSYVLSGNEKRTCOQNGEMSGHOPICAKREPKISDLVRR 358
DQ 301 LSLANHKVGFPIHFCNNSYVLSGNERACLOGAQSGHOPICAKREPKISDLVRR 360
QY 359 VLPNQVOSRETPHLQLYSAFSPKOKLOSAPTKKRALPFGDLPNGYQILHQLQYECISPF 418
DQ 361 VLPNQVOSRETPHLQLYSAFSPKOKLOSAPTKKRALPFGDLPNGYQILHQLQYECISPF 420
QY 419 YBRIGSSRRCTLRGKMSGRAPSCIPICGKIENNTAPKTQGLRMPQAAIYRRTSGVHG 478
DQ 421 YBRIGSSRRCTLRGKMSGRAPSCIPICGKIENNTAPKTQGLRMPQAAIYRRTSGVHG 480
QY 479 SLHKGAFLVCSGALVNERTVVVAACHVTDLGKVTMIKTADLKVVLGKFFRDDRDEXTI 538
DQ 481 SLHKGAFLVCSGALVNERTVVVAACHVTDLGKVTMIKTADLKVVLGKFFRDDRDEXTI 540
QY 539 QSLQISAIILHPNYDPIILDADIAIKLIDKARISTRVOPICLAASRDLSFQESHITV 598
DQ 541 QSLQISAIILHPNYDPIILDADIAIKLIDKARISTRVOPICLAASRDLSFQESHITV 600
QY 599 AGMVLADVRSPGKNDTLRSQGVSVVSDSLCEQEHEDHGPVSVYDNMFCAWSMETAP 658
DQ 601 AGMVLADVRSPGKNDTLRSQGVSVVSDSLCEQEHEDHGPVSVYDNMFCAWSMETAP 660
QY 659 DICTAETGGAIVAFSPGRASPEPRMHLMGVSVSYKTCGSHRLSTAFTKVLPEKWIERN 718
DQ 661 DICTAETGGAIVAFSPGRASPEPRMHLMGVSVSYKTCGSHRLSTAFTKVLPEKWIERN 720
QY 719 MK 720
DQ 721 MK 722

RESULT 7
Q7IRE9


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ID Q71R9 PRELIMINARY; PRT; 417 AA.
AC Q71R9;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Huang Y., Zhou X.M., Zhang P.P., Jiang H.Q., Qin W.X., Zhao X.T.,
RA Man D.F., Gu J.R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to peptidase family S1.
DR EMBL: AF370386; AAQ524.1; -.
DR HSSP: P00734; 1B80.
DR GO: GO:0004263; F:chymotrypsin activity; IEA.
DR GO: GO:0008233; F:peptidase activity; IEA.
DR GO: GO:0004295; F:trypsin activity; IEA.
DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
DR Interpro: IPR001254; Peptidase_S1.
DR Interpro: IPR001314; Peptidase_S1A.
DR Interpro: IPR000436; Sushi_SCR_CCP.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR SMART: SM00020; TRYPSIN_1.
DR PROSITE: PSS0923; SUSHI_1.
DR PROSITE: PSS0240; TRYPSIN_DOM_1.
DR Hydrolase: Protease; Serine protease.
SQ SEQUENCE 417 AA; 46703 MW; 2546A52A3697C1C4 CRC64;

Query Match 53.2%; Score 2059; DB 2; Length 417;
Best Local Similarity 95.6%; Pred. No. 3.5e-146;
Matches 389; Conservative 1; Mismatches 17; Indels 0; Gaps 0;

QY 314 FCNNSVYLGNKERTCOQNGEMSGKOPICIKACREPKISDLVRRRLVPMQVSHETPLHQ 373
DB 11 FVTTPMLVAMRKELARMERMSKOPICIKACEPKISDLVRRRLVPMQVSHETPLHQ 70
QY 374 LYSAAFSKQKLSAFTKPPALPFGLDPMGYQHLLTOLQYECISPFYRLGSSRRRTCLRTG 433
DB 71 LYSAAFSKQKLSAFTKPPALPFGLDPMGYQHLLTOLQYECISPFYRLGSSRRRTCLRTG 130
QY 434 KMSGRAASCIPICKIKENITAPKTQGLRWPMQAAIYRTSGVNDGSLHKGMFLVCGAL 493
DB 131 KMSGRAASCIPICKIKENITAPKTQGLRWPMQAAIYRTSGVNDGSLHKGMFLVCGAL 190
QY 494 VNERTVVAHACVTDLAKVMIKTADLKVVLGKFRDDDDDEKTIQSLQISATILHPNYD 553
DB 191 VNERTVVAHACVTDLAKVMIKTADLKVVLGKFRDDDDDEKTIQSLQISATILHPNYD 250
QY 554 PILLDDIALIKLIDKARISTRVOPICLAASRDISTSFQSHITVAGMNLADVRSPGPK 613
DB 251 PILLDDIALIKLIDKARISTRVOPICLAASRDISTSFQSHITVAGMNLADVRSPGPK 310
QY 614 NDTLRSGVSVVDSLLCEQHEHGHGIVSTDMFCASMEPTAPSDICTAETGIAAVSF 673
DB 311 NDTLRSGVSVVDSLLCEQHEHGHGIVSTDMFCASMEPTAPSDICTAETGIAAVSF 370
QY 674 PGRASPEPRMHLGLVMSYDKTSHRLSTAFTVLPFKMIEBNMK 720
DB 371 PGRASPEPRMHLGLVMSYDKTSHRLSTAFTVLPFKMIEBNMK 417

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DE Hypothetical protein DKFZp586H2123 (Fragment).
GN Name=DKFZp586H2123;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=Uterus;
RA Ansgorge W., Winkner U., Mewes H.W., Gaassenhuber J., Wiemann S.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL050214; CAB43317.1; -.
DR PIR: T08805; T08805.
DR HSSP: P00736; 1MD7.
DR MEROPS: S01.998; -.
DR GO: GO:0008233; F:peptidase activity; IEA.
DR GO: GO:0004295; F:trypsin activity; IEA.
DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
DR Interpro: IPR001254; Peptidase_S1.
DR Interpro: IPR000436; Peptidase_S1A.
DR Pfam: PF00089; Trypsin_1.
DR SMART: SM00020; TRYPSIN_1.
DR PROSITE: PSS0240; TRYPSIN_DOM_1.
DR Hydrolase: Hypothetical protein; Protease; Serine protease.
FT NON TER 1
SQ SEQUENCE 181 AA; 19962 MW; ABC793BE682D439 CRC64;

Query Match 24.1%; Score 949; DB 2; Length 181;
Best Local Similarity 99.4%; Pred. No. 2.9e-63;
Matches 180; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 540 SLQISAILHPNDPILLDDIALIKLIDKARISTRVOPICLAASRDISTSFQSHITVA 599
DB 1 SLQISAILHPNDPILLDDIALIKLIDKARISTRVOPICLAASRDISTSFQSHITVA 60
QY 600 GNVVLADVSPGPKNDTLRSGVSVVDSLLCEQHEHGHGIVSTDMFCASMEPTAPSD 659
DB 61 GNVVLADVSPGPKNDTLRSGVSVVDSLLCEQHEHGHGIVSTDMFCASMEPTAPSD 120
QY 660 ICTAETGIAAVSFGRASPEPRMHLGLVMSYDKTSHRLSTAFTKVLFPKMIERNM 719
DB 121 ICTAETGIAAVSFGRASPEPRMHLGLVMSYDKTSHRLSTAFTKVLFPKMIERNM 180
QY 720 K 720
DB 181 K 181

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RESULT 9

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ID Q8T9S1 PRELIMINARY; PRT; 1019 AA.
AC Q8T9S1;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Factor C precursor.
OS Tachypleus tridentatus (Japanese horseshoe crab).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Metostomata; Xiphosura;
OC Limulidae; Tachypleus.
OX NCBI_TaxID=6853;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=21955715; PubMed=11958140;
RA Wang D., Liu Y., Chen L., Wang L., Yang G., Wu X., Zhang W.;
RT Cloning and expression of Tachypleus tridentatus factor C.;
RL Acta Biochim. Biophys. Sin. 34:77-82(2002).
CC -1- SIMILARITY: Belongs to peptidase family S1.
DR EMBL: AF467804; AAL75577.1; -.
DR HSSP: P00745; 1FDP.
DR GO: GO:0004263; F:chymotrypsin activity; IEA.
DR GO: GO:0008233; F:peptidase activity; IEA.
DR GO: GO:0005529; F:sugar binding; IEA.
DR GO: GO:0004295; F:trypsin activity; IEA.

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DR GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR00742; EGF_2.
 DR InterPro; IPR006209; EGF_1like.
 DR InterPro; IPR006210; EGF.
 DR InterPro; IPR003006; Ig MHC.
 DR InterPro; IPR004043; LCCl.
 DR InterPro; IPR01304; Lectin_C.
 DR InterPro; IPR01254; Peptidase_S1.
 DR InterPro; IPR00314; Peptidase_S1A.
 DR InterPro; IPR009003; Pept. Ser. Cys.
 DR InterPro; IPR000436; Sushi_scr_CCP.
 DR Pfam; PF03815; LCCl; 1.
 DR Pfam; PF00059; Lectin_C; 1.
 DR Pfam; PF00084; Sushi; 3.
 DR Pfam; PF00089; Trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00032; CCP; 5.
 DR SMART; SM00034; CLECT; 1.
 DR SMART; SM00181; EGF; 1.
 DR SMART; SM00603; LCCl; 1.
 DR SMART; SM00020; Tryp. SPC; 1.
 DR PROSITE; PS50041; C TYPE LECTIN 2; 1.
 DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE; PS50026; EGF_3; 1.
 DR PROSITE; PS00290; Ig_MHC; UNKNOWN_1.
 DR PROSITE; PS50820; LCCl; 1.
 DR PROSITE; PS50923; SUSH1; 5.
 DR PROSITE; PS50240; TRYPSIN DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 DR HydroBase; Protease; Serine protease; Signal.
 KW SIGNAL 1 25 Potential.
 FT CHAIN 1 1019 factor C.
 SQ SEQUENCE 1019 AA; 112248 MW; 88E51730AE595993 CRC64;
 Query Match 17.2%; Score 678; DB 2; Length 1019;
 Beet Local Similarity 25.6%; Pred. No. 5.5e-42;
 Matches 223; Conservative 117; Mismatches 308; Indels 222; Gaps 37;
 QY 34 PGAENIM-----CECECYDIE---CVCPRKEVVGTYIPCCRNNEECSCLIHPGCT 86
 DB 184 PNGWSSPPKCIIECAKAVSSPEHCKVTAAPSGNMIEGATL-----RSCDS----PHYL 233
 QY 87 IFENCKSGR-NGSWGTL----- 103
 DB 234 IGEFNLTCGNGQSGQIPCKKLVFCPLDPAVNAHEQVKGKYGQPGSTEVYTT 293
 QY 104 --DDPYVNGFYCAEGR--AGNYGG--DCMR-----CGQVLR--APKG 137
 DB 294 CSGNVFLMGFNTLKNLDGWSGSPSCVAVADREVDGSKAVDFLDVGEPRVRIHCPAG 353
 QY 138 QILLES-----YPLNAHCERTIHA---KPGFVI----- 163
 DB 354 CSLTAGTWGTAIYHELSSVCRRAIHAGKLRNSGGAHVANNPYSDFLSGLDNGIKXSEE 413
 QY 164 LRFVWLSLEPYDM-----COYDYVEVD-----GDNRDQIIRKVCGR--ERPAP 206
 DB 414 LKSLARSPRPDYVSSSTAGRSQCPDGPFEVEENCVYVTSKQRAWERAGVCTNMAARLAV 473
 QY 207 IQS--IGSSLVLPHISDG--SKPFGFH-----AIYEETACSSSCF 245
 DB 474 LDKDVIPLSLTEALNGKGLTTWTGLRLDAEKPFWEIMDRSNVVDNLTTFWASGEPG 533
 QY 246 HDGTCV-LDKXGS-----YKACIAGYTGRCENLLEERN---CSDPGVNVGYOKITGP 297
 DB 534 NETNVCVYLDIDQOLPWKTKRSCFPSSFPACMDLSDNNKAKCDPPGSLENGHATLHQGS 593
 QY 298 GLINGRHAKIGTVVSPFCNNSVYLSGNEKRTCOQNGESGKQPICIK--ACREPRIISDV 355
 DB 594 --IDGFVA--GSSINYSCEVLAHLSGTETVCTTGTSAPKPRCTIKYITQGNPVPVSYG 649
 QY 356 RRRVLPVQVSGRETPHLQLYSAPSKQYLQ--SAPTKKPLPFED-----LP 400

DB 650 SVEIKP---PSRINSISRVGSPFLRLPLPLARAKPPKRRSSQPSITVDLASKVKLP 706
 QY 401 MGQYHLHTOLOYECEIPFYRRLLGSSRRCTLRFGKSGRAPSCTPIGKIENTAP----- 455
 DB 707 EGHYRVSGRAIYTCESRYELLGSGRRCCSNMNMGRAPASCIPVGRSDSPSPFTWNG 766
 QY 456 -KTQGLRMPWQALYRTSGVHDGSLHKGAWELVCSGALVNERTVVAACHCVTLGKVTM 514
 DB 767 NSTEIQWPMQAGISWMLA-----DHNMFLOCGSLNEXMIVYAAACVYSATAEI 819
 QY 515 IKTADLKVVNGKPYRDDDEKTIQSLQISAILHPHYPIILDADIAIKLIDKARIST 574
 DB 820 IDPSQFKIYIGKYYRDSRDDVQVREALEIHVNNYDGNLNFIDALLQLTPTVLT 879
 QY 575 RVQPICLASRDLSFQESH-----TYAGNNVLADVRSPGKNDLRSVGVSYDSL 628
 DB 880 RVQPICLPT--DITL---REHLKEGLAVVTGNG---LNNENYTSSEMIOQAVLPVVAAS 930
 QY 629 LCEQEHEDHGIPIVSVDNMCASWEPTAPSDICTAETGIAVSPGRASPEPRHLMGL 688
 DB 931 TCEEGYKPADLPVTYENNECAGYK-KGRYDACSQSGG--PLVPADDSRTERRWLEGI 987
 QY 689 VSWSYDKTCSH-RLSTAFTKVLPEKMIER 717
 DB 988 VSWGSPSGCGKANQYGGFTVNVFLSMIRQ 1017
 RESULT 10
 ID LFC_TACTR STANDARD; PRT; 1019 AA.
 AC P28175;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 25-OCT-1994 (Rel. 30, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Limulus clotting factor C precursor (EC 3.4.21.84) (FC).
 OS Tachyples tridentatus (Japanese horseshoe crab).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
 OC Limulidae; Tachyples.
 OX NCBI_TaxID=6853;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT), AND PARTIAL SEQUENCE.
 RX MEDLINE=9117916; PubMed=2007602;
 RA Muta T., Miyata T., Misumi Y., Tokunaga F., Nakamura T., Toh Y.,
 RA Ikehara Y., Iwanaga S.;
 RT "Limulus factor C. An endotoxin-sensitive serine protease zymogen with
 RT a mosaic structure of complement-like, epidermal growth factor-like,
 RT and lectin-like domains".
 RL J. Biol. Chem. 266:6554-6561(1991).
 CC -1- FUNCTION: This enzyme is closely associated with an endotoxin-
 CC sensitive hemolymph coagulation system which may play important
 CC roles in both hemostasis and host defense mechanisms. Its active
 CC form catalyzes the activation of factor B.
 CC -1- CATALYTIC ACTIVITY: Selective cleavage of 103-Arg-Ser-104 and
 CC 124-Ile-Ile-125 bonds in Limulus clotting factor B to form
 CC activated factor B. Cleavage of Pro-Arg-I-Xaa bonds in synthetic
 CC substrates.
 CC -1- ENZYME REGULATION: Activated by Gram-negative bacterial
 CC lipopolysaccharides and chymotrypsin.
 CC -1- SUBUNIT: Heterodimer of a light chain and a heavy chain linked by
 CC a disulfide bond.
 CC -1- SUBCELLULAR LOCATION: Secreted in hemolymph.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named Isoforms=2;
 CC Name=long;
 CC IsoId=P28175-1; Sequence=Displayed;
 CC Name=short;
 CC IsoId=P28175-2; Sequence=VSP_005413, VSP_005414;
 CC -1- SIMILARITY: Belongs to the peptidase S1 family.
 CC -1- SIMILARITY: Contains 1 C-type lectin family domain.
 CC -1- SIMILARITY: Contains 1 EGF-like domain.
 CC -1- SIMILARITY: Contains 1 LCCl domain.
 CC -1- SIMILARITY: Contains 5 Sushi (CCP/SCR) domains.
 CC -----


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QY      689 VSMWYDTCGH-RISTAFKYLPPKWIIR 717
Db      988 VSMGSPGCGKANGYCGFTKVNVLISWIRQ 1017

RESULT 11
LFC_CARRO STANDARD; PRT; 1019 AA.
ID LFC_CARRO
AC 026422;
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Limulus clotting factor C precursor (EC 3.4.21.84) (PC).
OS Carinoscorpius rotundicauda (Southeast Asian horseshoe crab).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
OC Limulidae; Carinoscorpius.
OX NCBI_TaxID=6848;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=95268506; PubMed=7538401;
RA Ding J.L., Navas M.A., III, Ho B.;
RT "Molecular cloning and sequence analysis of factor C cDNA from the
RL Singapore horseshoe crab, Carinoscorpius rotundicauda.";
CC -1- FUNCTION: This enzyme is closely associated with an endotoxin-
CC sensitive hemolymph coagulation system which may play important
CC roles in both hemostasis and host defense mechanisms. Its active
CC form catalyzes the activation of factor B.
CC -1- CATALYTIC ACTIVITY: Selective cleavage of 103-Arg-Ser-104 and
CC 124-Ile-Ile-125 bonds in Limulus clotting factor B to form
CC activated factor B. Cleavage of Pro-Arg-Xaa bonds in synthetic
CC substrates.
CC -1- ENZYME REGULATION: Activated by Gram-negative bacterial
CC 1 lipopolysaccharides and chymotrypsin (by similarity).
CC -1- SUBUNIT: Heterodimer of a light chain and a heavy chain linked by
CC a disulfide bond (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted in hemolymph.
CC -1- SIMILARITY: Belongs to the peptidase S1 family.
CC -1- SIMILARITY: Contains 1 C-type lectin family domain.
CC -1- SIMILARITY: Contains 1 EGF-like domain.
CC -1- SIMILARITY: Contains 1 LCCU domain.
CC -1- SIMILARITY: Contains 5 Sushi (CCP/SCR) domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; S77063; AA834361.1; -.
DR HSSP; P00746; IEDP.
DR MEROPS; S01.219; -.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR006210; EGF.
DR InterPro; IPR004043; LCCU.
DR InterPro; IPR001304; Lectin_C.
DR InterPro; IPR001354; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR InterPro; IPR000436; Sushi_SCR_CCP.
DR Pfam; PF03815; LCCU; 1.
DR Pfam; PF00059; Lectin_C; 1.
DR Pfam; PF00084; Sushi; 5.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00032; CCP; 5.
DR SMART; SM00034; CLECT; 1.
DR SMART; SM00181; EGF; 1.
DR SMART; SM00603; LCCU; 1.

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DR SMART; SM00020; TRYP_SPC; 1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE_NEG.
DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; FALSE_NEG.
DR PROSITE; PS50026; EGF_3; 1.
DR PROSITE; PS50820; LCCU; 1.
DR PROSITE; PS50923; SUSHI; 5.
DR PROSITE; PS50240; TRYP_SIN_DOM; 1.
DR PROSITE; PS00134; TRYP_SIN_HIS; 1.
DR PROSITE; PS00135; TRYP_SIN_SER; 1.
KW Cell adhesion; EGF-like domain; Glycoprotein; Hemolymph clotting;
KW Hydrolyase; Lectin; Repeat; Serine protease; Signal; Sushi.
FT SIGNAL 1 25
FT CHAIN 1 25
FT CHAIN 26 690
FT CHAIN 691 1019
FT CHAIN 691 762
FT CHAIN 763 1019
FT DOMAIN 102 137
FT DOMAIN 137 197
FT DOMAIN 140 197
FT DOMAIN 198 256
FT DOMAIN 258 323
FT DOMAIN 325 421
FT DOMAIN 436 568
FT DOMAIN 574 636
FT DOMAIN 689 750
FT DOMAIN 763 1019
FT ACT_SITE 809 809
FT ACT_SITE 865 865
FT ACT_SITE 966 966
FT BINDING 960 960
FT DOMAIN 643 689
FT DISULFID 106 118
FT DISULFID 112 125
FT DISULFID 127 135
FT DISULFID 436 447
FT DISULFID 464 564
FT DISULFID 538 556
FT DISULFID 794 810
FT DISULFID 932 951
FT DISULFID 962 966
FT CARBOHYD 523 523
FT CARBOHYD 534 534
FT CARBOHYD 624 624
FT CARBOHYD 740 740
FT CARBOHYD 767 767
FT CARBOHYD 912 912
SQ SEQUENCE 1019 AA; 112429 MW; 918A1ED8B817B6C3 CRC64;

Query Match 16.9%; Score 665; DB 1; Length 1019;
Best Local Similarity 25.4%; Pred. No. 5.2e-41;
Matches 222; Conservative 118; Mismatches 304; Indels 230; Gaps 37;

QY 34 PGAEWNTMCRBCEYDIEVCYCEKRE-----VGYTTPCCRNENEDSCLIH 82
Db 184 PNGQWSNFPKPCIR---ECAMVSSPEHGKVNALSGDMIGATL---RFSCDS--- 229
QY 83 PGCTIFENCKSCR-NGSMWGTL-----
Db 230 PYVILIGQETLTCQANGMNGOIPQCKRLVFCPDLDPVNHAEHKYIGVEQKYGFPQCTE 289
QY 104 -----DDFYVKGFYCAECR--AGWYG--DKMR-----CGQVLR-- 133
Db 290 VTYTCSGNFYLMGFDTLKCNPDGWSGSPSCVAVADREVDCSKAVDFLDVGEPIRIH 349
QY 134 APKQQLLES-----YPLNAHCEWTIHA---KSGFYI----- 162
Db 350 CPAGCSLTAGTVMGTALYHEHSVCRAAIHAGKLPNSGAVHVYVNNGPSDFLQSDINGI 409
QY 163 ---QLRFVNLISLEFDY-----CGYDVVEYRD-----GDRPDQIILKRVCGN--E 202
Db 410 KSEELKSLANSFRPDVYRSSTAGSGCPDGGFEFVENCYVYTSKQRAWERAQSYCTINMAA 469

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QY 203 RPAPIGS--IGSSLHVLPHSDG-SKNPDGFH-----AIYEITACSS 241
D 470 RLAVLDKDVLPNSLTETLRGKGLTTTWIGLRLDAEKPIWEIMLDRSNVLANLDTFWMAS 529
QY 242 SPCHDGTCLV---DKAGS-YKACACLAGTGCENULEBERN---CSDPGCVNGYQKI 293
D 530 GEPENETNCVMDIQDQLQSVWTKKSCFQPSFACMMDLSDRNKAKDDPSLENGATL 589
QY 294 TGGPGLNGHAKIGTAVSPFCNNSVYLSGNEKRTCOONGEMSGKOPICIK--ACREPKI 351
D 590 HGGS--IDGYYA--GSSIRSCVLAHLSTETVCTTNGTWSAPKRCIKVITCQNPV 645
QY 352 SDLVRRRLPMQVOSRETPHLQLYSAFSAKQKIQ---SAPTKPALPFGD----- 398
D 646 PSYGSVEIKP---PSRTNSISRVGSPFLRLPLPLARAKAPPKRSPSTVDLASK 702
QY 399--LPMGQHHTLOLOECISPFYRLGSSRRTCLRTGKSGRAPSCIPICGKENTAP- 455
D 703 VKLPEGHYRVGSRAIYTCESRYELLQSGRRCDNNGNSGRPASCI PVCGRSDSPSPF 762
QY 456-----KTQGLRMPQAAIYRTSGVHDGSLHKAMFLVCSGALVNERTVVAACHVTDLG 510
D 763 IMNGNSTEIGQMPQAGISRWLA-----DHNMFLQCGSSLNEMKVIYTAACVYISA 815
QY 511 KVTMIKTADLKVVLGKPYRDDDEKTIQSLQISAILHPVYPIILDADIAILKLDKA 570
D 816 TAEIIDNQPVMYLGKYYRDSRDDYVYREALEIHVNPYDGNLNPDIALLQKTPV 875
QY 571 RISTRVOPICLAASRLDSTSFQESH-----TVAGNNVLADVSPGPKDTRLGVS 624
D 876 TLATRVOPICLP---DIYTT--REHLKEGLAVVTGWC---LNENNTYSETTIOAALPV 926
QY 625 VDSLCEGHEHDGIPVSYDNMFCASMEPTAPSDICTAETGIAVASPGRASPEBRMH 684
D 927 VAASTCEEGKEADLPITVENMFCAGIK-KGRYDACSQSGG--PLVFADDSKTERRW 983
QY 685 LMGVLSVYDKTCSH-RLSTAFTKVLPEFKWIER 717
D 984 LEGIVSWGSPSGCGKANQYGFTRKVNPLFWSIRQ 1017

RESULT 12
Q26423
ID 026423 PRELIMINARY; PRT; 1083 AA.
AC 026423;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Factor C.
GN Name:Factor C;
OS Carcinoscorpius rotundicauda (Southeast Asian horseshoe crab).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
OC Lmulidae; Carcinoscorpius.
OX NCBI_TaxID=6848;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95268506; Pubmed=7538401;
RA Ding J.L., Navas M.A. III, Ho B.;
RT "Molecular cloning and sequence analysis of factor C cDNA from the
RT Singapore horseshoe crab, Carcinoscorpius rotundicauda."
RL Mol. Mar. Biol. Biotechnol. 4:90-103 (1995).
CC -1- SIMILARITY: Belongs to peptidase family S1.
EMBL: S77064; AAB34362.1; -.
DR HESP; P00746; 1FDP.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000743; EGF_2.
DR InterPro; IPR006209; EGF_1like.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR003006; Ig_MHC.

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DR InterPro; IPR004043; LCCL.
DR InterPro; IPR001304; Lectin_C.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR InterPro; IPR000436; Sushi_SCR_CCP.
DR Pfam; PF03815; LCCL; 2.
DR Pfam; PF00059; Lectin_C; 1.
DR Pfam; PF00084; Sushi; 3.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00032; CCP; 5.
DR SMART; SM00034; CLECT; 1.
DR SMART; SM00181; EGF; 1.
DR SMART; SM00603; LCCL; 1.
DR SMART; SM00020; TRYP_SPC; 1.
DR PROSITE; PS50041; C-TYPE_LECTIN_2; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS50026; EGF_3; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR PROSITE; PS50820; LCCL; 1.
DR PROSITE; PS50923; SUSHI; 5.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR Hydrobase; Protease; Serine protease.
SM SEQUENCE 1083 AA; 120227 MW; C82CC45ACF9CB7 CRC64;

Query Match 16.9%; Score 665; DB 2; Length 1083;
Best Local Similarity 25.4%; Pred. No. 5,6e-41;
Matches 222; Conservative 118; Mismatches 304; Indels 230; Gaps 37;

QY 34 PGAEWNIMCECEYDQIEVCYCKE-----VVGYTIPCCRNENECDSCLIH 82
D 248 PNGQMSNFPKCLR---ECAMVSPBHKVNALSGDMIGAIL-----RFSQDS----- 293
QY 83 PGCTIFENCKSCR-NGSWGTL----- 103
D 294 PYVLIGDETITCQNGQNGQIQPCKNLVFCPDLVPVNAHKKYKIGVEQKGFQPGTE 353
QY 104-----DDFYVKGFCYAEGR--AGWTGG--DCNR-----CGQVLR-- 133
D 354 VITYSGNYFLMGFDLTKCNPDSGWSGSPSCVAVDREYDCDSKAVDFLDVGBPVRIH 413
QY 134 APKQILLES-----YPLNAHCWTHA---KRGFVI----- 162
D 414 CPAGCSLTAGTWTGTAIYHLLSSVCRAIHAQKLPSNGGAVHVNNGPYSDPLASDLNGI 473
QY 163---QLAFVMLSLFEDYV-----CQDYVEVRD-----GDNRDGQIIRKVCN--E 202
D 474 KSEELKSLARSFRFDVSSSTAGKSGCPDGMFEVDENCVYVTSKQAMERAGVCTNMAA 533
QY 203 RPAPIGS--IGSSLHVLPHSDG-SKNPDGFH-----AIYEITACSS 241
D 534 RLAVLDKDVLPNSLTETLRGKGLTTTWIGLRLDAEKPIWEIMLDRSNVLANLDTFWMAS 593
QY 242 SPCHDGTCLV---DKAGS-YKACACLAGTGCENULEBERN---CSDPGCVNGYQKI 293
D 594 GEPENETNCVMDIQDQLQSVWTKKSCFQPSFACMMDLSDRNKAKDDPSLENGATL 653
QY 294 TGGPGLNGHAKIGTAVSPFCNNSVYLSGNEKRTCOONGEMSGKOPICIK--ACREPKI 351
D 654 HGGS--IDGYYA--GSSIRSCVLAHLSTETVCTTNGTWSAPKRCIKVITCQNPV 709
QY 352 SDLVRRRLPMQVOSRETPHLQLYSAFSAKQKIQ---SAPTKPALPFGD----- 398
D 710 PSYGSVEIKP---PSRTNSISRVGSPFLRLPLPLARAKAPPKRSPSTVDLASK 766
QY 399--LPMGQHHTLOLOECISPFYRLGSSRRTCLRTGKSGRAPSCIPICGKENTAP- 455
D 767 VKLPEGHYRVGSRAIYTCESRYELLQSGRRCDNNGNSGRPASCI PVCGRSDSPSPF 826
QY 456-----KTQGLRMPQAAIYRTSGVHDGSLHKAMFLVCSGALVNERTVVAACHVTDLG 510

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Db      827  IMNGNSTEIGQWQAGISRWLA-----DHNMFLQCCGSLNEMKIVTAACVITYSA  879
Oy      511  KVTWIKTADLKVNVGKFRYDDDDREKTIQSLQISAILHPNYPDILDLADIAILKLDKA  570
Db      880  TAEIIDENQFMVIGKTYRDRSDDDVQVVEALEIHVNPYDGNLFDALQLKTPV  939
Oy      571  RISTRVOPICLAASRDLSFQESH-----TVAGNVLADVRSFGKNDTLRSQVSV  624
Db      940  TLTRVQPICLPF--DITF---REHLKEGTLAVVTGNG---LNENNTYSETIQOAVLPV  990
Oy      625  VDSLCEQHEDHGIPIVSYTNMFCASWEPTASDICTAETGTGIAAVSFPRASPEPRM  684
Db      991  VAASTCEGYKADLPVTVTNMFCAQYK-KGRYDACSQSGG--PLVFADDSKTERRW  1047
Oy      685  LMGVMSYDKTCSH-RLSTAFTKVLPEKDWIER  717
Db      1048  LEGIVMSGSPSGCGKANQYGGFTKVNVTLSMIRQ  1081

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RESULT 13

0868H7 PRELIMINARY, PRT, 680 AA.

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AC      0868H7, PRELIMINARY, PRT, 680 AA.
DT      01-JUN-2003 (TREMblrel. 24, Created)
DT      01-JUN-2003 (TREMblrel. 24, Last sequence update)
DT      01-MAR-2004 (TREMblrel. 26, Last annotation update)
DE      Mannose-binding lectin associated serine protease-1.
GN      Name=MASP-1;
OS      Branchiostoma belcheri (Amphioxus).
OC      Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
OX      Branchiostoma.
RN      NCBI_TaxID=7741;
RP      [1]
RC      SEQUENCE FROM N.A.
RX      TISSUE=Notochord; PubMed=12707349;
RA      Endo Y., Nonaka M., Saiga H., Kakimura Y., Matsushita M., Takahashi M.,
RA      Matsushita M., Fujita T.;
RT      "Origin of mannose-binding lectin-associated serine protease (MASP)-1
RT      and MASP-3 involved in the lectin complement pathway traced back to
RT      the invertebrate, amphioxus.";
RL      J. Immunol. 170:4701-4707(2003).
CC      -1- SIMILARITY: Belongs to peptidase family S1.
DR      EMBL; AB089267; BAC75886.1; -.
DR      HSSP; P00736; IAPQ.
DR      GO; GO:0005576; C:extracellular; IEA.
DR      GO; GO:0005509; F:calcium ion binding; IEA.
DR      GO; GO:0004263; F:chymotrypsin activity; IEA.
DR      GO; GO:0008233; F:peptidase activity; IEA.
DR      GO; GO:0005529; F:sugar binding; IEA.
DR      GO; GO:0004295; F:trypsin activity; IEA.
DR      GO; GO:0006956; P:complement activation; IEA.
DR      GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR      InterPro; IPR00152; Asx_hydroxyl_S.
DR      InterPro; IPR000859; CUB.
DR      InterPro; IPR001881; EGF_Ca.
DR      InterPro; IPR006209; EGF_like.
DR      InterPro; IPR001254; Peptidase_S1.
DR      InterPro; IPR001154; Peptidase_S1A.
DR      InterPro; IPR011361; Pept_S1_Comp_Act.
DR      InterPro; IPR009003; Pept_ser_Cys.
DR      InterPro; IPR000436; Sushi_SCR_CCP.
DR      Pfam; PF00431; CUB; 2.
DR      Pfam; PF00008; EGF; 1.
DR      Pfam; PF00084; Sushi; 2.
DR      Pfam; PF00089; Trypsin; 1.
DR      PIRSF; PIRSF001155; Clr_Cls_MASP; 1.
DR      PRINTS; PR00722; CHYMOTRYPSIN.
DR      SMART; SM00032; CCP; 2.
DR      SMART; SM00043; CUB; 2.
DR      SMART; SM00179; EGF_CA; 1.
DR      SMART; SM00020; Tryp_Spc; 1.

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DR      PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR      PROSITE; PS01180; CUB; 2.
DR      PROSITE; PS01186; EGF_2; 1.
DR      PROSITE; PS01187; EGF_CA; 1.
DR      PROSITE; PS50923; SUSHI; 2.
DR      PROSITE; PS50240; TRYPSIN_DOM; 1.
DR      PROSITE; PS00135; TRYPSIN_SER; 1.
DR      PROSITE; PS00135; TRYPSIN_HIS; UNKNOWN_1.
DR      EGF-like domain; Hydroxylase; Lectin; Protease; Serine protease.
KW      SEQUENCE 680 AA; 75871 MW; 496985A9A728318 CRC64;

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Query Match 15.4%; Score 608.5; DB 2; Length 680;
 Best Local Similarity 26.3%; Pred. No. 5.5e-37;
 Matches 195; Conservative 92; Mismatches 239; Indels 215; Gaps 35;

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Oy      46  CEYDQIECV-----CEPKREV-----VGYT  65
Db      84  CEYDYVVMGDKLVGLFCGETDPTREKVGDRVIBSTGSLSEPKSPSNVDRHGFV  143
Oy      66  IPCCRNENECDSCLHPGCTIFENCKSCNNGSGTLDPFYKGFACACRAG-WTGD  124
Db      144  VHYRVVDRDEC--AVNNGCHNF---CHN-----YISGYCS-CRAGWTMKD  185
Oy      125  ---C-WRCG-QVLRAPKGILLLES---YPLNAHCENTHAKGFVQLRFVMSLEFD-  174
Db      186  RETCKEGCGQVLTOUSGTTSSPEYRLPKVLDLDCDKIOVEBQVVTLOF--DDFDV  242
Oy      175  ----YWCQDYVEVRDNDQDIKRVCGNERPAPIOISGLHYLFHSDGSKNPDG  229
Db      243  EQHPEVSCPYDLHKVQAGDEKGP---YCGKTVPTITSTDHGMHVFPHSDSGENKGF  298
Oy      230  HAIYEITACSSBPCFHDGTCVLDKAGSYCACLAAGTGCRCENLEBRNCSDDGVNG  289
Db      299  RAYTYT-----TARPCAL-----SAP-----  315
Oy      290  YQKITGPGPLINGHAKIGTVSPFCNNSYVLGSENERTCOONGESGKPICTKACREP  349
Db      316  ----AYGMESGNFYSGRVSPACGEYGLDGPDRVCOADGSMGQVPTC-----  362
Oy      350  KISDLVRRRLPMQVOSRETPRLHQLVSAFSSKOKLQSPATKPKALPGDLPNGYHLHQ  409
Db      363  ---ELVVGCPLP-NISNGELEVDGNFS-----YADLAI-----  391
Oy      410  LQYECISPPFRRLGSSRRCTLRGKSGRAPSCPTPGKIENTAPKTQGLR-----WP  463
Db      392  --YRC-DQFYEMAGEGTRFCGADGKMTGNBSPCKPTGCKEFPVTRGLVGGRPARGAP  448
Oy      464  WQAIYVRTSGVHDGSLHKGAMFLVCSGALVNERTVVAACVTDLCKVTMIKTADLKV  523
Db      449  WMAHLHTRPRG-----FCGGTLGDQWVLTAAHCLVSPVTSPLIDSSSVI  496
Oy      524  LGKF-YRDDRDREKTIQSLQISAILHPNYPDILDLADIAILKLDKARISTRVOPICLA  582
Db      497  LGRKAKDKOTBTGTV---QVAQIVHAPAFNFTFLADIALKLESAPRLNPIYTPICLL  553
Oy      583  ASRDLSF---QESHITVAGNVLADVRSBGFNDTLRSQVSVVDSLCEQEHEDHGI  639
Db      554  SEERATATLVGREAATV--GNG---HSDQGFANLRLREFLPLVDTSTCNKYD-----  603
Oy      640  PVSYTDNMFCAWSEPTASDICTAETGTGIAAVSFPRASPEPRNHLGLVMSYDKTCSH  699
Db      604  -FTVTSMTICAGFO-EGGKACRGDSGG--PLAFERTTA-EKVVQGEVVTWNG--CGR  655
Oy      700  RLS-TAFTKVLPEKDWIERM  719
Db      656  KNKYGVTNVIVQLPWLDEVM  676

```

RESULT 14

0868H5 PRELIMINARY, PRT, 680 AA.

AC 0868H5, PRELIMINARY, PRT, 680 AA.
 DT 01-JUN-2003 (TREMblrel. 24, Created)

DT 01-JUN-2003 (TrEMBLrel. 24, last sequence update)
 DE 01-MAR-2004 (TrEMBLrel. 26, last annotation update)
 DT Manose-binding lectin associated serine protease-1.
 GN Name=MASP1/3;
 OS Branchiostoma belcheri (Amphioxus).
 OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
 OC Branchiostoma.
 NCBI_TaxID=7741;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=2593355; PubMed=12707349;
 RA Endo Y., Nonaka M., Saiga H., Kakinuma Y., Matsusita A., Takahashi M.,
 RA Matsushita M., Fujita T.;
 RT Origin of manose-binding lectin-associated serine protease (MASP)-1
 RT and MASP-3 involved in the lectin complement pathway traced back to
 RT the invertebrate, amphioxus.";
 RL J. Immunol. 170:4701-4707(2003).
 CC -1- SIMILARITY: Belongs to peptidase family S1.
 DR EMBL; AB089507; BAC75888.1; -.
 DR HSSP; P00736; IAPQ.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0005529; F:sugar binding; IEA.
 DR GO; GO:0004295; F:trypsin activity; IEA.
 DR GO; GO:0006956; P:complement activation; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR000153; Axx_hydroxyl_S.
 DR InterPro; IPR000859; CUB.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR001254; Peptidase_S1.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR InterPro; IPR011361; Pept_S1_Comp_Act.
 DR InterPro; IPR009003; Pept_Ser_Cys.
 DR InterPro; IPR000436; Sushi_SCR_CCP.
 DR Pfam; PF00431; CUB; 2.
 DR Pfam; PF00008; EGF; 1.
 DR Pfam; PF00084; Sushi; 2.
 DR Pfam; PF00089; Trypsin; 1.
 DR PIRSF; PIRSF001155; C1r_C1s_MASP; 1.
 DR PRINTS; PRO0722; CHYMOTRYPSIN.
 DR SMART; SM00032; CCP; 2.
 DR SMART; SM00042; CUB; 2.
 DR SMART; SM00179; EGF_CA; 1.
 DR SMART; SM00020; Tryp_Sec; 1.
 DR PROSITE; PS00010; Axx_HYDROXYL; UNKNOWN_1.
 DR PROSITE; PS01180; CUB; 2.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS01187; EGF_CA; 1.
 DR PROSITE; PS50923; SUSHI; 2.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR PROSITE; PS50134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KM EGF-like domain; Hydroxylase; Lectin; Protease; Serine protease.
 SQ SEQUENCE 680 AA; 75394 MW; 9837DF68B1C6766 CRC64;

Query Match 15.34; Score 604; DB 2; Length 680;
 Best Local Similarity 27.64; Pred. No. 1.2e-36;
 Matches 186; Conservative 80; Mismatches 229; Indels 178; Gaps 32;

QY 77 DSCLI-HPGCTIFENCSCKNGSGTLDDFYKGFCAECRAG-WTGGD---C-MRCG- 129
 DB 152 DECAVNDGGGHF-----CHN-----YISGYCS-CRAGYIMKRETCFGCGR 195
 QY 130 QVLRAPKGOILLBS-----YPLNAHCEWTIAKPGFVQLRPFVMSLEFD-----YVCOY 179
 DB 196 QVLTQLSGTISSEPPYPLRYLVDCDKIKQVEPVTTLQF---DDPFDVQEQHEVSCPY 252
 QY 180 DYVEVRDGDNRDGGIIRKVCGERPADIQSIGSLHVLFFHSDGSKNDFGFAHYEETIAC 239
 DB 253 DHIKIQAGDEKYGK---CCGKTVPPTITSDHNMVRVFFHSDGSKNDFGFAHYEETIAC 304

QY 240 SSSPCFHDGTCVLDAKAGSYKACLAGYTGRCENLLEERNCSDPGGPVNGYOKITGGPGL 299
 DB 305 -----TAPFCAL-----SAP-----AYGT 319
 QY 300 INGRHAKIGTVSPFCNNSVLSGNEKRTQONGESGKQPI-C-IAACRPKISDLVRR 358
 DB 320 MEGSNFTYSQKVSFACGEGYLLDPDHRVCOADGSGVGPTELVNCGPP----- 370
 QY 359 VLMQVQSRTEPLHQLYSAFNSKQKLSAPTKKPAVFGDLPMGYOHLHTQLQ-YECTISP 417
 DB 371 -----PNSNGEIEVDGNFSTADIAIYRC-DQ 396
 QY 418 FYRRLGSSRRCTCLRTGKMSGRAPSCIPICGKINENITAPKTQGR-----WPMQALYRR 471
 DB 397 FYEMAGGGRFCFCAADGKWTENEPSCKPTGCKPEFVTRGKLVGRPAMRGMPMAMLHRT 456
 QY 472 TSGVHDGSLHKAMFLVCSGALVNERTVVAACVTDLGKVTMIKTLADLKVYLGKF-YRD 530
 DB 457 PRGP-----FCGGTLIGDQWVLTAAHCLVSPVTSPILDKSFVILGKHVARD 504
 QY 531 DDDDEKTIOSLOISATIIHENVPIILLDDIATIKLIDKARISTRVQPICLAASRDISTS 590
 DB 505 KDTTEQTVQVAQTAA--HPAFNFTTSLADIALKLASPARLNPYITPICLSSEEXTAT 561
 QY 591 F---QESHITVAGMNVLADVRSPGKNDTLRSGVSVDSILCEQGHEDHIGIPSVYTDNM 647
 DB 562 LVREGRAVY--GNG-----HSDGFIANEIREVFLPLVDINTCNKTYD-----FTYISDM 610
 QY 648 FCASWEPTAPSDICTAETGIIAIVSPGGRASPPRRHMLGLVMSYDKTCSHLS-TAFT 706
 DB 611 ICAGFO-EGGKDCARGDSG--PLAFFERTA--EKWQGVVSMGNG--CGRKRYGVYT 663
 QY 707 KYLPFKDMIERNM 719
 DB 664 NVQYLPWIDEVM 676

RESULT 15
 ID 0868H6 PRELIMINARY; PRT; 688 AA.
 AC 0868H6;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, last annotation update)
 DE Manose-binding lectin associated serine protease-3.
 GN Name=MASP-3;
 OS Branchiostoma belcheri (Amphioxus).
 OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
 OC Branchiostoma.
 NCBI_TaxID=7741;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Notochord;
 RX MEDLINE=2593355; PubMed=12707349;
 RA Endo Y., Nonaka M., Saiga H., Kakinuma Y., Matsusita A., Takahashi M.,
 RA Matsushita M., Fujita T.;
 RT Origin of manose-binding lectin-associated serine protease (MASP)-1
 RT and MASP-3 involved in the lectin complement pathway traced back to
 RT the invertebrate, amphioxus.";
 RL J. Immunol. 170:4701-4707(2003).
 CC -1- SIMILARITY: Belongs to peptidase family S1.
 DR EMBL; AB089268; BAC75887.1; -.
 DR HSSP; P00760; IEXX.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0005529; F:sugar binding; IEA.
 DR GO; GO:0004295; F:trypsin activity; IEA.
 DR GO; GO:0006956; P:complement activation; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR000153; Axx_hydroxyl_S.

DR InterPro; IPR000859; CUB.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR006209; EGF_Like.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR001361; Pept_S1_Comp_Act.
DR InterPro; IPR009003; Pept_Set_Cys.
DR InterPro; IPR00436; Subst_SCR_CCP.
DR Pfam; PF00431; CUB; 2.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF00084; Subst; 2.
DR Pfam; PF00089; Trypsin; 1.
DR PIRSF; PIRSF001155; C1r_C1s_MASP; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00032; CCP; 2.
DR SMART; SM00042; CUB; 2.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
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DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS01187; EGF_CA; 1.
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DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR EGF-like domain; Hydrolyase; Lectin; Protease; Serine protease.
SQ SEQUENCE 688 AA; 76890 MW; 14B3AD8215BD4D15 CRC64;

Query Match 15.1%; Score 597; DB 2; Length 688;

Best local similarity 26.6%; Pred. No. 4.1e-36;
Matches 197; Conservative 88; Mismatches 244; Indels 212; Gaps 36;

QY 46 CEYDQIECV-----CPGKREV-----VGYT 65
DB 84 CEYDYVKMEBDKLVGLFCGTEDTDTEQVPGDRVIESGSQLSEFKSDFSNADRHGFA 143
QY 66 IPCNENECDSCLIRPGCTIFENCKSCRNKSGWGTLDIFYKGFYCAECRAG-WYGGD 124
DB 144 VHYRVVDREDC--AVDNGSCHHF-----CHN-----YISGYCS-CRAGYWMKD 185
QY 125 ---C-MRGS-QVLRAPKQIILLES---YPLAHCEWTIAKPGFVQLRFVMTLSLEPD- 174
DB 186 RETCFPGCGQVLYTLSTGISSEYPRLYPVYLDQDMKIQVEPGYVTLQF---DDDFV 242
QY 175 ---YMCQYDVEYRDGNDNRDQIIRKVCNERPAPIQSIGSLHVLFHSDGSKNPDGF 229
DB 243 EQHPEVSCPYDHLTKYKADKGP---YCGKIVPPTITSDHNMHVFFHSDDSGENKGF 298
QY 230 HAIYEITACSSSPCFHDGTCVLDAKASYKCACLAGYTGRCENILLEENCSDPGGPVNG 289
DB 299 RAYVFT-----TARPCAL-----SAP----- 315
QY 290 YQKITGPGGLNGRHAIGTVVSPFCNNSYVLSGNEKRTCOQNGEMSGKQPICIKACREP 349
DB 316 -----AVGTMEGSMFTYSQKVSFACGEGYILDGPHRVCOADGWSGVPQC----- 362
QY 350 KISDLVRRARVLPWQVQSRREPLHQLYSAFQKQLQSAPTKKPALFGDLPMGYOHLHTQ 409
DB 363 ---ELVNGGRLP-NISNGEIVDGNFS-----YADIAI----- 391
QY 410 LQYECISPFYRRLLGSSRRTCLRTGMSGRAPSCIPICGI-----ENIT--APKTQGLRW 462
DB 392 ---YRC-DQFYEMAGEGTRFCEAGKMTGNEPSCKPICGESSFPSSRDRIVGGGPKKG-AW 447
QY 463 PMQAAIYRTSGVNDGSLHKAMFL---VCSGALVNERTVVAACHVTDLCKVTMIKTAD 519
DB 448 PMQAAV-----IHQGAPRIKRCFCGALVDKMIILTAACV---GENDILPTGY 493
QY 520 LKVVIGKPYRDDDEKTIQSLQISAILHPYVDPIILDADIAIKLIDKARISTRVQPI 579
DB 494 FNVSLGLHKKEKPEDDNVVFP--EVERVIRHPMDKDNFSDIALLEKEEVDLTDYIRPV 551

QY 580 CLAAS--RDISTFOESHI-TVAGMNVLDVRSRGFNDTLRSGVSVYVDLLCEBOHD 636
DB 552 CLQSRSGRQSAQVQGRAGVVTGKGRTSMLF--GSEANTLQEVVVPVDOECVSAVEG 609
QY 637 HGIPVSYTDNMFQASMEPTAPSDICTAETGIAAVSFPGRASPEPRWHLMLGLVSWSYDKT 636
DB 610 ---DYPVTGMLCAGLR-IGKXDCDGDSCGPIILFDQDPDT-----RYVAGLVSWGEPS 661
QY 697 CSH-RUSTAFTKVLPPFKWIE 716
DB 662 CGRAKKYGVARYENFVQWIK 682

Search completed: July 12, 2005, 17:13:18
Job time : 199 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 12, 2005, 17:08:11 ; Search time 43 Seconds
(without alignments)
1249.938 Million cell updates/sec

Title: US-10-063-546-38

Perfect score: 3945
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Scoring table: BLOSUM62
Gap 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : Issued Patents AA:*
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6: /cgn2_6/prodata/1/aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2946.5	74.7	570	4	US-10-067-422-9
2	665	16.9	1019	1	US-08-296-014A-4
3	665	16.9	1019	2	US-08-596-405-4
4	665	16.9	1019	2	US-08-877-620-4
5	665	16.9	1019	4	US-09-287-368-4
6	665	16.9	1019	4	US-09-626-795-4
7	665	16.9	1083	1	US-08-296-014A-2
8	665	16.9	1083	2	US-08-596-405-2
9	665	16.9	1083	2	US-08-877-620-2
10	665	16.9	1083	4	US-09-287-368-2
11	665	16.9	1083	4	US-09-626-795-2
12	482	12.2	699	4	US-09-949-016-6138
13	475	12.0	717	4	US-09-949-016-1182
14	399.5	10.1	691	4	US-09-949-016-7775
15	327	8.3	855	4	US-09-027-337-2
16	327	8.3	855	4	US-09-644-600-2
17	327	8.3	855	4	US-09-654-600A-2
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37	310.5	7.9	461	4	US-09-054-272-32	Sequence 32, Appl1
38	310.5	7.9	461	4	US-09-949-016-5921	Sequence 5921, Ap
39	310.5	7.9	461	6	5225537-2	Patent No. 5225537
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41	310.5	7.9	485	4	US-09-949-016-10882	Sequence 10882, A
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45	309	7.8	461	6	5270178-2	Patent No. 5270178
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48	307	7.8	460	6	5270178-15	Patent No. 5270178
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55	302.5	7.7	461	6	5270178-18	Patent No. 5270178
56	302.5	7.7	461	6	5270178-17	Patent No. 5270178
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59	288.5	7.3	902	4	US-09-654-600A-10	Sequence 10, Appl1
60	287.5	7.3	356	4	US-09-054-272-18	Sequence 18, Appl1
61	283.5	7.2	587	4	US-09-949-016-11501	Sequence 11501, A
62	282	7.1	527	6	5520913-1	Patent No. 5520913
63	282	7.1	527	6	5520913-1	Patent No. 5520913
64	281	7.1	487	1	US-08-469-486-53	Sequence 53, Appl1
65	281	7.1	487	2	US-08-469-658-53	Sequence 53, Appl1
66	281	7.1	488	4	US-09-367-777-44	Sequence 44, Appl1
67	281	7.1	488	4	US-09-367-791A-27	Sequence 27, Appl1
68	281	7.1	492	1	US-08-469-486-2	Sequence 2, Appl1
69	281	7.1	492	2	US-08-469-658-2	Sequence 2, Appl1
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71	280	7.1	527	1	US-07-609-5108-16	Sequence 16, Appl1
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74	280	7.1	527	4	US-09-612-314A-51	Sequence 51, Appl1
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78	280	7.1	562	2	US-08-811-949-43	Sequence 43, Appl1
79	280	7.1	562	2	US-08-560-098A-50	Sequence 50, Appl1
80	280	7.1	562	2	US-08-883-795A-38	Sequence 38, Appl1
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83	280	7.1	562	6	5185259-3	Patent No. 5185259
84	280	7.1	562	6	5200340-2	Patent No. 5200340
85	280	7.1	562	6	5344773-2	Patent No. 5344773
86	280	7.1	562	6	5185259-3	Patent No. 5185259
87	280	7.1	562	6	5200340-2	Patent No. 5200340
88	280	7.1	562	6	5344773-2	Patent No. 5344773
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92	278.5	7.1	466	3	US-08-321-777-4	Sequence 4, Appl1
93	278.5	7.1	466	3	US-09-009-217-14	Sequence 14, Appl1
94	278.5	7.1	466	3	US-09-009-656-14	Sequence 14, Appl1
95	278.5	7.1	466	5	PCT-US93-04493-4	Sequence 4, Appl1
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102	276	7.0	448	2	US-08-955-471-3	Sequence 3, Appl1	175	248	6.3	230	3	US-08-944-483-62	Sequence 62, Appl1
103	276	7.0	448	5	PCT-US92-10242-3	Sequence 3, Appl1	176	248	6.3	231	2	US-09-027-337-6	Sequence 6, Appl1
104	276	7.0	527	4	US-09-600-985-3	Sequence 3, Appl1	177	248	6.3	221	4	US-09-644-600-6	Sequence 6, Appl1
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109	275.5	7.0	406	5	PCT-US92-10242-5	Sequence 5, Appl1	182	247	6.3	986	4	US-09-949-016-6650	Sequence 6650, Ap
110	275.5	7.0	444	1	US-08-475-845-2	Sequence 2, Appl1	183	246.5	6.2	259	3	US-08-944-483-52	Sequence 52, Appl1
111	275.5	7.0	444	2	US-08-337-690-2	Sequence 2, Appl1	184	246.5	6.2	295	3	US-08-338-368-2	Sequence 2, Appl1
112	275.5	7.0	444	2	US-08-660-289-2	Sequence 2, Appl1	185	246.5	6.2	376	2	US-08-558-269-10	Sequence 10, Appl1
113	275.5	7.0	444	2	US-08-537-807-2	Sequence 2, Appl1	186	246.5	6.2	376	3	US-09-410-882-10	Sequence 10, Appl1
114	275.5	7.0	444	2	US-08-871-003-2	Sequence 2, Appl1	187	246.5	6.2	579	2	US-08-395-411-4	Sequence 4, Appl1
115	275.5	7.0	444	3	US-08-464-233-2	Sequence 2, Appl1	188	246.5	6.2	579	2	US-08-955-471-4	Sequence 4, Appl1
116	275.5	7.0	444	3	US-09-189-607-2	Sequence 2, Appl1	189	246.5	6.2	579	3	US-09-117-708-14	Sequence 14, Appl1
117	275.5	7.0	444	3	US-09-378-907-2	Sequence 2, Appl1	190	246.5	6.2	579	5	PCT-US92-10242-4	Sequence 4, Appl1
118	275.5	7.0	444	5	PCT-US94-05779-2	Sequence 2, Appl1	191	246.5	6.2	615	1	US-07-998-972A-3	Sequence 3, Appl1
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121	275	7.0	562	6	5244676-5	Sequence 6458, Ap	194	246.5	6.2	615	5	PCT-US92-11357-3	Sequence 3, Appl1
122	275	7.0	1113	4	US-09-959-392-4	Sequence 4, Appl1	195	246.5	6.2	622	4	US-09-054-272-42	Sequence 42, Appl1
123	273	6.9	560	4	US-09-912-559-3	Sequence 3, Appl1	196	246.5	6.2	812	4	US-08-991-761A-7	Sequence 7, Appl1
124	273	6.9	560	4	US-09-912-559-3	Sequence 3, Appl1	197	246	6.2	812	4	US-08-278-091-10	Sequence 10, Appl1
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135	263	6.7	431	4	US-09-101-272G-1	Sequence 1, Appl1	208	245	6.2	228	3	US-09-106-466A-10	Sequence 10, Appl1
136	263	6.7	431	6	5188829-1	Sequence 1, Appl1	209	245	6.2	228	3	US-09-106-467-10	Sequence 10, Appl1
137	263	6.7	431	6	5188829-1	Sequence 1, Appl1	210	245	6.2	228	3	US-09-115-994-2	Sequence 2, Appl1
138	262.5	6.7	461	3	US-08-742-877-2	Sequence 2, Appl1	211	244.5	6.2	259	4	US-09-000-846-2	Sequence 2, Appl1
139	262.5	6.7	461	3	US-09-053-871A-21	Sequence 21, Appl1	212	242.5	6.1	416	2	US-08-872-757-2	Sequence 2, Appl1
140	262.5	6.7	461	4	US-10-133-907-5	Sequence 5, Appl1	213	242	6.1	730	3	US-08-872-757-2	Sequence 2, Appl1
141	262.5	6.7	461	6	5521070-2	Sequence 2, Appl1	214	242	6.1	730	4	US-09-850-048A-2	Sequence 4, Appl1
142	262.5	6.7	461	6	5521070-2	Sequence 2, Appl1	215	242	6.1	730	4	US-08-811-849-1	Sequence 1, Appl1
143	262.5	6.7	480	4	US-09-949-016-11123	Sequence 11123, A	216	241.5	6.1	768	1	US-08-572-225-1	Sequence 1, Appl1
144	262.5	6.7	1042	4	US-09-959-392-2	Sequence 2, Appl1	217	241	6.1	354	2	US-08-811-949-61	Sequence 61, Appl1
145	261.5	6.6	415	4	US-09-118-748-2	Sequence 2, Appl1	218	241	6.1	986	4	US-08-872-757-4	Sequence 4, Appl1
146	260.5	6.6	437	1	US-08-487-037-2	Sequence 2, Appl1	219	241	6.1	986	4	US-09-850-048A-4	Sequence 4, Appl1
147	260	6.6	477	2	US-08-560-098A-51	Sequence 51, Appl1	220	240.5	6.1	356	1	US-08-427-640-8	Sequence 8, Appl1
148	258.5	6.6	411	1	US-08-087-163-1	Sequence 1, Appl1	221	240.5	6.1	357	4	US-09-911-842A-2	Sequence 2, Appl1
149	258.5	6.6	411	1	US-08-286-748B-18	Sequence 18, Appl1	222	240	6.1	242	4	US-09-959-392-34	Sequence 34, Appl1
150	258.5	6.6	411	1	US-08-153-799-18	Sequence 18, Appl1	223	239.5	6.1	432	2	US-08-560-098A-47	Sequence 47, Appl1
151	258.5	6.6	411	3	US-09-181-816-1	Sequence 3, Appl1	224	239.5	6.1	1015	4	US-09-285-385C-2	Sequence 2, Appl1
152	258.5	6.6	411	4	US-09-880-503-3	Sequence 3, Appl1	225	239.5	6.1	3594	4	US-09-911-842A-4	Sequence 4, Appl1
153	257.5	6.5	430	6	5219569-2	Sequence 2, Appl1	226	239	6.1	230	4	US-09-601-318-3	Sequence 3, Appl1
154	257.5	6.5	430	6	5219569-2	Sequence 2, Appl1	227	239	6.1	356	2	US-08-681-151-1	Sequence 1, Appl1
155	256.5	6.5	411	4	US-09-403-736-2	Sequence 2, Appl1	228	238.5	6.1	389	2	US-08-811-949-67	Sequence 67, Appl1
156	256.5	6.5	430	1	US-07-944-157A-3	Sequence 3, Appl1	229	238.5	6.0	437	2	US-08-811-949-49	Sequence 49, Appl1
157	255.5	6.5	244	4	US-09-618-259-11	Sequence 11, Appl1	230	238.5	6.0	437	2	US-08-811-949-55	Sequence 55, Appl1
158	254.5	6.5	437	1	US-08-487-037-3	Sequence 3, Appl1	231	238.5	6.0	437	2	US-08-811-949-57	Sequence 57, Appl1
159	254	6.4	261	6	5270178-21	Sequence 21, Appl1	232	238.5	6.0	437	2	US-08-811-949-57	Sequence 57, Appl1
160	254	6.4	261	6	5270178-21	Sequence 21, Appl1	233	238	6.0	237	3	US-08-163-919A-3	Sequence 3, Appl1
161	251	6.4	261	6	5270178-5	Sequence 5, Appl1	234	238	6.0	237	4	US-08-462-515-3	Sequence 3, Appl1
162	251	6.4	261	6	5270178-5	Sequence 5, Appl1	235	238	6.0	237	5	PCT-US94-14073-3	Sequence 3, Appl1
163	250.5	6.3	229	2	US-08-557-146-13	Sequence 13, Appl1	236	236.5	6.0	274	2	US-08-978-404B-5	Sequence 5, Appl1
164	250.5	6.3	229	2	US-09-154-344-13	Sequence 13, Appl1	237	236.5	6.0	355	1	US-08-17-116-1	Sequence 1, Appl1
165	250.5	6.3	411	2	US-08-560-098A-48	Sequence 48, Appl1	238	236.5	6.0	355	1	US-08-217-618-1	Sequence 1, Appl1
166	249.5	6.3	403	4	US-09-880-503-6	Sequence 6, Appl1	239	236.5	6.0	355	1	US-08-427-640-2	Sequence 2, Appl1
167	249.5	6.3	986	4	US-09-285-385C-19	Sequence 19, Appl1	240	236.5	6.0	355	1	US-08-427-640-6	Sequence 6, Appl1
168	249	6.3	251	3	US-08-944-483-47	Sequence 47, Appl1	241	236.5	6.0	355	1	US-08-217-617A-1	Sequence 1, Appl1
169	248.5	6.3	250	3	US-08-944-483-51	Sequence 51, Appl1	242	236.5	6.0	355	2	US-08-217-616-1	Sequence 1, Appl1
170	248.5	6.3	261	6	5270178-19	Sequence 19, Appl1	243	236.5	6.0	355	2	US-08-811-949-45	Sequence 45, Appl1
171	248.5	6.3	261	6	5270178-19	Sequence 19, Appl1	244	236.5	6.0	355	3	US-08-811-949-47	Sequence 47, Appl1
172	248.5	6.3	261	6	5270178-19	Sequence 19, Appl1	245	236.5	6.0	355	3	US-08-794-528-1	Sequence 1, Appl1
173	248.5	6.3	261	6	5270178-20	Sequence 20, Appl1	246	236.5	6.0	355	6	5223256-1	Sequence 1, Appl1

247	236.5	6.0	355	6	5223256-1	Patent No. 5223256	320	228	5.8	812	4	US-09-192-012-3	Sequence 3, Appl1
248	236.5	6.0	356	1	US-08-427-640-4	Sequence 4, Appl1	321	228	5.8	812	4	US-09-335-325-1	Sequence 1, Appl1
249	236.5	6.0	378	1	US-09-553-988-10	Sequence 10, Appl1	322	228	5.8	812	4	US-08-991-761A-12	Sequence 12, Appl1
250	236.5	6.0	378	4	US-09-618-869-10	Sequence 10, Appl1	323	228	5.8	812	5	PCT-US95-05107-1	Sequence 1, Appl1
251	236.5	6.0	472	2	US-08-811-949-63	Sequence 63, Appl1	324	227	5.8	241	4	US-09-657-986B-2	Sequence 2, Appl1
252	236.5	6.0	871	3	US-09-245-041-19	Sequence 19, Appl1	325	227	5.8	265	4	US-09-023-942A-26	Sequence 26, Appl1
253	236.5	6.0	871	4	US-09-358-055B-19	Sequence 19, Appl1	326	227	5.8	308	3	US-08-705-875A-10	Sequence 10, Appl1
254	236.5	6.0	871	4	US-09-893-338-19	Sequence 19, Appl1	327	227	5.8	308	4	US-09-242-999-10	Sequence 10, Appl1
255	236.5	6.0	1013	2	US-08-866-650-3	Sequence 3, Appl1	328	226.5	5.7	443	3	US-09-518-046-2	Sequence 2, Appl1
256	236.5	6.0	1013	2	US-09-021-287-3	Sequence 3, Appl1	329	226.5	5.7	2787	4	US-09-245-041-15	Sequence 15, Appl1
257	236.5	6.0	1013	3	US-09-240-473-1	Sequence 3, Appl1	330	226.5	5.7	2787	4	US-09-358-055B-15	Sequence 15, Appl1
258	236.5	6.0	1350	3	US-09-245-041-17	Sequence 17, Appl1	331	226.5	5.7	2787	4	US-09-893-238-15	Sequence 15, Appl1
259	236.5	6.0	1350	4	US-09-358-055B-17	Sequence 17, Appl1	332	226	5.7	406	4	US-09-851-588-6	Sequence 6, Appl1
260	236.5	6.0	1350	4	US-09-893-338-17	Sequence 17, Appl1	333	226	5.7	423	3	US-09-656-002-2	Sequence 2, Appl1
261	236	6.0	355	2	US-08-811-949-53	Sequence 53, Appl1	334	226	5.7	435	3	US-09-008-971A-6	Sequence 6, Appl1
262	236	6.0	355	2	US-08-811-949-59	Sequence 59, Appl1	335	226	5.7	435	4	US-09-607-745-2	Sequence 2, Appl1
263	235	6.0	270	2	US-08-978-404B-8	Sequence 8, Appl1	336	226	5.7	435	4	US-09-851-588-8	Sequence 8, Appl1
264	233.5	5.9	252	3	US-08-944-483-72	Sequence 72, Appl1	337	226	5.7	471	4	US-09-949-016-9238	Sequence 9238, Ap
265	233.5	5.9	253	2	US-09-027-337-8	Sequence 8, Appl1	338	226	5.7	481	4	US-09-949-016-9239	Sequence 9239, Ap
266	233.5	5.9	253	4	US-09-644-600-8	Sequence 8, Appl1	339	226	5.7	637	4	US-09-949-016-11538	Sequence 11538, A
267	233.5	5.9	253	4	US-09-654-600A-8	Sequence 8, Appl1	340	226	5.7	637	4	US-09-949-016-11539	Sequence 11539, A
268	233.5	5.9	383	2	US-08-558-269-6	Sequence 6, Appl1	341	225.5	5.7	348	4	US-09-949-016-6979	Sequence 6979, Ap
269	233.5	5.9	383	6	US-09-410-882-6	Sequence 6, Appl1	342	224.5	5.7	222	4	US-09-959-392-32	Sequence 32, Appl1
270	233.5	5.9	546	6	5200340-6	Patent No. 5200340	343	224.5	5.7	235	3	US-08-944-483-65	Sequence 65, Appl1
271	233.5	5.9	546	6	5200340-6	Patent No. 5200340	344	224	5.7	235	2	US-09-016-366A-17	Sequence 17, Appl1
272	232.5	5.9	259	4	US-10-165-442-2	Sequence 2, Appl1	345	224	5.7	275	2	US-08-978-404B-12	Sequence 12, Appl1
273	232.5	5.9	295	4	US-10-165-442-1	Sequence 5, Appl1	346	224	5.7	276	4	US-09-880-503-5	Sequence 5, Appl1
274	232.5	5.9	1013	2	US-08-866-650-5	Sequence 5, Appl1	347	224	5.7	306	2	US-08-560-098A-45	Sequence 45, Appl1
275	232.5	5.9	1013	2	US-09-021-287-5	Sequence 5, Appl1	348	224	5.7	323	4	US-09-880-503-7	Sequence 7, Appl1
276	232.5	5.9	1013	3	US-08-991-408-2	Sequence 2, Appl1	349	224	5.7	331	2	US-08-560-098A-46	Sequence 46, Appl1
277	232.5	5.9	1013	3	US-09-240-473-5	Sequence 5, Appl1	350	223.5	5.7	245	3	US-08-944-483-69	Sequence 69, Appl1
278	232.5	5.9	1013	3	US-09-432-473-2	Sequence 2, Appl1	351	223.5	5.7	346	4	US-09-949-016-9000	Sequence 9000, Ap
279	232.5	5.9	1013	4	US-09-285-385C-20	Sequence 20, Appl1	352	223	5.7	238	3	US-08-944-483-64	Sequence 64, Appl1
280	232	5.9	638	2	US-08-681-151-3	Sequence 3, Appl1	353	223	5.7	521	4	US-09-949-016-11081	Sequence 11081, A
281	231.5	5.9	399	2	US-08-811-949-65	Sequence 65, Appl1	354	223	5.7	521	4	US-09-949-016-11082	Sequence 11082, A
282	231.5	5.9	417	4	US-09-820-002-4	Sequence 4, Appl1	355	223	5.7	521	4	US-09-949-016-11083	Sequence 11083, Ap
283	231	5.9	365	1	US-08-093-741-83	Sequence 83, Appl1	356	222.5	5.6	452	4	US-09-949-016-7182	Sequence 7182, Ap
284	231	5.9	365	1	US-08-720-012-83	Sequence 83, Appl1	357	222.5	5.6	790	4	US-08-991-761A-13	Sequence 13, Appl1
285	231	5.9	333	2	US-08-560-098A-44	Sequence 44, Appl1	358	222	5.6	274	2	US-09-016-366A-21	Sequence 21, Appl1
286	231	5.9	333	3	US-08-967-024C-24	Sequence 24, Appl1	359	222	5.6	274	2	US-08-978-404B-16	Sequence 16, Appl1
287	231	5.9	333	3	US-08-967-024C-25	Sequence 25, Appl1	360	222	5.6	233	3	US-09-734-675-4	Sequence 73, Appl1
288	231	5.9	1012	4	US-09-285-385C-4	Sequence 4, Appl1	361	222	5.6	407	3	US-08-944-483-73	Sequence 73, Appl1
289	230.5	5.8	295	4	US-10-165-442-3	Sequence 4, Appl1	362	221	5.6	273	2	US-08-978-404B-6	Sequence 6, Appl1
290	230.5	5.8	295	4	US-10-165-442-4	Sequence 4, Appl1	363	221	5.6	300	3	US-08-705-875A-6	Sequence 6, Appl1
291	230.5	5.8	302	3	US-09-230-731-26	Sequence 26, Appl1	364	221	5.6	300	4	US-09-242-999-6	Sequence 6, Appl1
292	230.5	5.8	302	4	US-09-242-999-22	Sequence 22, Appl1	365	221	5.6	1193	4	US-09-949-016-10498	Sequence 10498, A
293	230	5.8	222	4	US-09-959-392-21	Sequence 31, Appl1	366	220.5	5.6	376	4	US-09-820-002-2	Sequence 2, Appl1
294	230	5.8	248	3	US-08-944-483-63	Sequence 63, Appl1	367	220	5.6	273	2	US-09-016-366A-19	Sequence 19, Appl1
295	230	5.8	387	3	US-09-032-215-8	Sequence 8, Appl1	368	220	5.6	273	2	US-08-978-404B-14	Sequence 14, Appl1
296	230	5.8	387	3	US-09-032-215-13	Sequence 13, Appl1	369	219.5	5.6	254	3	US-08-944-483-50	Sequence 50, Appl1
297	229	5.8	242	3	US-09-004-731-36	Sequence 36, Appl1	370	219.5	5.6	255	2	US-09-027-337-7	Sequence 7, Appl1
298	229	5.8	242	3	US-08-749-699-36	Sequence 36, Appl1	371	219.5	5.6	255	4	US-09-644-600-7	Sequence 7, Appl1
299	229	5.8	242	3	US-09-004-729-36	Sequence 36, Appl1	372	219.5	5.6	255	4	US-09-654-600A-7	Sequence 7, Appl1
300	229	5.8	400	3	US-09-004-731-30	Sequence 30, Appl1	373	218.5	5.5	244	4	US-09-601-318-4	Sequence 4, Appl1
301	229	5.8	400	3	US-09-004-731-33	Sequence 33, Appl1	374	218.5	5.5	244	4	US-09-601-318-5	Sequence 5, Appl1
302	229	5.8	400	3	US-08-749-699-30	Sequence 30, Appl1	375	218.5	5.5	244	4	US-09-601-318-6	Sequence 6, Appl1
303	229	5.8	400	3	US-08-749-699-33	Sequence 33, Appl1	376	218.5	5.5	245	4	US-09-601-318-7	Sequence 7, Appl1
304	229	5.8	400	4	US-09-004-729-30	Sequence 30, Appl1	377	218.5	5.5	245	4	US-09-079-970A-6	Sequence 6, Appl1
305	229	5.8	400	4	US-09-004-729-33	Sequence 33, Appl1	378	218.5	5.5	245	4	US-09-601-318-1	Sequence 1, Appl1
306	228.5	5.8	235	3	US-08-807-151-3	Sequence 3, Appl1	379	218.5	5.5	1198	3	US-09-079-970A-5	Sequence 5, Appl1
307	228.5	5.8	235	3	US-09-478-957-3	Sequence 3, Appl1	380	217.5	5.5	1198	3	US-09-245-041-131	Sequence 131, App
308	228	5.8	591	3	US-08-991-408-4	Sequence 4, Appl1	381	217.5	5.5	1198	4	US-09-794-236-3	Sequence 3, Appl1
309	228	5.8	591	3	US-09-432-473-4	Sequence 4, Appl1	382	217.5	5.5	1198	4	US-09-432-473-4	Sequence 132, App
310	228	5.8	809	4	US-08-991-761A-9	Sequence 9, Appl1	383	217.5	5.5	1439	3	US-09-558-055B-11	Sequence 130, App
311	228	5.8	812	1	US-08-248-629A-1	Sequence 1, Appl1	384	217.5	5.5	1439	4	US-09-358-055B-11	Sequence 131, App
312	228	5.8	812	1	US-08-451-932A-1	Sequence 1, Appl1	385	217	5.5	268	4	US-08-944-483-61	Sequence 61, Appl1
313	228	5.8	812	1	US-08-452-260-1	Sequence 1, Appl1	386	217	5.5	273	2	US-09-613-822B-2	Sequence 2, Appl1
314	228	5.8	812	1	US-08-336-785-1	Sequence 1, Appl1	387	217	5.5	273	2	US-08-978-404B-3	Sequence 3, Appl1
315	228	5.8	812	2	US-08-612-788-1	Sequence 1, Appl1	388	217	5.5	791	1	US-08-643-219-1	Sequence 1, Appl1
316	228	5.8	812	2	US-08-605-598B-1	Sequence 1, Appl1	389	217	5.5	791	3	US-08-851-350-1	Sequence 1, Appl1
317	228	5.8	812	2	US-08-429-743-1	Sequence 1, Appl1	390	217	5.5	2703	1	US-08-185-432-19	Sequence 19, Appl1
318	228	5.8	812	2	US-08-866-735-1	Sequence 1, Appl1	391	217	5.5	2703	4	US-08-899-232-4	Sequence 4, Appl1
319	228	5.8	812	3	US-09-066-028-1	Sequence 1, Appl1	392	217	5.5	2703	4	US-09-121-457-4	Sequence 4, Appl1

393	216	5.5	267	2	US-09-016-366A-23	Sequence 23, Appl	466	211	5.3	1218	4	US-09-917-254-85	Sequence 85, Appl
394	216	5.5	267	2	US-08-978-404B-18	Sequence 18, Appl	467	211	5.3	1218	4	US-09-195-524-6	Sequence 6, Appl
395	216	5.5	267	4	US-09-917-254-101	Sequence 101, App	468	211	5.3	1218	4	US-09-579-536-1	Sequence 1, Appl
396	216	5.5	268	1	US-08-568-031-2	Sequence 2, Appl	469	211	5.3	1218	4	US-09-949-016-5992	Sequence 5992, Ap
397	216	5.5	268	2	US-08-966-319-2	Sequence 2, Appl	470	211	5.3	1254	4	US-09-949-016-10297	Sequence 10297, A
398	216	5.5	268	3	US-09-153-304-2	Sequence 2, Appl	471	210.5	5.3	418	4	US-09-370-838-62	Sequence 62, Appl
399	216	5.5	268	3	US-08-944-483-66	Sequence 66, Appl	472	210.5	5.3	418	4	US-08-882-046-5	Sequence 5, Appl
400	216	5.5	299	3	US-09-386-642-12	Sequence 12, Appl	473	210.5	5.3	1219	3	US-09-566-047-5	Sequence 5, Appl
401	216	5.5	328	4	US-09-386-642-11	Sequence 11, Appl	474	210.5	5.3	1219	4	US-09-661-416-5	Sequence 24, Appl
402	216	5.5	790	1	US-08-469-486-54	Sequence 54, Appl	475	210	5.3	154	3	US-09-61-416-5	Sequence 5, Appl
403	216	5.5	790	2	US-08-469-658-54	Sequence 54, Appl	476	210	5.3	248	3	US-08-944-483-24	Sequence 24, Appl
404	216	5.5	810	6	5200340-8	Patent No. 5200340	477	210	5.3	446	4	US-10-177-661-4	Sequence 4, Appl
405	216	5.5	810	6	5200340-8	Patent No. 5200340	478	209.5	5.3	477	4	US-10-177-661-2	Sequence 2, Appl
406	215.5	5.5	317	4	US-09-386-629-7	Sequence 7, Appl	479	209.5	5.3	562	4	US-09-879-792-12	Sequence 12, Appl
407	215.5	5.5	317	4	US-09-907-794A-263	Sequence 263, App	480	208.5	5.3	492	4	US-09-885-166A-895	Sequence 895, App
408	215.5	5.5	317	4	US-09-905-125A-263	Sequence 263, App	481	208.5	5.3	492	4	US-09-879-792-14	Sequence 14, Appl
409	215.5	5.5	317	4	US-09-902-775A-263	Sequence 263, App	482	208.5	5.3	492	4	US-09-879-426-895	Sequence 895, App
410	215.5	5.5	317	4	US-09-906-700-263	Sequence 263, App	483	208.5	5.3	492	4	US-09-759-143-895	Sequence 895, App
411	215.5	5.5	317	4	US-09-903-603A-263	Sequence 263, App	484	208	5.3	268	2	US-08-765-192-2	Sequence 2, Appl
412	215.5	5.5	317	4	US-09-904-920A-263	Sequence 263, App	485	208	5.3	268	1	US-08-765-192-2	Sequence 2, Appl
413	215.5	5.5	317	4	US-09-909-064-263	Sequence 263, App	486	208	5.3	268	1	US-09-199-793-2	Sequence 2, Appl
414	215.5	5.5	317	4	US-09-905-381A-263	Sequence 263, App	487	208	5.3	268	1	US-08-467-155A-10	Sequence 10, Appl
415	215.5	5.5	317	4	US-09-906-618-263	Sequence 263, App	488	208	5.3	271	2	US-08-628-198-10	Sequence 10, Appl
416	215	5.4	713	4	US-09-949-016-8-9983	Sequence 9983, Ap	489	208	5.3	271	2	US-09-201-038-10	Sequence 10, Appl
417	215	5.4	791	2	US-09-131-995-1	Sequence 1, Appl	490	208	5.3	271	5	PCT-US96-0734A-10	Sequence 10, Appl
418	215	5.4	791	2	US-08-832-087B-1	Sequence 1, Appl	491	207.5	5.3	211	3	US-08-944-483A-59	Sequence 59, Appl
419	215	5.4	791	3	US-09-132-154-1	Sequence 1, Appl	492	206.5	5.2	235	1	US-08-650-129-5	Sequence 5, Appl
420	215	5.4	791	4	US-08-991-761A-6	Sequence 6, Appl	493	206.5	5.2	255	3	US-08-984-417-5	Sequence 5, Appl
421	215	5.4	791	4	US-08-924-287A-1	Sequence 1, Appl	494	206.5	5.2	284	4	US-09-387-375-7	Sequence 7, Appl
422	215	5.4	810	1	US-07-854-603-2	Sequence 2, Appl	495	206.5	5.2	284	4	US-10-041-400A-7	Sequence 7, Appl
423	215	5.4	810	1	US-08-147-000B-29	Sequence 29, Appl	496	206.5	5.2	284	4	US-10-042-091A-7	Sequence 7, Appl
424	215	5.4	810	3	US-09-086-514-1	Sequence 1, Appl	497	206.5	5.2	316	4	US-09-387-375-9	Sequence 9, Appl
425	215	5.4	810	4	US-09-192-012-5	Sequence 5, Appl	498	206.5	5.2	316	4	US-10-041-400A-9	Sequence 9, Appl
426	215	5.4	810	4	US-09-403-736-1	Sequence 1, Appl	499	206.5	5.2	316	4	US-10-042-091A-9	Sequence 9, Appl
427	215	5.4	810	4	US-09-701-265-1	Sequence 1, Appl	500	205.5	5.2	235	3	US-08-944-483-48	Sequence 48, Appl
428	214	5.4	254	2	US-08-560-098A-49	Sequence 49, Appl	501	205.5	5.2	269	2	US-08-978-404B-10	Sequence 10, Appl
429	214	5.4	292	4	US-09-607-745-9	Sequence 9, Appl	502	205.5	5.2	288	4	US-09-386-629-13	Sequence 13, Appl
430	213.5	5.4	255	3	US-08-944-483-67	Sequence 67, Appl	503	205.5	5.2	337	4	US-09-386-629-8	Sequence 8, Appl
431	213.5	5.4	256	2	US-09-027-317-3	Sequence 3, Appl	504	205.5	5.2	432	3	US-09-342-749-2	Sequence 2, Appl
432	213.5	5.4	256	4	US-09-644-600A-3	Sequence 3, Appl	505	205.5	5.2	492	4	US-09-691-840-2	Sequence 2, Appl
433	213.5	5.4	256	4	US-09-654-600A-3	Sequence 3, Appl	506	205.5	5.2	492	4	US-09-759-143-932	Sequence 932, App
434	212.5	5.4	250	4	US-09-205-228-427	Sequence 427, App	507	205.5	5.2	510	4	US-09-949-016-11074	Sequence 11074, A
435	212.5	5.4	282	3	US-09-025-059-1	Sequence 1, Appl	508	205	5.2	393	4	US-09-759-143-934	Sequence 934, App
436	212.5	5.4	289	4	US-09-386-642-14	Sequence 14, Appl	509	204.5	5.2	439	4	US-09-949-016-9260	Sequence 9260, App
437	212	5.4	260	3	US-09-025-059-3	Sequence 3, Appl	510	204	5.2	260	3	US-09-070-526-2	Sequence 2, Appl
438	212	5.4	260	4	US-09-618-259-8	Sequence 8, Appl	511	204	5.2	260	4	US-09-618-259-7	Sequence 7, Appl
439	212	5.4	814	1	US-08-750-711-1	Sequence 1, Appl	512	203.5	5.2	224	3	US-08-944-483-34	Sequence 34, Appl
440	211.5	5.4	232	1	US-08-508-448C-19	Sequence 19, Appl	513	203.5	5.2	3623	4	US-09-341-461-2	Sequence 2, Appl
441	211.5	5.4	418	1	US-08-508-448C-25	Sequence 25, Appl	514	203.5	5.2	283	3	US-08-807-151-1	Sequence 1, Appl
442	211.5	5.4	418	4	US-09-370-838-82	Sequence 82, Appl	515	203	5.1	283	3	US-09-478-957-1	Sequence 1, Appl
443	211.5	5.4	418	4	US-09-370-838-83	Sequence 83, Appl	516	203	5.1	231	4	US-09-230-652-2	Sequence 2, Appl
444	211.5	5.4	418	4	US-09-854-133-82	Sequence 83, Appl	517	202	5.1	226	1	US-08-650-129-4	Sequence 4, Appl
445	211.5	5.4	418	4	US-09-854-133-83	Sequence 83, Appl	518	200.5	5.1	226	1	US-08-482-816-8	Sequence 8, Appl
446	211	5.3	276	2	US-09-016-366A-15	Sequence 15, Appl	519	200.5	5.1	226	1	US-08-984-417-4	Sequence 4, Appl
447	211	5.3	276	2	US-08-978-404B-21	Sequence 21, Appl	520	200.5	5.1	232	1	US-08-278-091-8	Sequence 8, Appl
448	211	5.3	300	3	US-08-978-404B-21	Sequence 21, Appl	521	200.5	5.1	232	1	US-08-463-859-8	Sequence 8, Appl
449	211	5.3	300	3	US-08-705-875A-4	Sequence 4, Appl	522	200.5	5.1	232	1	US-08-472-173-8	Sequence 8, Appl
450	211	5.3	300	4	US-09-220-731-21	Sequence 21, Appl	523	200.5	5.1	232	2	US-08-467-167-8	Sequence 8, Appl
451	211	5.3	300	4	US-09-242-999-4	Sequence 4, Appl	524	200.5	5.1	232	2	US-08-482-816-8	Sequence 8, Appl
452	211	5.3	433	4	US-09-949-016-8220	Sequence 8220, Ap	525	200.5	5.1	232	2	US-08-286-149-8	Sequence 8, Appl
453	211	5.3	1010	4	US-08-882-046-7	Sequence 7, Appl	526	200.5	5.1	232	2	US-08-801-499-8	Sequence 8, Appl
454	211	5.3	1010	4	US-09-566-047-7	Sequence 7, Appl	527	200.5	5.1	232	2	US-08-615-271-8	Sequence 8, Appl
455	211	5.3	1067	4	US-09-068-740A-6	Sequence 6, Appl	528	200.5	5.1	232	3	US-08-615-271-8	Sequence 8, Appl
456	211	5.3	1187	4	US-09-579-536C-18	Sequence 18, Appl	529	200.5	5.1	232	3	US-09-074-660-8	Sequence 8, Appl
457	211	5.3	1208	4	US-09-068-740A-7	Sequence 7, Appl	530	200.5	5.1	232	3	US-09-074-659-8	Sequence 8, Appl
458	211	5.3	1208	4	US-09-199-865-1	Sequence 1, Appl	531	200.5	5.1	232	3	US-09-106-468-8	Sequence 8, Appl
459	211	5.3	1208	4	US-10-213-329-1	Sequence 1, Appl	532	200.5	5.1	232	3	US-09-106-466A-8	Sequence 8, Appl
460	211	5.3	1218	2	US-08-400-159-6	Sequence 6, Appl	533	200.5	5.1	247	2	US-09-106-467-8	Sequence 8, Appl
461	211	5.3	1218	3	US-08-611-729A-6	Sequence 6, Appl	534	200.5	5.1	247	2	US-08-956-267A-2	Sequence 2, Appl
462	211	5.3	1218	3	US-08-882-046-2	Sequence 2, Appl	535	200.5	5.1	415	4	US-09-636-382A-2	Sequence 2, Appl
463	211	5.3	1218	3	US-09-214-278-7	Sequence 7, Appl	536	200.5	5.1	415	4	US-09-907-794A-104	Sequence 104, App
464	211	5.3	1218	3	US-09-068-740A-11	Sequence 11, Appl	537	200.5	5.1	415	4	US-09-905-125A-104	Sequence 104, App
465	211	5.3	1218	4	US-09-855-722-7	Sequence 7, Appl	538	200.5	5.1	415	4	US-09-902-775A-104	Sequence 104, App
					US-09-566-047-2	Sequence 2, Appl							

539	200.5	5.1	415	4	US-09-903-603A-104	Sequence 104, App	612	193	4.9	228	3	US-08-944-483-44	Sequence 44, Appl
540	200.5	5.1	415	4	US-09-904-920A-104	Sequence 104, App	613	193	4.9	223	6	5223425-8	Patent No. 5223425
541	200.5	5.1	415	4	US-09-909-064-104	Sequence 104, App	614	193	4.9	253	6	5223425-8	Patent No. 5223425
542	200.5	5.1	415	4	US-09-905-381A-104	Sequence 104, App	615	193	4.9	268	3	US-09-032-215-42	Sequence 42, Appl
543	200.5	5.1	415	4	US-09-906-618-104	Sequence 104, App	616	192.5	4.9	225	2	US-08-557-146-12	Sequence 12, Appl
544	200.5	5.1	769	4	US-09-949-016-11019	Sequence 1019, A	617	192.5	4.9	225	2	US-09-154-344-12	Sequence 12, Appl
545	200.5	5.1	810	4	US-08-991-761A-11	Sequence 11, Appl	618	192.5	4.9	221	1	US-08-467-155A-7	Sequence 7, Appl
546	200	5.1	385	4	US-09-163-951-16	Sequence 16, Appl	619	192.5	4.9	221	2	US-08-628-198-7	Sequence 7, Appl
547	200	5.1	385	4	US-09-345-881-16	Sequence 16, Appl	620	192.5	4.9	221	1	US-09-201-038-7	Sequence 7, Appl
548	199.5	5.1	1193	2	US-08-400-159-10	Sequence 10, Appl	621	192.5	4.9	221	5	PCT-US96-07343-7	Sequence 7, Appl
549	199.5	5.1	1193	3	US-08-611-729A-10	Sequence 10, Appl	622	192	4.9	199	3	US-09-518-046-20	Sequence 20, Appl
550	199.5	5.1	1193	4	US-09-195-542-10	Sequence 10, Appl	623	191.5	4.9	221	4	US-09-959-992-33	Sequence 33, Appl
551	199.5	5.1	2556	1	US-08-185-432-17	Sequence 17, Appl	624	191.5	4.9	224	2	US-08-766-982-13	Sequence 13, Appl
552	199.5	5.1	2556	1	US-08-083-590A-20	Sequence 20, Appl	625	191.5	4.9	224	3	US-08-944-483-36	Sequence 36, Appl
553	199.5	5.1	2556	3	US-08-532-384-20	Sequence 20, Appl	626	191.5	4.9	224	3	US-09-296-219-13	Sequence 13, Appl
554	199.5	5.1	2556	4	US-08-899-232-2	Sequence 2, Appl	627	191.5	4.9	225	2	US-09-027-337-5	Sequence 5, Appl
555	199.5	5.1	2556	4	US-09-121-457-2	Sequence 2, Appl	628	191.5	4.9	225	4	US-09-644-600-5	Sequence 5, Appl
556	199	5.0	249	4	US-09-949-016-8151	Sequence 8151, Ap	629	191.5	4.9	225	4	US-09-654-600A-5	Sequence 5, Appl
557	199	5.0	260	3	US-09-008-271A-7	Sequence 7, Appl	630	191.5	4.9	223	4	US-09-636-382A-24	Sequence 24, Appl
558	199	5.0	278	3	US-08-392-828C-4	Sequence 4, Appl	631	191.5	4.9	830	1	US-08-110-158-4	Sequence 4, Appl
559	199	5.0	278	3	US-09-330-945-9	Sequence 4, Appl	632	191	4.8	250	6	5223425-4	Patent No. 5223425
560	198.5	5.0	223	1	US-08-278-091-9	Sequence 9, Appl	633	191	4.8	250	6	5223425-4	Patent No. 5223425
561	198.5	5.0	223	1	US-08-483-859-9	Sequence 9, Appl	634	191	4.8	254	3	US-09-439-213-525	Sequence 525, App
562	198.5	5.0	223	1	US-08-472-173-9	Sequence 9, Appl	635	191	4.8	254	4	US-09-636-215-525	Sequence 525, App
563	198.5	5.0	223	2	US-08-487-167-9	Sequence 9, Appl	636	191	4.8	254	4	US-09-685-166A-525	Sequence 525, App
564	198.5	5.0	223	2	US-08-482-816-9	Sequence 9, Appl	637	191	4.8	254	4	US-09-679-426-525	Sequence 525, App
565	198.5	5.0	223	2	US-08-296-149-9	Sequence 9, Appl	638	191	4.8	254	4	US-09-759-143-525	Sequence 525, App
566	198.5	5.0	223	2	US-08-801-499-9	Sequence 9, Appl	639	191	4.8	254	4	US-09-651-236-525	Sequence 525, App
567	198.5	5.0	223	2	US-08-615-271-9	Sequence 9, Appl	640	191	4.8	455	3	US-09-261-416-2	Sequence 2, Appl
568	198.5	5.0	223	3	US-09-074-660-9	Sequence 9, Appl	641	190	4.8	284	4	US-09-386-642-54	Sequence 54, Appl
569	198.5	5.0	223	3	US-09-074-659-9	Sequence 9, Appl	642	189	4.8	220	3	US-09-439-313-327	Sequence 327, App
570	198.5	5.0	223	3	US-09-106-468-9	Sequence 9, Appl	643	189	4.8	220	4	US-09-352-616A-327	Sequence 327, App
571	198.5	5.0	223	3	US-09-106-466A-9	Sequence 9, Appl	644	189	4.8	220	4	US-09-232-149A-327	Sequence 327, App
572	198.5	5.0	223	3	US-09-106-467-9	Sequence 9, Appl	645	189	4.8	220	4	US-09-636-215-327	Sequence 327, App
573	198.5	5.0	223	4	US-09-601-318-2	Sequence 2, Appl	646	189	4.8	220	4	US-09-685-166A-327	Sequence 327, App
574	198.5	5.0	223	4	US-08-978-404B-45	Sequence 45, Appl	647	189	4.8	220	4	US-09-688-489-327	Sequence 327, App
575	198.5	5.0	232	2	US-08-978-404B-45	Sequence 46, Appl	648	189	4.8	220	4	US-09-679-426-327	Sequence 327, App
576	198.5	5.0	849	4	US-09-949-016-10271	Sequence 10271, A	649	189	4.8	220	4	US-09-759-143-327	Sequence 327, App
577	198	5.0	242	3	US-08-944-483-57	Sequence 57, Appl	650	189	4.8	220	4	US-09-651-236-327	Sequence 327, App
578	197.5	5.0	221	3	US-08-944-483-54	Sequence 54, Appl	651	189	4.8	224	3	US-08-944-483-33	Sequence 33, Appl
579	197.5	5.0	222	1	US-08-266-840-46	Sequence 46, Appl	652	189	4.8	225	2	US-09-027-337-4	Sequence 4, Appl
580	197.5	5.0	222	1	US-08-456-407A-46	Sequence 46, Appl	653	189	4.8	225	2	US-09-644-600-4	Sequence 4, Appl
581	197.5	5.0	222	2	US-08-892-544-46	Sequence 46, Appl	654	189	4.8	225	4	US-09-654-600A-4	Patent No. 5223425
582	197	5.0	338	4	US-08-991-761A-10	Sequence 10, Appl	655	189	4.8	228	6	5223425-5	Patent No. 5223425
583	196.5	5.0	241	3	US-08-944-483-50	Sequence 60, Appl	656	189	4.8	228	6	5223425-5	Patent No. 5223425
584	196.5	5.0	248	3	US-08-944-483-71	Sequence 71, Appl	657	189	4.8	223	2	US-08-557-146-2	Sequence 2, Appl
585	196.5	5.0	300	1	US-08-148-910-1	Sequence 1, Appl	658	189	4.8	223	2	US-08-824-874-3	Sequence 3, Appl
586	196.5	5.0	300	1	US-08-448-937A-1	Sequence 1, Appl	659	189	4.8	223	2	US-09-154-344-2	Sequence 2, Appl
587	196.5	5.0	2523	1	US-08-185-432-18	Sequence 18, Appl	660	189	4.8	253	3	US-08-930-188-2	Sequence 2, Appl
588	196.5	5.0	2523	4	US-08-899-232-3	Sequence 3, Appl	661	189	4.8	253	3	US-09-210-084-3	Sequence 3, Appl
589	196.5	5.0	2523	4	US-09-121-457-3	Sequence 3, Appl	662	189	4.8	253	4	US-09-764-762-3	Sequence 3, Appl
590	195.5	5.0	232	3	US-08-944-483-55	Sequence 45, Appl	663	189	4.8	253	5	PCT-US96-04294-2	Sequence 2, Appl
591	195.5	5.0	241	1	US-08-330-978-4	Sequence 4, Appl	664	189	4.8	255	4	US-09-949-016-7776	Sequence 7716, Ap
592	195.5	5.0	241	1	US-08-474-042-4	Sequence 4, Appl	665	189	4.8	312	4	US-09-023-942A-4	Sequence 4, Appl
593	195.5	5.0	241	1	US-08-484-558-4	Sequence 4, Appl	666	189	4.8	449	4	US-09-636-215-617	Sequence 617, App
594	195.5	5.0	241	1	US-08-774-592-4	Sequence 4, Appl	667	189	4.8	449	4	US-09-685-166A-617	Sequence 617, App
595	195.5	5.0	254	1	US-08-330-978-3	Sequence 3, Appl	668	189	4.8	449	4	US-09-679-426-617	Sequence 617, App
596	195.5	5.0	254	1	US-08-474-042-3	Sequence 3, Appl	669	189	4.8	449	4	US-09-759-143-617	Sequence 617, App
597	195.5	5.0	254	1	US-08-484-558-3	Sequence 3, Appl	670	189	4.8	449	4	US-09-651-236-617	Sequence 617, App
598	195.5	5.0	254	1	US-08-774-592-3	Sequence 3, Appl	671	188.5	4.8	200	4	US-09-386-653A-7	Sequence 7, Appl
599	195.5	5.0	306	1	US-08-330-978-1	Sequence 1, Appl	672	188	4.8	248	1	US-08-744-026-1	Sequence 1, Appl
600	195.5	5.0	306	1	US-08-474-042-1	Sequence 1, Appl	673	188	4.8	248	2	US-09-102-732-1	Sequence 1, Appl
601	195.5	5.0	306	1	US-08-484-558-1	Sequence 1, Appl	674	188	4.8	248	3	US-09-261-617-3	Sequence 1, Appl
602	195.5	5.0	306	1	US-08-774-592-1	Sequence 1, Appl	675	188	4.8	254	3	US-09-439-213-523	Sequence 523, App
603	195.5	5.0	2471	1	US-08-185-432-16	Sequence 16, Appl	676	188	4.8	254	4	US-09-636-215-523	Sequence 523, App
604	195.5	5.0	2471	1	US-08-083-590A-19	Sequence 19, Appl	677	188	4.8	254	4	US-09-685-166A-523	Sequence 523, App
605	195.5	5.0	2471	3	US-08-532-384-19	Sequence 19, Appl	678	188	4.8	254	4	US-09-679-426-523	Sequence 523, App
606	195.5	5.0	2471	4	US-08-899-232-1	Sequence 1, Appl	679	188	4.8	254	4	US-09-759-143-523	Sequence 523, App
607	195.5	5.0	2471	2	US-09-121-457-1	Sequence 1, Appl	680	188	4.8	254	4	US-09-651-236-523	Sequence 523, App
608	194.5	4.9	246	2	US-08-978-404B-44	Sequence 44, Appl	681	188	4.8	253	2	US-08-790-137-4	Sequence 4, Appl
609	194.5	4.9	415	3	US-09-032-523-2	Sequence 2, Appl	682	188	4.8	253	2	US-08-824-874-5	Sequence 5, Appl
610	194.5	4.9	415	3	US-09-802-633-2	Sequence 2, Appl	683	188	4.8	253	3	US-08-807-151-5	Sequence 5, Appl
611	194	4.9	113	4	US-09-438-046-20	Sequence 20, Appl	684	188	4.8	253	3	US-09-210-084-5	Sequence 5, Appl

685	188	4.8	263	3	US-09-478-957-5	Sequence 5, Appl1	758	181.5	4.6	258	1	US-07-990-301A-2	Sequence 2, Appl1
686	188	4.8	263	4	US-09-764-762-5	Sequence 5, Appl1	759	181.5	4.6	259	1	US-08-467-155A-8	Sequence 8, Appl1
687	188	4.8	333	4	US-08-991-761A-8	Sequence 8, Appl1	760	181.5	4.6	259	2	US-08-528-198-8	Sequence 8, Appl1
688	187.5	4.8	224	3	US-08-944-483-35	Sequence 35, Appl1	761	181.5	4.6	299	3	US-09-201-038-8	Sequence 8, Appl1
689	187.5	4.8	242	3	US-08-944-483-39	Sequence 29, Appl1	762	181.5	4.6	299	5	PCT-US96-07343-8	Sequence 8, Appl1
690	187.5	4.8	255	3	US-08-906-769-83	Sequence 83, Appl1	763	181	4.6	336	4	US-09-800-729-86	Sequence 648, Ap
691	187.5	4.8	255	3	US-08-906-616-83	Sequence 83, Appl1	764	180	4.6	254	4	US-09-949-016-6948	Sequence 68, Appl
692	187.5	4.8	255	3	US-08-817-795-83	Sequence 83, Appl1	765	180	4.6	200	6	5223425-10	Sequence 68, Ap
693	187.5	4.8	255	3	US-08-639-075A-83	Sequence 83, Appl1	766	180	4.6	200	6	5223425-10	Sequence 68, Ap
694	187.5	4.8	255	3	US-09-012-431-93	Sequence 83, Appl1	767	179.5	4.6	205	3	US-09-020-956-176	Sequence 176, App
695	187.5	4.8	255	3	US-09-012-692-83	Sequence 83, Appl1	768	179.5	4.6	205	3	US-09-030-607-176	Sequence 176, App
696	187.5	4.8	255	3	US-08-906-613-83	Sequence 83, Appl1	769	179.5	4.6	205	4	US-09-439-113-176	Sequence 176, App
697	187.5	4.8	255	5	PCT-US95-14442A-83	Sequence 83, Appl1	770	179.5	4.6	205	3	US-09-352-616A-176	Sequence 176, App
698	186	4.7	110	4	US-09-341-461-28	Sequence 28, Appl1	771	179.5	4.6	205	4	US-09-232-149A-176	Sequence 176, App
699	186	4.7	230	1	US-08-456-840-47	Sequence 47, Appl1	772	179.5	4.6	205	4	US-09-159-812-176	Sequence 176, App
700	186	4.7	230	1	US-08-266-407A-47	Sequence 47, Appl1	773	179.5	4.6	205	4	US-09-636-215-176	Sequence 176, App
701	186	4.7	230	1	US-08-892-544-47	Sequence 47, Appl1	774	179.5	4.6	205	4	US-09-685-166A-176	Sequence 176, App
702	186	4.7	230	2	US-08-766-982-12	Sequence 12, Appl1	775	179.5	4.6	205	4	US-09-115-453-176	Sequence 176, App
703	186	4.7	230	3	US-08-944-483-53	Sequence 53, Appl1	776	179.5	4.6	205	4	US-09-688-489-176	Sequence 176, App
704	186	4.7	230	3	US-09-296-219-12	Sequence 12, Appl1	777	179.5	4.6	205	4	US-09-679-426-176	Sequence 176, App
705	186	4.7	232	2	US-08-897-340-31	Sequence 31, Appl1	778	179.5	4.6	205	4	US-09-759-143-176	Sequence 176, App
706	186	4.7	232	3	US-09-252-329-31	Sequence 31, Appl1	779	179.5	4.6	205	4	US-09-651-236-176	Sequence 176, App
707	186	4.7	326	3	US-09-411-977-3	Sequence 3, Appl1	780	179.5	4.6	259	6	5223425-2	Sequence 176, App
708	186	4.7	326	3	US-10-057-951-3	Sequence 3, Appl1	781	179.5	4.6	259	6	5223425-2	Sequence 176, App
709	185.5	4.7	256	3	US-09-032-215-27	Sequence 27, Appl1	782	179.5	4.6	728	3	US-08-981-392-2	Sequence 2, Appl1
710	185.5	4.7	261	3	US-08-163-919A-2	Sequence 2, Appl1	783	179.5	4.6	728	4	US-09-908-322-2	Sequence 2, Appl1
711	185.5	4.7	261	4	US-08-462-515-2	Sequence 2, Appl1	784	179.5	4.6	830	5	PCT-US91-05059-2	Sequence 2, Appl1
712	185.5	4.7	261	5	PCT-US94-14073-2	Sequence 2, Appl1	785	179	4.5	230	1	US-08-379-621-2	Sequence 2, Appl1
713	185.5	4.7	306	4	US-09-386-642-53	Sequence 53, Appl1	786	179	4.5	230	1	US-08-147-000B-2	Sequence 2, Appl1
714	185.5	4.7	711	1	US-08-184-012C-8	Sequence 8, Appl1	787	179	4.5	230	2	US-08-889-078-2	Sequence 2, Appl1
715	185.5	4.7	711	1	US-08-334-177-2	Sequence 8, Appl1	788	179	4.5	233	3	US-09-578-303-4	Sequence 4, Appl1
716	185.5	4.7	711	1	US-08-666-082B-1	Sequence 2, Appl1	789	179	4.5	334	3	US-09-032-215-22	Sequence 22, Appl1
717	185.5	4.7	711	5	PCT-US95-13830-2	Sequence 5, Appl1	790	178.5	4.5	250	3	US-08-944-683-68	Sequence 66, Appl1
718	185.5	4.7	713	3	US-08-872-855-5	Sequence 5, Appl1	791	178.5	4.5	315	4	US-09-386-653A-9	Sequence 9, Appl1
719	185	4.7	247	1	US-08-944-483-9	Sequence 49, Appl1	792	178.5	4.5	401	2	US-08-839-008-5	Sequence 5, Appl1
720	185	4.7	258	1	US-08-744-023-3	Sequence 3, Appl1	793	178.5	4.5	468	2	US-08-839-008-5	Sequence 5, Appl1
721	185	4.7	258	2	US-09-102-732-3	Sequence 3, Appl1	794	178.5	4.5	468	3	US-09-032-523-8	Sequence 8, Appl1
722	185	4.7	258	3	US-09-261-767-3	Sequence 3, Appl1	795	178.5	4.5	468	4	US-09-802-633-8	Sequence 8, Appl1
723	185	4.7	314	4	US-09-023-942A-6	Sequence 6, Appl1	796	178.5	4.5	922	4	US-09-116-473-4	Sequence 4, Appl1
724	184	4.7	144	4	US-09-618-259-1	Sequence 1, Appl1	797	178.5	4.5	923	3	US-08-936-135-6	Sequence 6, Appl1
725	184	4.7	314	3	US-09-008-271A-3	Sequence 3, Appl1	798	178.5	4.5	923	3	US-09-439-711C-6	Sequence 6, Appl1
726	184	4.7	314	4	US-09-907-794A-257	Sequence 257, App	799	177.5	4.5	248	2	US-08-851-974-3	Sequence 3, Appl1
727	184	4.7	314	4	US-09-905-125A-257	Sequence 257, App	800	177.5	4.5	248	2	US-09-213-390-3	Sequence 3, Appl1
728	184	4.7	314	4	US-09-902-775A-257	Sequence 257, App	801	177.5	4.5	1964	3	US-09-467-997-1	Sequence 1, Appl1
729	184	4.7	314	4	US-09-906-700-257	Sequence 257, App	802	177	4.5	110	4	US-09-314-135-7	Sequence 7, Appl1
730	184	4.7	314	4	US-09-903-603A-257	Sequence 257, App	803	177	4.5	110	4	US-09-270-767-45768	Sequence 45768, A
731	184	4.7	314	4	US-09-904-920A-257	Sequence 257, App	804	177	4.5	223	4	US-08-278-091-11	Sequence 11, Appl1
732	184	4.7	314	4	US-09-909-064-257	Sequence 257, App	805	177	4.5	240	1	US-08-483-859-11	Sequence 11, Appl1
733	184	4.7	314	4	US-09-905-381A-257	Sequence 257, App	806	177	4.5	240	1	US-08-483-859-11	Sequence 11, Appl1
734	184	4.7	314	4	US-09-906-618-257	Sequence 257, App	807	177	4.5	240	1	US-08-472-173-11	Sequence 11, Appl1
735	183.5	4.7	711	2	US-08-766-982-2	Sequence 2, Appl1	808	177	4.5	240	2	US-08-487-167-11	Sequence 11, Appl1
736	183.5	4.7	711	3	US-09-296-219-2	Sequence 2, Appl1	809	177	4.5	240	2	US-08-482-816-11	Sequence 11, Appl1
737	183.5	4.7	711	4	US-09-600-991-20	Sequence 20, Appl1	810	177	4.5	240	2	US-08-296-149-11	Sequence 11, Appl1
738	183.5	4.7	711	4	US-09-601-040A-12	Sequence 12, Appl1	811	177	4.5	240	2	US-08-801-499-11	Sequence 11, Appl1
739	183.5	4.7	711	4	US-09-949-016-6981	Sequence 12, Appl1	812	177	4.5	240	2	US-08-615-271-11	Sequence 11, Appl1
740	183.5	4.7	722	3	US-08-981-392-12	Sequence 12, Appl1	813	177	4.5	240	3	US-09-074-660-11	Sequence 11, Appl1
741	183.5	4.7	722	4	US-09-908-322-12	Sequence 12, Appl1	814	177	4.5	240	3	US-09-074-659-11	Sequence 11, Appl1
742	183	4.6	418	4	US-10-177-661-6	Sequence 6, Appl1	815	177	4.5	240	3	US-09-106-468-11	Sequence 11, Appl1
743	182.5	4.6	258	4	US-09-023-942A-8	Sequence 8, Appl1	816	177	4.5	240	3	US-09-106-466A-11	Sequence 11, Appl1
744	182.5	4.6	484	2	US-08-252-493C-9	Sequence 9, Appl1	817	177	4.5	240	3	US-09-106-467-11	Sequence 11, Appl1
745	182.5	4.6	484	2	US-09-276-197-9	Sequence 9, Appl1	818	177	4.5	729	3	US-08-872-855-8	Sequence 8, Appl1
746	182.5	4.6	720	3	US-08-872-855-4	Sequence 4, Appl1	819	177	4.5	830	6	5378464-2	Sequence 8, Appl1
747	182	4.6	405	3	US-09-734-675-2	Sequence 2, Appl1	820	177	4.5	830	6	5378464-2	Sequence 8, Appl1
748	182	4.6	721	3	US-08-872-855-7	Sequence 7, Appl1	821	176.5	4.5	232	1	US-08-990-301A-4	Sequence 22, Appl1
749	182	4.6	1055	3	US-09-214-278-2	Sequence 2, Appl1	822	176.5	4.5	901	3	US-08-936-135-12	Sequence 22, Appl1
750	182	4.6	1055	4	US-09-855-722-2	Sequence 2, Appl1	823	176.5	4.5	901	3	US-09-439-711C-22	Sequence 22, Appl1
751	182	4.6	1065	2	US-08-400-159-8	Sequence 8, Appl1	824	176.5	4.5	906	3	US-08-936-135-24	Sequence 24, Appl1
752	182	4.6	1212	3	US-09-214-278-3	Sequence 3, Appl1	825	176.5	4.5	906	4	US-09-439-711C-24	Sequence 24, Appl1
753	182	4.6	1212	4	US-09-855-722-3	Sequence 3, Appl1	826	176.5	4.5	909	3	US-08-936-135-8	Sequence 8, Appl1
754	182	4.6	1238	3	US-09-214-278-5	Sequence 5, Appl1	827	176.5	4.5	909	3	US-08-936-135-10	Sequence 10, Appl1
755	182	4.6	1238	4	US-09-855-722-5	Sequence 5, Appl1	828	176.5	4.5	909	4	US-09-439-711C-8	Sequence 8, Appl1
756	182	4.6	1257	3	US-08-611-729A-8	Sequence 8, Appl1	829	176.5	4.5	909	4	US-09-439-711C-10	Sequence 10, Appl1
757	182	4.6	1257	4	US-09-195-524-8	Sequence 8, Appl1	830	176.5	4.5	914	3	US-08-936-135-12	Sequence 12, Appl1

831	176.5	4.5	914	4	US-09-439-711C-12	Sequence 12, Appl	904	170	4.3	213	3	US-08-306-769-149	Sequence 149, App
832	176.5	4.5	925	4	US-09-116-473-2	Sequence 2, Appl	905	170	4.3	213	3	US-08-306-616-149	Sequence 149, App
833	176.5	4.5	926	3	US-08-936-135-14	Sequence 14, Appl	906	170	4.3	213	3	US-08-639-075A-149	Sequence 149, App
834	176.5	4.5	926	4	US-09-439-711C-14	Sequence 14, Appl	907	170	4.3	213	3	US-09-012-431-149	Sequence 149, App
835	176.5	4.5	926	3	US-08-936-135-16	Sequence 16, Appl	908	170	4.3	213	3	US-09-012-692-149	Sequence 149, App
836	176.5	4.5	931	4	US-09-439-711C-16	Sequence 16, Appl	909	170	4.3	213	3	US-08-306-613-149	Sequence 149, App
837	176	4.5	233	3	US-09-004-731-17	Sequence 27, Appl	910	170	4.3	717	4	US-09-601-040A-8	Sequence 8, Appl
838	176	4.5	233	3	US-08-749-699-27	Sequence 27, Appl	911	170	4.3	729	4	US-09-601-040A-4	Sequence 4, Appl
839	176	4.5	233	3	US-09-004-729-27	Sequence 27, Appl	912	170	4.3	1148	4	US-08-882-046-4	Sequence 4, Appl
840	176	4.5	242	3	US-08-944-483-58	Sequence 58, Appl	913	170	4.3	1148	4	US-09-566-047-4	Sequence 4, Appl
841	176	4.5	266	3	US-09-004-731-24	Sequence 24, Appl	914	169	4.3	95	3	US-09-374-135-5	Sequence 8, Appl
842	176	4.5	266	3	US-08-749-699-24	Sequence 24, Appl	915	169	4.3	110	4	US-09-341-461-25	Sequence 25, Appl
843	176	4.5	266	4	US-09-004-729-24	Sequence 24, Appl	916	169	4.3	237	5	US-08-096-946-11	Sequence 11, Appl
844	175.5	4.4	921	4	US-09-439-711C-4	Sequence 4, Appl	917	169	4.3	237	5	PCT-US94-07329-11	Sequence 11, Appl
845	175	4.4	112	4	US-09-438-046-21	Sequence 21, Appl	918	169	4.3	237	5	PCT-US95-06157-1	Sequence 11, Appl
846	175	4.4	909	3	US-08-936-135-18	Sequence 18, Appl	919	169	4.3	375	4	US-09-755-100A-11	Sequence 11, Appl
847	175	4.4	909	4	US-09-439-711C-18	Sequence 18, Appl	920	168.5	4.3	222	6	5223425-6	Patent No. 5223425
848	175	4.4	926	3	US-08-936-135-20	Sequence 20, Appl	921	168.5	4.3	222	6	5223425-6	Patent No. 5223425
849	175	4.4	926	4	US-09-439-711C-20	Sequence 20, Appl	922	168.5	4.3	333	4	US-09-142-027A-12	Sequence 12, Appl
850	175	4.4	931	4	US-09-583-638-4	Sequence 4, Appl	923	168	4.3	245	3	US-08-306-769-121	Sequence 12, Appl
851	174	4.4	265	2	US-08-177-109A-57	Sequence 57, Appl	924	168	4.3	245	3	US-08-306-616-121	Sequence 12, Appl
852	174	4.4	265	2	US-08-687-706-57	Sequence 57, Appl	925	168	4.3	245	3	US-08-639-075A-121	Sequence 12, Appl
853	174	4.4	286	1	US-08-467-155A-9	Sequence 9, Appl	926	168	4.3	245	3	US-09-012-431-121	Sequence 12, Appl
854	174	4.4	286	2	US-08-628-198-9	Sequence 9, Appl	927	168	4.3	245	3	US-09-012-692-121	Sequence 12, Appl
855	174	4.4	286	3	US-09-201-038-9	Sequence 9, Appl	928	168	4.3	245	3	US-08-306-613-121	Sequence 12, Appl
856	174	4.4	286	5	PCT-US96-07343-9	Sequence 9, Appl	929	167.5	4.2	261	1	US-08-744-026-5	Sequence 5, Appl
857	173.5	4.4	294	4	US-09-800-729-146	Sequence 146, Appl	930	167.5	4.2	261	2	US-09-102-732-5	Sequence 6, Appl
858	173.5	4.4	294	4	US-10-067-422-12	Sequence 12, Appl	931	167.5	4.2	261	3	US-09-083-521-6	Sequence 6, Appl
859	173.5	4.4	414	4	US-09-270-767-16426	Sequence 46426, A	932	167.5	4.2	261	3	US-09-261-767-5	Sequence 5, Appl
860	173.5	4.4	717	3	US-08-872-855-9	Sequence 9, Appl	933	167.5	4.2	261	4	US-09-413-049-1	Sequence 1, Appl
861	173	4.4	211	3	US-09-242-931-25	Sequence 25, Appl	934	167.5	4.2	261	4	US-09-907-402-1	Sequence 1, Appl
862	173	4.4	211	4	US-09-242-939-20	Sequence 20, Appl	935	167.5	4.2	261	4	US-09-618-259-10	Sequence 10, Appl
863	172.5	4.4	449	2	US-08-839-008-2	Sequence 2, Appl	936	167.5	4.2	262	1	US-08-744-026-4	Sequence 4, Appl
864	172.5	4.4	449	4	US-09-919-497-89	Sequence 89, Appl	937	167.5	4.2	262	2	US-09-102-732-4	Sequence 4, Appl
865	172.5	4.4	449	4	US-09-949-016-1238	Sequence 7238, Ap	938	167.5	4.2	262	3	US-09-261-767-4	Sequence 4, Appl
866	172.5	4.4	458	4	US-08-882-046-6	Sequence 6, Appl	939	167.5	4.2	933	4	US-09-583-638-2	Sequence 2, Appl
867	172.5	4.4	1248	3	US-09-566-047-6	Sequence 6, Appl	940	167	4.2	103	3	US-09-374-135-5	Sequence 5, Appl
868	172.5	4.4	1248	4	US-09-270-767-33709	Sequence 33709, A	941	166.5	4.2	520	3	US-09-068-740A-3	Sequence 3, Appl
869	172	4.4	250	4	US-09-270-767-33709	Sequence 33709, A	942	166.5	4.2	702	3	US-09-068-740A-4	Sequence 4, Appl
870	172	4.4	357	4	US-09-270-767-33564	Sequence 43564, A	943	166.5	4.2	723	3	US-09-068-740A-9	Sequence 9, Appl
871	172	4.4	357	4	US-09-270-767-58936	Sequence 58936, A	944	166.5	4.2	723	4	US-09-423-753-27	Sequence 27, Appl
872	172	4.4	721	3	US-08-961-392-5	Sequence 5, Appl	945	166.5	4.2	723	4	US-09-641-612-6	Sequence 6, Appl
873	172	4.4	721	3	US-09-908-322-5	Sequence 39, Appl	946	166	4.2	124	6	5514582-38	Patent No. 5514582
874	171.5	4.3	238	3	US-08-944-483-39	Sequence 190, App	947	166	4.2	124	6	5514582-38	Patent No. 5514582
875	171.5	4.3	259	3	US-08-906-769-190	Sequence 190, App	948	166	4.2	237	3	US-08-768-859A-1	Sequence 1, Appl
876	171.5	4.3	259	3	US-08-906-616-190	Sequence 190, App	949	166	4.2	237	3	US-08-767-820A-1	Sequence 1, Appl
877	171.5	4.3	259	3	US-08-639-075A-190	Sequence 190, App	950	166	4.2	237	3	US-08-622-046B-7	Sequence 7, Appl
878	171.5	4.3	259	3	US-09-004-731-85	Sequence 85, Appl	951	166	4.2	237	3	US-08-944-483-38	Sequence 38, Appl
879	171.5	4.3	259	3	US-09-012-431-190	Sequence 190, App	952	166	4.2	237	3	US-09-100-264-3	Sequence 3, Appl
880	171.5	4.3	259	3	US-08-749-699-85	Sequence 85, Appl	953	166	4.2	237	4	US-09-303-339-2	Sequence 2, Appl
881	171.5	4.3	259	3	US-09-012-692-190	Sequence 190, App	954	166	4.2	237	4	US-08-843-076D-7	Sequence 7, Appl
882	171.5	4.3	259	3	US-08-906-613-190	Sequence 190, App	955	166	4.2	237	4	US-09-303-208-1	Sequence 1, Appl
883	171.5	4.3	259	4	US-09-004-729-85	Sequence 85, Appl	956	166	4.2	237	4	US-08-944-483-70	Sequence 70, Appl
884	171.5	4.3	262	2	US-08-790-137-1	Sequence 1, Appl	957	166	4.2	441	3	US-09-949-016-10792	Sequence 10792, A
885	171.5	4.3	262	2	US-08-790-137-3	Sequence 3, Appl	958	166	4.2	923	4	US-09-439-711C-2	Sequence 2, Appl
886	171.5	4.3	262	2	US-08-681-151-4	Sequence 4, Appl	959	165.5	4.2	240	1	US-08-472-228A-1	Sequence 1, Appl
887	171.5	4.3	262	2	US-08-824-874-4	Sequence 4, Appl	960	165.5	4.2	240	3	US-09-146-831-1	Sequence 1, Appl
888	171.5	4.3	262	3	US-08-807-151-4	Sequence 4, Appl	961	165.5	4.2	240	3	PCT-US96-09303-1	Sequence 1, Appl
889	171.5	4.3	262	3	US-09-210-084-4	Sequence 4, Appl	962	165.5	4.2	363	1	US-08-597-545-2	Sequence 2, Appl
890	171.5	4.3	262	3	US-09-478-957-4	Sequence 4, Appl	963	165.5	4.2	363	1	US-08-457-135-2	Sequence 2, Appl
891	171.5	4.3	262	4	US-09-764-762-4	Sequence 4, Appl	964	165	4.2	101	3	US-09-374-135-4	Sequence 4, Appl
892	171.5	4.3	262	4	US-09-618-359-9	Sequence 9, Appl	965	164	4.2	351	3	US-09-345-041-11	Sequence 11, Appl
893	171.5	4.3	666	3	US-09-341-587-1	Sequence 1, Appl	966	164	4.2	351	4	US-09-358-055B-11	Sequence 11, Appl
894	171.5	4.3	1785	3	US-09-341-587-3	Sequence 3, Appl	967	164	4.2	351	4	US-09-993-238-11	Sequence 11, Appl
895	171	4.3	262	4	US-09-025-059-4	Sequence 4, Appl	968	164	4.2	812	4	US-09-192-012-9	Sequence 9, Appl
896	171	4.3	262	4	US-09-755-100A-14	Sequence 14, Appl	969	163	4.1	441	4	US-09-949-016-11196	Sequence 11196, A
897	171	4.3	287	4	US-09-270-767-33263	Sequence 33263, A	970	163	4.1	607	4	US-09-907-794A-190	Sequence 190, App
898	171	4.3	287	4	US-09-270-767-48480	Sequence 48480, A	971	163	4.1	607	4	US-09-905-125A-190	Sequence 190, App
899	171	4.3	290	4	US-09-949-016-8166	Sequence 8166, Ap	972	163	4.1	607	4	US-09-902-775A-190	Sequence 190, App
900	171	4.3	717	4	US-09-601-040A-6	Sequence 6, Appl	973	163	4.1	607	4	US-09-906-700-190	Sequence 190, App
901	171	4.3	729	4	US-09-601-040A-2	Sequence 2, Appl	974	163	4.1	607	4	US-09-903-603A-190	Sequence 190, App
902	171	4.3	737	4	US-09-866-028-15	Sequence 15, Appl	975	163	4.1	607	4	US-09-904-920A-190	Sequence 190, App
903	171	4.3	737	4	US-09-944-457-15	Sequence 15, Appl	976	163	4.1	607	4	US-09-909-064-190	Sequence 190, App

977	163	4.1	607	US-09-905-381A-190	Sequence 190, App	1050	156	4.0	238	5	PCT-US95-06157-8	Sequence 8, Appl
978	163	4.1	607	US-09-906-618-190	Sequence 190, App	1051	156	4.0	244	3	US-08-768-859A-10	Sequence 10, Appl
979	162.5	4.1	1290	US-08-470-350B-2	Sequence 2, Appl	1052	156	4.0	244	3	US-08-767-820A-10	Sequence 10, Appl
980	161.5	4.1	251	US-08-944-483-28	Sequence 28, Appl	1053	156	4.0	244	3	US-08-622-046B-5	Sequence 5, Appl
981	161.5	4.1	832	US-08-981-392-6	Sequence 6, Appl	1054	156	4.0	244	3	US-08-622-046B-16	Sequence 16, Appl
982	161.5	4.1	832	US-09-908-322-6	Sequence 6, Appl	1055	156	4.0	244	3	US-09-100-264-5	Sequence 5, Appl
983	161.5	4.1	1025	US-09-834-309-5	Sequence 5, Appl	1056	156	4.0	244	3	US-08-843-076B-5	Sequence 5, Appl
984	161	4.1	270	US-09-949-016-7712	Sequence 7712, Ap	1057	156	4.0	244	5	PCT-US95-06157-10	Sequence 10, Appl
985	161	4.1	293	US-09-509-908-2	Sequence 2, Appl	1058	156	4.0	261	3	US-08-768-859A-6	Sequence 6, Appl
986	160.5	4.1	238	US-09-664-595A-15	Sequence 15, Appl	1059	156	4.0	261	3	US-08-767-820A-19	Sequence 19, Appl
987	160.5	4.1	263	US-09-949-016-6072	Sequence 9072, Ap	1060	156	4.0	261	3	US-08-767-820A-6	Sequence 6, Appl
988	160.5	4.1	329	US-09-270-767-42672	Sequence 42672, A	1061	156	4.0	261	3	US-08-767-820A-19	Sequence 19, Appl
989	160.5	4.1	661	US-09-949-016-6157	Sequence 6157, Ap	1062	156	4.0	261	3	US-08-622-046B-3	Sequence 3, Appl
990	160.5	4.1	665	US-09-949-016-10776	Sequence 10776, A	1063	156	4.0	261	3	US-08-622-046B-14	Sequence 14, Appl
991	160	4.1	207	US-10-000-489-54	Sequence 54, Appl	1064	156	4.0	261	3	US-09-100-264-7	Sequence 7, Appl
992	160	4.1	234	US-08-944-483-46	Sequence 46, Appl	1065	156	4.0	261	3	US-08-983-0750-7	Sequence 7, Appl
993	160	4.1	268	US-09-949-016-60712	Sequence 10712, A	1066	156	4.0	261	3	US-08-843-076B-3	Sequence 3, Appl
994	160	4.1	2871	US-09-538-092-1076	Sequence 1076, Ap	1067	156	4.0	261	5	PCT-US95-06157-6	Sequence 6, Appl
995	159.5	4.0	228	US-08-768-982-11	Sequence 11, Appl	1068	156	4.0	278	2	US-09-949-016-7711	Sequence 7711, Ap
996	159.5	4.0	228	US-09-296-219-41	Sequence 11, Appl	1069	155.5	3.9	247	2	US-08-651-974-1	Sequence 1, Appl
997	159.5	4.0	228	US-09-270-767-32048	Sequence 32048, A	1070	155.5	3.9	247	2	US-09-213-390-1	Sequence 1, Appl
998	159.5	4.0	276	US-09-270-767-47265	Sequence 47265, A	1071	155.5	3.9	830	3	US-08-622-046B-11	Sequence 11, Appl
999	159	4.0	237	US-08-844-024-2	Sequence 2, Appl	1072	155	3.9	2489	4	US-09-911-842A-5	Sequence 5, Appl
1000	159	4.0	237	US-08-718-547-2	Sequence 2, Appl	1073	154.5	3.9	228	1	US-08-278-091-7	Sequence 7, Appl
1001	158.5	4.0	283	US-09-244-111-2	Sequence 2, Appl	1074	154.5	3.9	228	1	US-08-472-173-7	Sequence 7, Appl
1002	158.5	4.0	385	US-08-597-545-1	Sequence 1, Appl	1075	154.5	3.9	228	1	US-08-487-167-7	Sequence 7, Appl
1003	158.5	4.0	385	US-08-457-135-1	Sequence 1, Appl	1076	154.5	3.9	228	2	US-08-482-816-7	Sequence 7, Appl
1004	158.5	4.0	385	US-09-142-027A-10	Sequence 10, Appl	1077	154.5	3.9	228	2	US-08-482-816-7	Sequence 7, Appl
1005	158.5	4.0	833	US-08-264-534-6	Sequence 6, Appl	1078	154.5	3.9	228	2	US-08-296-149-7	Sequence 7, Appl
1006	158.5	4.0	833	US-08-083-590A-2	Sequence 2, Appl	1079	154.5	3.9	228	2	US-08-615-371-7	Sequence 7, Appl
1007	158.5	4.0	833	US-08-465-500-6	Sequence 6, Appl	1080	154.5	3.9	228	2	US-08-615-371-7	Sequence 7, Appl
1008	158.5	4.0	833	US-08-346-126-6	Sequence 6, Appl	1081	154.5	3.9	228	3	US-09-074-650-7	Sequence 7, Appl
1009	158.5	4.0	833	US-08-346-128-6	Sequence 6, Appl	1082	154.5	3.9	228	3	US-09-074-659-7	Sequence 7, Appl
1010	158.5	4.0	833	US-08-523-384-2	Sequence 2, Appl	1083	154.5	3.9	228	3	US-08-482-816-7	Sequence 7, Appl
1011	158.5	4.0	833	US-08-893-828-6	Sequence 6, Appl	1084	154.5	3.9	228	3	US-09-106-466A-7	Sequence 7, Appl
1012	158	4.0	156	US-09-261-416-6	Sequence 6, Appl	1085	154.5	3.9	228	3	US-09-106-466A-7	Sequence 7, Appl
1013	157.5	4.0	190	US-08-845-998-4	Sequence 4, Appl	1086	154	3.9	101	3	US-09-374-135-6	Sequence 6, Appl
1014	157.5	4.0	190	US-09-206-537-4	Sequence 4, Appl	1087	154	3.9	224	1	US-08-553-516-2	Sequence 2, Appl
1015	157.5	4.0	190	US-09-430-854-4	Sequence 4, Appl	1088	154	3.9	227	3	US-08-944-483-10	Sequence 40, Appl
1016	157.5	4.0	226	US-09-601-040A-28	Sequence 28, Appl	1089	154	3.9	248	2	US-08-921-426-4	Sequence 2, Appl
1017	157.5	4.0	228	US-08-944-483-55	Sequence 55, Appl	1090	154	3.9	248	2	US-08-921-426-4	Sequence 4, Appl
1018	157.5	4.0	255	US-08-906-769-91	Sequence 91, Appl	1091	154	3.9	248	3	US-08-816-915-4	Sequence 4, Appl
1019	157.5	4.0	255	US-08-906-616-91	Sequence 91, Appl	1092	154	3.9	248	5	PCT-US95-07743-4	Sequence 37, Appl
1020	157.5	4.0	255	US-08-817-795-91	Sequence 91, Appl	1093	154	3.9	248	5	US-08-824-874-1	Sequence 4, Appl
1021	157.5	4.0	255	US-08-639-075A-91	Sequence 91, Appl	1094	154	3.9	268	2	US-09-210-084-1	Sequence 1, Appl
1022	157.5	4.0	255	US-09-012-431-91	Sequence 91, Appl	1095	154	3.9	268	2	US-09-210-084-1	Sequence 1, Appl
1023	157.5	4.0	255	US-09-012-692-91	Sequence 91, Appl	1096	154	3.9	268	4	US-09-764-762-1	Sequence 1, Appl
1024	157.5	4.0	255	US-08-906-613-91	Sequence 91, Appl	1097	154	3.9	321	4	US-09-270-767-33762	Sequence 33762, A
1025	157.5	4.0	255	PCT-US95-14442A-91	Sequence 91, Appl	1098	154	3.9	321	4	US-09-270-767-48979	Sequence 48979, A
1026	157	4.0	185	US-08-906-769-141	Sequence 141, App	1099	154	3.9	1466	6	5256642-6	Patent No. 5256642
1027	157	4.0	185	US-08-906-616-141	Sequence 141, App	1100	154	3.9	1466	6	5472939-6	Patent No. 5472939
1028	157	4.0	185	US-08-639-075A-141	Sequence 141, App	1101	154	3.9	1466	6	5256642-6	Patent No. 5256642
1029	157	4.0	185	US-09-012-431-141	Sequence 141, App	1102	154	3.9	1466	6	5472939-6	Patent No. 5472939
1030	157	4.0	185	US-09-012-692-141	Sequence 141, App	1103	154	3.9	1537	6	5256642-5	Patent No. 5256642
1031	157	4.0	185	US-08-906-613-141	Sequence 141, App	1104	154	3.9	1537	6	5472939-5	Patent No. 5472939
1032	157	4.0	610	5217870-2	Patent No. 5217870	1105	154	3.9	1537	6	5256642-5	Patent No. 5256642
1033	157	4.0	610	5217870-2	Patent No. 5217870	1106	154	3.9	1537	6	5472939-5	Patent No. 5472939
1034	157	4.0	647	US-09-949-016-10272	Sequence 10272, A	1107	154	3.9	1847	6	5256642-10	Patent No. 5256642
1035	156.5	4.0	312	US-09-636-382A-15	Sequence 15, Appl	1108	154	3.9	1847	6	5256642-10	Patent No. 5256642
1036	156.5	4.0	3635	US-09-845-583A-2	Sequence 2, Appl	1109	154	3.9	1847	6	5256642-10	Patent No. 5256642
1037	156	4.0	237	US-08-768-859A-16	Sequence 16, Appl	1110	154	3.9	1847	6	5472939-10	Patent No. 5472939
1038	156	4.0	237	US-08-768-859A-21	Sequence 21, Appl	1111	154	3.9	1947	6	US-09-612-314A-52	Patent No. 5256642
1039	156	4.0	237	US-08-767-820A-16	Sequence 16, Appl	1112	154	3.9	2039	6	5256642-2	Patent No. 5256642
1040	156	4.0	237	US-08-767-820A-21	Sequence 21, Appl	1113	154	3.9	2039	6	5472939-2	Patent No. 5472939
1041	156	4.0	237	US-08-622-046B-1	Sequence 1, Appl	1114	154	3.9	2039	6	5256642-2	Patent No. 5256642
1042	156	4.0	237	US-08-622-046B-12	Sequence 12, Appl	1115	154	3.9	2039	6	5472939-2	Patent No. 5472939
1043	156	4.0	237	US-08-944-483-37	Sequence 37, Appl	1116	153.5	3.9	185	3	US-08-705-875A-5	Sequence 5, Appl
1044	156	4.0	237	US-09-100-264-1	Sequence 1, Appl	1117	153.5	3.9	185	3	US-09-220-731-22	Sequence 22, Appl
1045	156	4.0	237	US-09-100-264-12	Sequence 12, Appl	1118	153.5	3.9	185	3	US-09-242-999-5	Sequence 5, Appl
1046	156	4.0	237	US-08-843-076D-1	Sequence 1, Appl	1119	153.5	3.9	190	2	US-08-845-998-6	Sequence 6, Appl
1047	156	4.0	237	US-08-843-076D-8	Sequence 8, Appl	1120	153.5	3.9	190	3	US-09-206-537-6	Sequence 6, Appl
1048	156	4.0	238	US-08-768-859A-8	Sequence 8, Appl	1121	153.5	3.9	190	3	US-09-430-854-6	Sequence 6, Appl
1049	156	4.0	238	US-08-767-820A-8	Sequence 8, Appl	1122	153.5	3.9	352	4	US-09-902-540-5796	Sequence 9796, Ap

1123	153.5	3.9	610	1	US-08-365-470-3	Sequence 3, Appl1	1196	148.5	3.8	111	4	US-09-341-461-30	Sequence 30, Appl1
1124	153.5	3.9	610	3	US-09-209-668-19	Sequence 19, Appl1	1197	148	3.8	113	4	US-09-438-046-23	Sequence 23, Appl1
1125	153.5	3.9	610	3	US-09-490-490A-89	Sequence 89, Appl1	1198	148	3.8	218	3	US-09-578-303-3	Sequence 3, Appl1
1126	153.5	3.9	610	4	US-09-949-016-5942	Sequence 5942, Ap	1199	148	3.8	242	3	US-09-332-215-47	Sequence 47, Appl1
1127	153.5	3.9	1725	4	US-09-562-702A-20	Sequence 20, Appl1	1200	148	3.8	657	4	US-09-949-016-11365	Sequence 11365, A
1128	153.5	3.9	1725	4	US-09-561-818A-20	Sequence 20, Appl1	1201	148	3.8	657	4	US-09-949-016-11365	Sequence 11365, A
1129	153.5	3.9	1786	4	US-09-562-702A-18	Sequence 18, Appl1	1202	148	3.8	657	4	US-09-949-016-11367	Sequence 11367, A
1130	153.5	3.9	1786	4	US-09-561-818A-18	Sequence 18, Appl1	1203	148	3.8	657	4	US-09-949-016-11367	Sequence 11367, A
1131	153	3.9	158	3	US-09-374-135-2	Sequence 2, Appl1	1204	148	3.8	1480	3	US-09-191-647-7	Sequence 7, Appl1
1132	153	3.9	248	3	US-08-906-769-111	Sequence 11, App	1205	148	3.8	1480	3	US-09-540-245A-7	Sequence 7, Appl1
1133	153	3.9	248	3	US-08-906-616-111	Sequence 11, App	1206	148	3.8	1480	5	US-09-540-153-7	Sequence 7, Appl1
1134	153	3.9	248	3	US-08-817-795-111	Sequence 11, App	1207	148	3.8	1480	5	PCT-US91-0905-2	Sequence 2, Appl1
1135	153	3.9	248	3	US-08-639-075A-111	Sequence 11, App	1208	147.5	3.7	137	1	US-08-456-840-48	Sequence 48, Appl1
1136	153	3.9	248	3	US-09-012-431-111	Sequence 11, App	1209	147.5	3.7	197	2	US-08-466-407A-48	Sequence 48, Appl1
1137	153	3.9	248	3	US-09-012-431-111	Sequence 11, App	1210	147.5	3.7	197	2	US-08-892-544A-48	Sequence 48, Appl1
1138	153	3.9	248	3	US-08-906-613-111	Sequence 11, App	1211	147.5	3.7	246	3	US-08-906-769-127	Sequence 127, App
1139	153	3.9	248	5	PCT-US95-14442A-111	Sequence 11, App	1212	147.5	3.7	246	3	US-08-906-616-127	Sequence 127, App
1140	153	3.9	254	3	US-09-578-303-5	Sequence 5, Appl1	1213	147.5	3.7	246	3	US-08-639-075A-127	Sequence 127, App
1141	153	3.9	286	4	US-09-270-767-45162	Sequence 45162, A	1214	147.5	3.7	246	3	US-09-012-431-127	Sequence 127, App
1142	152.5	3.9	267	4	US-09-949-016-10711	Sequence 10711, A	1215	147.5	3.7	246	3	US-09-012-431-127	Sequence 127, App
1143	152.5	3.9	642	2	US-08-872-855-10	Sequence 10, Appl1	1216	147.5	3.7	246	3	US-09-012-431-127	Sequence 127, App
1144	152	3.9	247	2	US-08-851-974-4	Sequence 4, Appl1	1217	147.5	3.7	574	6	US-08-906-613-127	Sequence 127, App
1145	152	3.9	247	2	US-09-213-190-4	Sequence 4, Appl1	1218	147.5	3.7	574	6	5378464-3	Patent No. 5378464
1146	152	3.9	247	4	US-09-949-016-6457	Sequence 6457, Ap	1219	147.5	3.7	1765	4	US-09-562-702A-16	Sequence 16, Appl1
1147	152	3.9	258	4	US-09-949-016-10661	Sequence 10661, A	1220	147.5	3.7	1765	4	US-09-561-818A-16	Sequence 16, Appl1
1148	152	3.9	1033	4	US-09-834-309-1	Sequence 1, Appl1	1221	147.5	3.7	1766	4	US-09-562-702A-14	Sequence 14, Appl1
1149	151.5	3.8	259	4	US-09-949-016-10954	Sequence 10954, A	1222	147.5	3.7	1766	4	US-09-561-818A-14	Sequence 14, Appl1
1150	151.5	3.8	716	2	US-08-766-982-1	Sequence 1, Appl1	1223	147.5	3.7	1786	4	US-09-561-709B-9	Sequence 9, Appl1
1151	151.5	3.8	716	2	US-08-296-219-1	Sequence 1, Appl1	1224	147.5	3.7	1786	4	US-10-006-011A-2	Sequence 669, App
1152	151	3.8	110	4	US-09-341-461-17	Sequence 27, Appl1	1225	147.5	3.7	4391	4	US-10-006-011A-2	Sequence 2, Appl1
1153	151	3.8	110	4	US-08-036-946-10	Sequence 10, Appl1	1226	147	3.7	229	3	US-09-004-731-44	Sequence 44, Appl1
1154	151	3.8	237	5	PCT-US94-07329-10	Sequence 10, Appl1	1227	147	3.7	229	3	US-08-749-699A-44	Sequence 44, Appl1
1155	151	3.8	237	5	PCT-US95-06157-16	Sequence 16, Appl1	1228	147	3.7	229	4	US-09-004-729-44	Sequence 44, Appl1
1156	150.5	3.8	277	1	US-08-024-868-2	Sequence 2, Appl1	1229	147	3.7	242	3	US-09-004-731-41	Sequence 41, Appl1
1157	150.5	3.8	277	2	US-08-242-097-2	Sequence 2, Appl1	1230	147	3.7	242	3	US-08-749-699A-41	Sequence 41, Appl1
1158	150.5	3.8	277	3	US-09-206-695-2	Sequence 2, Appl1	1231	147	3.7	242	4	US-09-004-729-41	Sequence 41, Appl1
1159	150.5	3.8	277	3	US-09-000-179-1	Sequence 1, Appl1	1232	147	3.7	466	4	US-09-949-016-11726	Sequence 11726, A
1160	150.5	3.8	277	4	US-09-799-118-2	Sequence 2, Appl1	1233	146.5	3.7	223	1	US-08-278-091-13	Sequence 13, Appl1
1161	150.5	3.8	277	5	PCT-US96-11995-1	Sequence 1, Appl1	1234	146.5	3.7	223	1	US-08-483-859-13	Sequence 13, Appl1
1162	150.5	3.8	500	4	US-09-423-753-2	Sequence 2, Appl1	1235	146.5	3.7	223	1	US-08-472-173-13	Sequence 13, Appl1
1163	150.5	3.8	659	4	US-09-423-753-3	Sequence 3, Appl1	1236	146.5	3.7	223	2	US-08-487-167-13	Sequence 13, Appl1
1164	150.5	3.8	685	3	US-08-872-855-2	Sequence 2, Appl1	1237	146.5	3.7	223	2	US-08-882-816-13	Sequence 13, Appl1
1165	150.5	3.8	685	4	US-09-423-753-25	Sequence 25, Appl1	1238	146.5	3.7	223	2	US-08-966-149-13	Sequence 13, Appl1
1166	150.5	3.8	685	4	US-09-641-612-7	Sequence 7, Appl1	1239	146.5	3.7	223	2	US-08-801-499-13	Sequence 13, Appl1
1167	150.5	3.8	1064	1	US-08-537-210A-3	Sequence 3, Appl1	1240	146.5	3.7	223	2	US-08-615-271-13	Sequence 13, Appl1
1168	150.5	3.8	1064	3	US-09-113-825-3	Sequence 3, Appl1	1241	146.5	3.7	223	3	US-09-074-659-13	Sequence 13, Appl1
1169	150	3.8	113	4	US-09-438-046-32	Sequence 22, Appl1	1242	146.5	3.7	223	3	US-09-074-659-13	Sequence 13, Appl1
1170	150	3.8	238	6	US-08-944-483-31	Sequence 31, Appl1	1243	146.5	3.7	223	3	US-09-106-468-13	Sequence 13, Appl1
1171	150	3.8	238	6	US-08-944-483-31	Sequence 31, Appl1	1244	146.5	3.7	223	3	US-09-106-468-13	Sequence 13, Appl1
1172	150	3.8	238	6	US-08-944-483-31	Sequence 31, Appl1	1245	146.5	3.7	223	3	US-09-106-468-13	Sequence 13, Appl1
1173	150	3.8	263	4	US-09-653-813-2	Sequence 2, Appl1	1246	146	3.7	137	3	US-09-518-046-23	Sequence 23, Appl1
1174	150	3.8	267	2	US-08-978-404B-46	Sequence 46, Appl1	1247	146	3.7	263	4	US-09-518-046-23	Sequence 23, Appl1
1175	150	3.8	276	1	US-08-467-155A-1	Sequence 1, Appl1	1248	146	3.7	263	4	US-09-518-046-23	Sequence 23, Appl1
1176	150	3.8	276	2	US-08-628-198-1	Sequence 1, Appl1	1249	146	3.7	263	4	US-09-518-046-23	Sequence 23, Appl1
1177	150	3.8	276	3	US-09-201-038-1	Sequence 1, Appl1	1250	145.5	3.7	108	4	US-09-341-461-22	Sequence 22, Appl1
1178	150	3.8	276	5	PCT-US96-07343-1	Sequence 1, Appl1	1251	145.5	3.7	222	3	US-09-949-016-11365	Sequence 11365, A
1179	150	3.8	677	4	US-09-949-016-11370	Sequence 11370, A	1252	145.5	3.7	222	3	US-08-906-616-103	Sequence 103, App
1180	150	3.8	677	4	US-09-949-016-11370	Sequence 11370, A	1253	145.5	3.7	222	3	US-08-817-795A-103	Sequence 103, App
1181	150	3.8	677	4	US-09-949-016-11371	Sequence 11371, A	1254	145.5	3.7	222	3	US-08-639-075A-103	Sequence 103, App
1182	150	3.8	677	4	US-09-949-016-11372	Sequence 11372, A	1255	145.5	3.7	222	3	US-09-012-431-103	Sequence 103, App
1183	149.5	3.8	46	4	US-10-067-422-17	Sequence 17, Appl1	1256	145.5	3.7	222	3	US-09-012-431-103	Sequence 103, App
1184	149.5	3.8	385	1	US-08-340-539A-2	Sequence 2, Appl1	1257	145.5	3.7	222	3	US-08-906-613-103	Sequence 103, App
1185	149.5	3.8	385	2	US-08-461-592B-2	Sequence 2, Appl1	1258	145.5	3.7	222	5	PCT-US95-14444A-103	Sequence 103, App
1186	149.5	3.8	1935	4	US-09-949-016-10403	Sequence 10403, A	1259	145	3.7	110	4	US-09-341-461-21	Sequence 21, Appl1
1187	149	3.8	263	1	US-07-906-983-2	Sequence 2, Appl1	1260	145	3.7	222	3	US-08-906-769-81	Sequence 81, Appl1
1188	149	3.8	575	4	US-09-949-016-11264	Sequence 11264, A	1261	145	3.7	222	3	US-08-906-616-81	Sequence 81, Appl1
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1194	149	3.8	1404	3	US-08-611-729A-2	Sequence 2, Appl1	1267	145	3.7	222	5	PCT-US95-14444A-81	Sequence 81, Appl1
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1487	127	3.2	1617	4	US-09-562-702A-26	Sequence 26, App1

1488 127 3.2 2123 4 US-09-949-016-7517 Sequence 7517, App

1489 127 3.2 3070 4 US-09-961-403-7 Sequence 7, App1

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1496 127 3.2 3110 4 US-09-561-709B-7 Sequence 7, App1

1497 127 3.2 3110 4 US-09-917-254-86 Sequence 86, App1

1498 127 3.2 3110 4 US-09-949-016-5937 Sequence 5937, App

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ALIGNMENTS

RESULT 1

US-10-067-422-9

Sequence 9, Application US/10067422

Patent No. 6743613

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APPLICANT: Ni et al.

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ORGANISM: Homo sapiens

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Best Local Similarity 96.8%; Pred. No. 9.5e-237;

Matches 552; Conservative 0; Mismatches 1; Indels 17; Gaps 1;

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228 GFPAIYEETACSSSPCFHDGTCVLDKAGSYKACACIAGYTGRCENL----- 274

61 GFPAIYEETACSSSPCFHDGTCVLDKAGSYKACACIAGYTGRCENLLEAGSKIRASED 120

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121 SLSTLEERNQSDGGGVNGQKTTGGPGLINGHAKIGTVVSFFCNNSVYLSGNERKTCQ 180

331 QNEMSGKOPICIKACREPKISDLVRRVLEPMVOGSEETPIHOLYLAASFQKQLQAPTK 390

181 QNEMSGKOPICIKACREPKISDLVRRVLEPMVOGSEETPIHOLYLAASFQKQLQAPTK 240

391 KPALPFGDLPNGYOHULTOLQYECISPPYRRLGSSRRCTLRGKSGRAPSCIPICGKIE 450

241 KPALPFGDLPNGYOHULTOLQYECISPPYRRLGSSRRCTLRGKSGRAPSCIPICGKIE 300

QY 451 NITAPKTOGLRMPQAAIYRTSGVNDGSLHKGMFLVCSGALVNERTVVAAHCVTDLG 510
DB 301 NITAPKTOGLRMPQAAIYRTSGVNDGSLHKGMFLVCSGALVNERTVVAAHCVTDLG 360
QY 511 KVTMIKTADLKVVYKGFRRDDREKTIQSLQISAILHPYDPIILDADIAIKLKDKA 570
DB 361 KVTMIKTADLKVVYKGFRRDDREKTIQSLQISAILHPYDPIILDADIAIKLKDKA 420
QY 571 RISTRVOPICLAASRDISTSFQESHITVAGNVLADVRSPGFKNDTLRSQVSVVDSILC 630
DB 421 RISTRVOPICLAASRDISTSFQESHITVAGNVLADVRSPGFKNDTLRSQVSVVDSILC 480
QY 631 BEQHEHDGIPVSVTDNMFCSWEPTAPSDICTAETGIIAIVSPGRASPEPRHMLGLVS 690
DB 481 BEQHEHDGIPVSVTDNMFCSWEPTAPSDICTAETGIIAIVSPGRASPEPRHMLGLVS 540
QY 691 WSYDKTCSHRLSTAFKVLPEFKMIERNMK 720
DB 541 WSYDKTCSHRLSTAFKVLPEFKMIERNMK 570

RESULT 2

US-08-296-014A-4
Sequence 4, Application US/08296014A
Patent No. 5716834
GENERAL INFORMATION:
APPLICANT: Ding, Jeak Ling
APPLICANT: Ho, Bow
TITLE OF INVENTION: The Cloned Factor C cDNA of the
TITLE OF INVENTION: Singapore Horseshoe Crab, Carcinoscorpius
TITLE OF INVENTION: rotundicauda and Purification of Factor C Proenzyme
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: 8110 Gatehouse Road, Suite 500 East
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
ZIP: 22042
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/296,014A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Murphy, Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1781-105P
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
TELEX: 248345
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1019 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-296-014A-4

Query Match 15.9%; Score 665; DB 1; Length 1019;
Best Local Similarity 25.4%; Pred. No. 1,7e-46;
Matches 222; Conservative 118; Mismatches 304; Indels 230; Gaps 37;
QY 34 PGAENINMRECECEQDOIECVCPGRK-----VVGTYLPCHNEENECDSCLIH 82
DB 184 PNGQNSNPPKICIR-----ECANVSSPEHGKNAALSGDMIEGATL-----RFSCHS----- 229
QY 83 PGCTIFENCKSCR-NGSWGTL----- 103

DB 230 PYLIGQETITCGANQOMNGIOPCKALVFCPDLDPVNAHEHKYKIGVEBKQGFPGTE 289
QY 104 -----DFFYKGFYCAECR--AGWYGG--DCNR-----CGQVLR-- 133
DB 290 VVTYCSGNVFLMGFDTLKCNPDGSMGSGPSGVKAVDRVDCSKAVDFLDVGEPIRIH 349
QY 134 APKQILLES-----YPLNAHCMTIHA--KRPVI----- 162
DB 350 CPAGCSITACTGWTGTAIYHLSISVCRRAIHAAGLPSNGGAVHVNNNGPYDPLGSDINGI 409
QY 163 -----QLRFVWLSLEFDYM-----CQYDYVEVRD-----GDNRDGQIIRKVCN--E 202
DB 410 KSEELKSIAASFEDYRSSTAGKSGCPDGMFEVDENCVVTSKQAMEAAGVCTMMA 469
QY 203 RPAPIOS--IGSSILHVLPHSDG--SKNDFGH-----AIYEETACSS 241
DB 470 RLAVLDKDVLPNSLTETLRGKGLTTWTGILHRLDAEKPIWEIMDRSNVNLNDLTFWAS 529
QY 242 SPCFHGTCVYL-----DKAGS--YKACIAGYTQRCENLLEERN-----CSDPGCPNGYQXI 293
DB 530 GERGENETCVMDIQQDLOSVMWTKSCFOPSPACMMDLDRNKAKCDDPGSLENGATL 589
QY 294 TGGPGLINGRHAKIGTVVSPFCNNSVYLSGENEKRTCCQNGMSGKOPICIK--ACREPKI 351
DB 590 HGQS--IDGFYA--GSSIRYSCVLAHLSGTETVTTTNGTWAPKRCIKVITCQNPV 645
QY 352 SDVLRRLVPMQVOSRETPHLQVYSAFSSKQKQ-----SAPTKKPALEPGD----- 398
DB 646 PSYGSAVIRK---PSRNTNSISRVGSPFLRLPLPLAARAKPPKRSQSPSTVDLASK 702
QY 399 -LPMGYQLHTQLOECISPPFYRLGSSRRCTLRGKMGGRAPSCPIPGKIENTIAP- 455
DB 703 VKLPEGIVRVGSAIYCESRYVELLSQGRCDSDNMGGRAPSCIPVGRSDSPSPFP 762
QY 456 -----KTQGLRMPQAAIYRTSGVNDGSLHKGMFLVCSGALVNERTVVAAHCVTDLG 510
DB 763 IMNGNSTEIGQMPWAGISRMLA-----DHMMFLQCCGSLINEKMIYTAHCVTYSA 815
QY 511 KVTMIKTADLKVVYKGFRRDDREKTIQSLQISAILHPYDPIILDADIAIKLKDKA 570
DB 816 TAEIIDNQFKMYLKGKRYRDSRDDVQVREALEIHNVNVDGNNFIDALILQKTPV 875
QY 571 RISTRVOPICLAASRDISTSFQESHITVAGNVLADVRSPGFKNDTLRSQVSVV 624
DB 876 TLTRVQPICLPT--DITT--REHLEKGTAAVVTGNG--LNENNTYBETIQOAVLPV 926
QY 625 VDSLCEQHEHDGIPVSVTDNMFCSWEPTAPSDICTAETGIIAIVSPGRASPEPRMH 684
DB 927 VAASTCEGKKEADLPVTENNFCAGYK--KRYDACSQSGG--PLVFADDSRTERRV 983
QY 685 LMGLVSWSYDKTCSH--RLSTAFTKVLPEFKMIER 717
DB 984 LEGIVSWGSPSGCGKANQYGGFTKVVNVLFWIRQ 1017

RESULT 3

US-08-596-405-4
Sequence 4, Application US/08596405
Patent No. 5858706
GENERAL INFORMATION:
APPLICANT: Ding, Jeak Ling
APPLICANT: Ho, Bow
TITLE OF INVENTION: The Cloned Factor C cDNA of the
TITLE OF INVENTION: Singapore Horseshoe Crab, Carcinoscorpius
TITLE OF INVENTION: rotundicauda and Purification of Factor C Proenzyme
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: 8110 Gatehouse Road, Suite 500 East
CITY: Falls Church
STATE: Virginia
COUNTRY: USA

```

      ZIP: 22042
      COMPUTER READABLE FORM:
      MEDIUM TYPE: Floppy disk
      COMPUTER: IBM PC compatible
      OPERATING SYSTEM: PC-DOS/MS-DOS
      SOFTWARE: Patent Release #1.0, Version #1.25
      CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/08/596,405
      FILING DATE:
      CLASSIFICATION: 435
      ATTORNEY/AGENT INFORMATION:
      NAME: Murphy, Jr., Gerald M.
      REGISTRATION NUMBER: 28,977
      REFERENCE/DOCKET NUMBER: 1781-105P
      TELECOMMUNICATION INFORMATION:
      TELEPHONE: (703) 205-8000
      TELEFAX: (703) 205-8050
      TELEX: 248345
      INFORMATION FOR SEQ ID NO: 4:
      SEQUENCE CHARACTERISTICS:
      LENGTH: 1019 amino acids
      TYPE: amino acid
      TOPOLOGY: linear
      MOLECULE TYPE: protein
      US-08-596-405-4

Query Match      16.9%; Score 665; DB 2; Length 1019;
Best Local Similarity 25.4%; Pred. No. 1.7e-46;
Matches 222; Conservative 118; Mismatches 304; Indels 230; Gaps 37;

QY      34 PGAEWNIMRCECEYDIEVCVCPKRE-----VGYTIIPCCRNENECDSCLIH 82
DB      184 PNGQWSNFPKCR-----ECAMVSSPEHGKVALSGDMIGATL-----RFSQDS----- 229
QY      83 PGCTIFENCSCR-NGSWGTL----- 103
DB      230 PYVLIGETLTCCQNGMNGQIIPQCKNLVPCPLDPVNAHAKVIGVEQYQGPQSGTE 289
QY      104 -----DDFYVKGFCYCAEGR--AGWYGG--DCMR-----GQVYR-- 133
DB      290 VTYTSGNFTLMGDTLCKNPDGSMGSGSCPSCKVADREVDSCSKAVPLDDVGEFVRIH 349
QY      134 APKQQLILES-----YPLNAHCEWTIHA--KPGFYI----- 162
DB      350 CPAGCSLTATGWTGTATYHLESLVCRAIHAQKLPNGGAVHVNNGPYSDPLGSLDNGI 409
QY      163 ---QLRFMLSLIEDYV-----CQDYVEYRD-----GDRDQIIRKVCN--E 202
DB      410 KSEBELKLSRFPDYVRSSTAGKSGCPDGMFEVDENCYVVTSKQAMBRAGVCTMAA 469
QY      203 RPARIQS--IGSSLHVLPHSDG--SKNFDGRH-----AIYEITACSS 241
DB      470 RLVLVDQVLPNSLTETLRKGLTTTIGLHRLDAEKPIWELMDRSNVVLANDLTFWAS 529
QY      242 SPCHDGTCLV-----DKVGS--YKCAAGYTGRCENLEERN-----CSDPGPVGXOXI 293
DB      530 GEPENENCYMDIQQDLOSLVWTKSKCFOPSSPACMDLSDRKAKACDDPSLENGHATL 589
QY      294 TGGPGLINGHAKIGTVSFFCNNSYVLSGNEKRTCOONGSEWSGKOPICIK--ACREPKI 351
DB      590 HGGS--IDGFYA--GSSIRVSCVLAHLSGTEVYTCCTNGWMSAPKRCIKVITCQRPV 645
QY      352 SDLVRRVLEMQVQSRETPHLQLYSAAFSKOKLQ---SAPTKKALPFGD----- 398
DB      646 PSYGSVETIKP---PSRTNISRVSQSPFLRLPLPLARAKAPPKRSPSSOPSTVDLASK 702
QY      399 --LPMGQHLHTLOQYECISPFYRLGSSRRTCLRTKMSGRAPSCIPICGKIENITAP- 455
DB      703 VKLPBEGHYRGSRAIYTCESRYIELLSQGRCLDSNGMGRAPSCIPVCGRSDSPSPF 762
QY      456 -----KTQGLRMPWQAAIYRTSGVHDGSLHKAMFLVCSGALVNERTVVAHAHCVTDLG 510
DB      763 IMMGNSTREIQGMQWQAGISRWLA-----DHNNWFLQCGGSLNLEKMTVTAHCVTYS 815

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QY      511 KTMITADLKVVLGFRYDDDEKTIQSLQISAIILHPNDPILDLADIALIKLIDKA 570
DB      816 TAEIIPNQFKVYGLGYRSDSDRDYVQVREALHVNPNDPGNLNDIALIQKTPV 875
QY      571 RISTRVOPICLAASRLSTSFQESH-----TVAGMVLADVRSPGKNDLTRSGVSV 624
DB      876 TLTRVQPICLPT--DITF--REHLKEGTLAVVTMG---LNENNTYSETIQQAVLPV 926
QY      625 VDSLCEQHEHDHPIVSYDNNMFCASWEPTASDICTAETGIAVSPGRASPEPRWH 684
DB      927 VASTCEBGKEADLDTLTENNFCAGYK--KGRYDACSQSDSG--PLVFADSRTERRW 983
QY      685 LMGVMSYDKTCSH-RLSTAFKVLPEFQWIER 717
DB      984 LEGIVSGSPSGCGKANQYCGFTKVVVFLSMIRQ 1017

RESULT 4
US-08-877-620-4
; Sequence 4, Application US/08877620
; Patent No. 5985590
; GENERAL INFORMATION:
; APPLICANT: Ding, Jeak Ling
; TITLE OF INVENTION: The Cloned Factor C cDNA of the
; TITLE OF INVENTION: Singapore Horseshoe Crab, Carcinoscopus
; TITLE OF INVENTION: roundicauda and Purification of Factor C Proenzyme
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolaach & Birch
; STREET: 8110 Gatehouse Road, Suite 500 East
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22042
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/877,620
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/596,405
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy, Jr., Gerald M.
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 1781-105P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1019 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-877-620-4

Query Match      16.9%; Score 665; DB 2; Length 1019;
Best Local Similarity 25.4%; Pred. No. 1.7e-46;
Matches 222; Conservative 118; Mismatches 304; Indels 230; Gaps 37;

QY      34 PGAEWNIMRCECEYDIEVCVCPKRE-----VGYTIIPCCRNENECDSCLIH 82
DB      184 PNGQWSNFPKCR-----ECAMVSSPEHGKVALSGDMIGATL-----RFSQDS----- 229
QY      83 PGCTIFENCSCR-NGSWGTL----- 103

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Db      984 LEGIVSWGSPGGCKANQYGFTRKANVFLSMIRO 1017

RESULT 6
US-09-626-795-4
; Sequence 4, Application US/09626795
; Patent No. 6719973
; GENERAL INFORMATION:
; APPLICANT: DING, Jeak Ling
; APPLICANT: HO, Bow
; TITLE OF INVENTION: Use of Recombinant Factor C to Induce Bacteriostasis
; FILE REFERENCE: 4810-61737
; CURRENT APPLICATION NUMBER: US/09/626,795
; CURRENT FILING DATE: 2000-07-26
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1019
; TYPE: PRT
; ORGANISM: Carcinoscopus rotundicauda
US-09-626-795-4

Query Match      16.9%; Score 665; DB 4; Length 1019;
Best Local Similarity 25.4%; Pred. No. 1.7e-46;
Matches 222; Conservative 118; Mismatches 304; Indels 230; Gaps 37;

Qy      34 PGABNMIMRCECEYDQIECVCPGKRE-----VVGYTIPCCRNENECDSCLIH 82
      184 PNGQMSNFPKICLR-----ECAMWSPEHGVNALSMDMIGATL-----RFGCDs----- 229
      83 PGCTIFENCKSCR-NGSMGGTL----- 103
      230 PYVLIGGETLTCCQNGQNGQIPQCKNLVFCPDLDPVNAHAKYKIGVEQKYGFPGTE 289
      104 -----DDFYVKGKFCACER--AGWYGG--DCMR-----CGQVLR-- 133
      290 VVTYCGSNYFLMGFDLTKCNPDGSGWSGSCVAVADREVDCSKAVDFLDVGEVRIH 349
      134 APKQIILLES-----YPLNAHCWETIHA-----KQFVYL----- 162
      350 CPAGCSLTAGTGWCTAIYHLLSVCRALIHAGKLPNSGGAHVHVNNGPYSDFLASDLNGI 409
      163 -----QLRFMLSLBEDYM-----COYDVEVRD-----GDNRDGQIIRKVCN--E 202
      410 KSEELKSLARSPRDYVRSSPAKSGCPDGFVEDENCVVTSKQRAHERAAGVCTMAA 469
      203 RPAPIQS--IGSSLIHLFHSOG--SKNFDGFH-----AIYEETLACSS 241
      470 RLAVLDDKVIPIINSLTETLRGKGLTTWIGLHRLDAEKPIWELMDRNSNVJLNDLTFMAS 529
      242 SPCHDGTCLV-----DKAGS--YKQACLAGITGQRCENLLEBRN-----GSDPGGPNVGOXI 293
      530 GEPENETNCVYMDIQDQISVWTKYSCFQPSSEFACMMDLSDRNKACDDPSLENGHATL 589
      294 TGGGGLINGHAKIGTIVVSFFCNNSVYLISGNEKATCOONGSEWSGKOPICIK--ACREPKI 351
      590 HGOS--IDGFRV--GSSIRVSCVHLHLSGETEYVCTTNGWWSAPKRCIKVITCONPV 645
      352 SDLVRRRVLPWQVSRETPHLQVLSAFSKQKIQ--SAPTKPALPFGD----- 398
      646 PSYGVSVEIKP--PSRTNISIRVGSFPLRLPLPLARAKAPPKPRSSQSPSTVDLASK 702
      399 --LPMGQHLHTOQYECISPFYRLGSSRTCTRTKMGSRASCIPICGKENTAP- 455
      703 VKLPEGHYRVGSRRAIYTCESRYELLDSQGRCDNSNWSGRPASCLPVCGRSDSPSPF 762
      456 -----KTQGLRWPMQAAIYRTSGVHDGSLHKGAMFVCSGALVNERTVVAACHVTDLG 510
      763 IMNNSNEIGQMPQAGISRWLA-----DHMMWFQCGSSLNEMKMTVYAAACVYISA 815
      511 KVTMIKTADLKVNLGKFYRDDRDDEKTIQSLQISAIILHPNYDPIILDADIAIKLIDKA 570
      816 TAEIIDNQFMVYIGKYRDDSDDDYQVVEALEIHVNPNYDPGNINFDIALIQLKTPV 875

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Qy      571 RISTRVQPICLAASRLSTSPQESH-----TVAGNVLADYVRSPGKNDITLRSQVSV 624
      876 TLTRVQPICLPT--DITT---REHLKEGTLAVVTGMG-----LNENNTYSEITIQOAVLPV 926
Qy      625 VBSLLCEBQHEHDIGIVSVTNDNMFECASWEPTAVSDICTAETGIGIAVSPFGRASPEPRM 684
      927 VASTCEBQKEDLPLVTENNFCAGYK--KGRYDCSGDSGG--PLVFPADSRTERRW 983
Qy      685 IMGVSMYDKTCSH--RLSTAFKVLFPKDWIER 717
      984 LEGIVSWGSPGGCKANQYGFTRKANVFLSMIRO 1017

RESULT 7
US-08-296-014A-2
; Sequence 2, Application US/08296014A
; Patent No. 5716834
; GENERAL INFORMATION:
; APPLICANT: Ding, Jeak Ling
; APPLICANT: HO, Bow
; TITLE OF INVENTION: The Cloned Factor C cDNA of the
; TITLE OF INVENTION: Singapore Horseshoe Crab, Carcinoscopus
; TITLE OF INVENTION: rotundicauda and Purification of Factor C Proenzyme
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Birch, Stewart, Kolaesch & Birch
; STREET: 810 Gatehouse Road, Suite 500 East
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22042
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/296,014A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy, Jr., Gerald M.
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 1781-105P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1083 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-296-014A-2

Query Match      16.9%; Score 665; DB 1; Length 1083;
Best Local Similarity 25.4%; Pred. No. 1.8e-46;
Matches 222; Conservative 118; Mismatches 304; Indels 230; Gaps 37;

Qy      34 PGABNMIMRCECEYDQIECVCPGKRE-----VVGYTIPCCRNENECDSCLIH 82
      248 PNGQMSNFPKICLR-----ECAMWSPEHGVNALSMDMIGATL-----RFGCDs----- 233
      83 PGCTIFENCKSCR-NGSMGGTL----- 103
      294 PYVLIGGETLTCCQNGQNGQIPQCKNLVFCPDLDPVNAHAKYKIGVEQKYGFPGTE 353
      104 -----DDFYVKGKFCACER--AGWYGG--DCMR-----CGQVLR-- 133
      354 VVTYCGSNYFLMGFDLTKCNPDGSGWSGSCVAVADREVDCSKAVDFLDVGEVRIH 413

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QY 134 APKGQILLES-----YPLNAHCEWTIHA-----KRGFVI-----162
DB 414 CPAGCSLTAGTGWGTALYHLSVVCRAIHAAGKLPNSGAAVHVNNGPYSDFLGSDINGI 473
QY 163 ---OLRFVMLSLFEDYM-----COYDVEVRD-----GDNRDGQIILKRYCGN--E 202
DB 474 KSEELKSLARFRFDYVSSSTAGKSGCPDGMFEVDENCYVYTSQKRAMERAQGYCTMAA 533
QY 203 RPAPIQS--IGSSLHVLFSHDG-SKNFDGFH-----AIYEETACSS 241
DB 534 RLAVLDKDVIPNSLTETLRGKGLTTWTWIGLHRLDAEKPFIMELMDRSNVVLDNLTFWAS 593
QY 242 SPCHDGTCTL---DKAGS--YKACACLAGYTGQRCENLLEERN---CSDPGFPNGYQKI 293
DB 594 GEPENETNCVYMDIODQLOSVWTKKSCFPSSPACMDLSRNNAKCDDPSGLENGATL 653
QY 294 TGGPGLNGRHAQIGTVVSPFCNNNSYVLSGNEKRTCOQNGEMSGKOPICIK--ACREPKI 351
DB 654 HGQS--IDGFYA--GSSIRYSCVHLHLSGTETVYCTTNGTWSAPKPRCLIVITCQNPV 709
QY 352 SDLVRRRLPMOVOSRETPHLQVSAFSAFQKQKQ---SAPTKKPALPFGD-----398
DB 710 PSYGSVEIKP---PSRTNISIRVGSPLRLPLPLABAKKPPKRRSQPSTVDLASK 766
QY 399 --LPMGYQHLHTQLOVEICISPPYRRLGSSRRTCLRTGKWSGRAPSCIPICGKIENITAP- 455
DB 767 VKLPEGHYRVGSRAIYTESRYELLGSGRCDSNGMWSGRPASCIIPVCGRSDSPSPFP 826
QY 456 -----KTQGLRMPMOAIIYRRTSGVHDGSLHKAMFIVCGALVNERTVVAAHCVTDLG 510
DB 827 IMNGNSTEIGQPMWQAGISRWLA-----DHNNMFLOCGGSLNEKIVTAACVYYSA 879
QY 511 KVTMIKTADLVVYKGFYRDDDRDEKTIQSLQISAIIHPNYPDILLADADIAIKLIDKA 570
DB 880 TAEIIPDNQFMVYLGKYYRDRSDDDVYQVREALEIHVNPNYDGNLNFIDALIQLTPTV 939
QY 571 RISTRVOPICLAASRDISTSFQESH-----TVAGNVLADVRSPPGKNDTLRSQVSV 624
DB 940 TLTRVQPICTPT--DITF---REHLKEGTLAVVTWGMG---LNNNTYSETIOOAVLPV 990
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DB 991 VAASTCEGYKEADPLVTENMFPCAGYK-KGRYDAGSGDSG--PLVFADSKTERRKV 1047
QY 685 IMGIVMSYDKTCSH-RLSTAFTKVLPEKDWIER 717
DB 1048 LEGIVMSGSPSGCGKANQYGGTTKYNVFLSMIRQ 1081

RESULT 8
US-08-596-405-2
: Sequence 2, Application US/08596405
: Patent No. 5858706
: GENERAL INFORMATION:
: APPLICANT: Ding, Jaek Ling
: APPLICANT: Ho, Bow
: TITLE OF INVENTION: The Cloned Factor C cDNA of the
: TITLE OF INVENTION: Singapore Horseshoe Crab, Carcinus scorpheus
: TITLE OF INVENTION: rotundicauda and Purification of Factor C Proenzyme
: NUMBER OF SEQUENCES: 4
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Birch, Stewart, Kolasch & Birch
: STREET: 8110 Gatehouse Road, Suite 500 East
: CITY: Falls Church
: STATE: Virginia
: COUNTRY: USA
: ZIP: 22042
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:

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: APPLICATION NUMBER: US/08/596,405
: FILING DATE:
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Murphy, Jr., Gerald M.
: REGISTRATION NUMBER: 28,977
: REFERENCE/DOCKET NUMBER: 1781-105P
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (703) 205-8000
: TELEFAX: (703) 205-8050
: TELEX: 248345
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1083 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-596-405-2

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Query Match 16.9%; Score 665; DB 2; Length 1083;
Best Local Similarity 25.4%; Pred. No. 1,8e-46;
Matches 222; Conservative 118; Mismatches 304; Indels 230; Gaps 37;

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QY 34 PGAEWNTMCECEYDIEGVCEPKRE-----VYGYTIPCCRNENEDGSLIH 82
DB 248 PNCQWMSFPKRCR---ECAMVSSPEHGKVALSGDMIGATL-----RFSQDS---293
QY 83 PGCTIFENCKSCR-NGSMGTL-----103
DB 294 PYVLIQGETLTCQNGNMGNOIQCKNLVFCRPLDPVNNHAHKYKIGVEQKYQFPQCTE 353
QY 104 -----DDEYKGPYCAEGR--AGWYGG--DCNR-----CGQVLR--133
DB 354 VTYTCSGNYFLMGFDLTKCNPDSGWSGQSPCVKVADEYVDCSKAVDFLDVGEPIVRIH 413
QY 134 APKGQILLES-----YPLNAHCEWTIHA-----KRGFVI-----162
DB 414 CPAGCSLTAGTGWGTALYHLSVVCRAIHAAGKLPNSGAAVHVNNGPYSDFLGSDINGI 473
QY 163 ---OLRFVMLSLFEDYM-----COYDVEVRD-----GDNRDGQIILKRYCGN--E 202
DB 474 KSEELKSLARFRFDYVSSSTAGKSGCPDGMFEVDENCYVYTSQKRAMERAQGYCTMAA 533
QY 203 RPAPIQS--IGSSLHVLFSHDG-SKNFDGFH-----AIYEETACSS 241
DB 534 RLAVLDKDVIPNSLTETLRGKGLTTWTWIGLHRLDAEKPFIMELMDRSNVVLDNLTFWAS 593
QY 242 SPCHDGTCTL---DKAGS--YKACACLAGYTGQRCENLLEERN---CSDPGFPNGYQKI 293
DB 594 GEPENETNCVYMDIODQLOSVWTKKSCFPSSPACMDLSRNNAKCDDPSGLENGATL 653
QY 294 TGGPGLNGRHAQIGTVVSPFCNNNSYVLSGNEKRTCOQNGEMSGKOPICIK--ACREPKI 351
DB 654 HGQS--IDGFYA--GSSIRYSCVHLHLSGTETVYCTTNGTWSAPKPRCLIVITCQNPV 709
QY 399 --LPMGYQHLHTQLOVEICISPPYRRLGSSRRTCLRTGKWSGRAPSCIPICGKIENITAP- 455
DB 767 VKLPEGHYRVGSRAIYTESRYELLGSGRCDSNGMWSGRPASCIIPVCGRSDSPSPFP 826
QY 456 -----KTQGLRMPMOAIIYRRTSGVHDGSLHKAMFIVCGALVNERTVVAAHCVTDLG 510
DB 827 IMNGNSTEIGQPMWQAGISRWLA-----DHNNMFLOCGGSLNEKIVTAACVYYSA 879
QY 511 KVTMIKTADLVVYKGFYRDDDRDEKTIQSLQISAIIHPNYPDILLADADIAIKLIDKA 570
DB 880 TAEIIPDNQFMVYLGKYYRDRSDDDVYQVREALEIHVNPNYDGNLNFIDALIQLTPTV 939
QY 571 RISTRVOPICLAASRDISTSFQESH-----TVAGNVLADVRSPPGKNDTLRSQVSV 624
DB 940 TLTRVQPICTPT--DITF---REHLKEGTLAVVTWGMG---LNNNTYSETIOOAVLPV 990

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Db 940 TLTRVQICLPT--DITT--REHLKEGLAVVTGNG---LNENNTSETIQOAVLPV 990
Qy 625 VDSLCEBOHEDHGIPIVSTDNMFCAWSEPTAPSDICTAETGIIAAVSPFGRAPEPRWH 684
Db 991 VAASTCEEGYKADLPLVTENNMFCAGYK-KGRYDACSGBSGG--PLVFADSDRTERRW 1047
Qy 685 LMGVMSWYDKTCSH-RLSTAFTKVLPEFKWMIER 717
Db 1048 LEGIVSWGSPSGCGKANQYGGFTKVVNVLFWIRQ 1081

RESULT 9
US-08-877-620-2
Sequence 2, Application US/08877620
Patent No. 5985590
GENERAL INFORMATION:
APPLICANT: Ding, Jeak Ling
APPLICANT: Ho, Bow
TITLE OF INVENTION: The Cloned Factor C cDNA of the
TITLE OF INVENTION: Singapore Horseshoe Crab, Carinoscorpis
TITLE OF INVENTION: rotundicauda and Purification of Factor C Proenzyme
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: 810 Gatehouse Road, Suite 500 East
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
ZIP: 22042
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/877,620
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/596,405
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Murphy, Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1781-105P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
TELEX: 248345
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1083 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-877-620-2

Query Match 16.9%, Score 665; DB 2; Length 1083;
Best Local Similarity 25.4%; Pred. No. 1.8e-46;
Matches 222; Conservative 110; Mismatches 304; Indels 230; Gaps 37;

Qy 34 PGAEWNTMCECEYDIECVPCPKR-----VVGTTTFCRMEENEDSLIH 82
Db 248 PNCQWSPFKRJR---ECAMVSPBHKVNALSGMIGATL-----RFSQDS--- 293
Qy 83 PGCTIFENKSCR-NGSMGTL----- 103
Db 294 PYVLIGETILTCQNGNGNGQIPIQCKNLVFCRDLDPVNAHKKYIGEVQKYGQPGCTE 353
Qy 104 -----DFTYVKGFFCAEGR--AGWYGG--DCKR-----CGQVLR-- 133
Db 354 VVTYSGSNVFLMGFDLTKNPDGSMGSGSPSCVAVADREVDCSKAVDFLDVGEPRVIRH 413

Qy 134 APKQIILLS-----YPLNAHCWETIHA---KPGFVI----- 162
Db 414 CPAGCCLTAGTGWTAIYHELSSVCAAIHAGCLPNSGGAVHVNNQPYSDFLGDLNGI 473
Qy 163 ---QLRFVHLSLEFDM-----CQYDYVEVRD-----GDNRDGOIKRVCGN--E 202
Db 474 KSEELASLARSFRFDVSSSTAGKSCPDGWFEBVENCYVTSKORAMEAQAQVCTMMA 533
Qy 203 RPAPIOS--IGSSLAHLFHSDG-SKNFDFH-----AIYEITACSS 241
Db 534 RLAVLDKQVYIENLTETLAKGLITTWIGLHRLDAKRFIWMELMDRNVNLANLIFWAS 593
Qy 242 SPCHDGTCLV---DKAGS-YKACIAGYTGRCENLLEBN---CSDFGCVNGYQKI 293
Db 594 GEPNETNCVYMDIQDQSVMTKSCFQPSSPACMMDLSBRKAKCDPDGSLENGHATL 653
Qy 294 TGSPGLINRHAKIGVSPFCNNSYVLSGNERKTCQCNEMSGKPICK--ACREPKI 351
Db 654 HGGS--IDGFYA--GSSIRSCVHLVLSGETVCTTNGTWSAPKPRCIKVIYQONPV 709
Qy 352 SDLVRRRVLPWQVSRBETPLHOLYSAAFSKQKQ---SAPTKPALPFQD----- 398
Db 710 PSYGSVEIKP---PSRTNISRVSSEPLRPLRPLAARAKPPRPSQSPSTVDLASK 766
Qy 399 --LPMGYOHLTQLOYECISPFYRLGSSRRRTCLRTGKMSGRAPSCIPICIKIENTAP- 455
Db 767 VKLPEGHYRVGSAIYTCESRYVELLGSQCRCDNSGNGSGRASCIPVCGRSDSPSPF 826
Qy 456 -----KTQGLRWQOAIYRISGVHDGSLHKAMFLVCSGALVNERTVVAAHCTYDLC 510
Db 827 INNGNSTEIGQWPMQGISRMLA-----DHNMFLOCGSSILNEKWIYTAHCVYSA 879
Qy 511 KYMIMTKADLVKLVGKPRVDRDEKTIOSLSAIIHPNYPYPIILDADIAILKLDKA 570
Db 880 TAEIIPNOFKMLGKXTRHDSRDDYVVRLELHVNNVDPGNLINFIAIYQLKTPV 939
Qy 571 RISTRVQICLARSRLSTSPQESH-----TVAGNNVLADYRSGPKNDTLRSGVSV 624
Db 940 TLTRVQICLPT--DITT--REHLKEGLAVVTGNG---LNENNTSETIQOAVLPV 990
Qy 625 VDSLCEBOHEDHGIPIVSTDNMFCAWSEPTAPSDICTAETGIIAAVSPFGRAPEPRWH 684
Db 991 VAASTCEEGYKADLPLVTENNMFCAGYK-KGRYDACSGBSGG--PLVFADSDRTERRW 1047
Qy 685 LMGVMSWYDKTCSH-RLSTAFTKVLPEFKWMIER 717
Db 1048 LEGIVSWGSPSGCGKANQYGGFTKVVNVLFWIRQ 1081

RESULT 10
US-09-287-368-2
Sequence 2, Application US/09287368A
Patent No. 6645724
GENERAL INFORMATION:
APPLICANT: Ding, Jeak Ling
APPLICANT: HO, Bow
TITLE OF INVENTION: Assays for Endotoxin and Methods for Removal of Endotoxin
TITLE OF INVENTION: From a Sample Using Recombinant Factor C
FILE REFERENCE: 1781-0165P
CURRENT APPLICATION NUMBER: US/09/287,368A
CURRENT FILING DATE: 1999-04-07
EARLIER APPLICATION NUMBER: 09/201,786
EARLIER FILING DATE: 1998-12-01
EARLIER APPLICATION NUMBER: 09/081,767
EARLIER FILING DATE: 1998-05-21
EARLIER APPLICATION NUMBER: 60/058,816
EARLIER FILING DATE: 1997-09-19
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patent in Ver. 2.1
SEQ ID NO 2
LENGTH: 1083
TYPE: PRT
ORGANISM: Carinoscorpis rotundicauda

FEATURE:
OTHER INFORMATION: any n or xaa = Unknown
US-09-287-368-2

16.9%; Score 665; DB 4; Length 1083;

Query Match
Best Local Similarity 25.4%; Pred. No. 1.8e-46;
Matches 222; Conservative 118; Mismatches 304; Indels 230; Gaps 37;

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QY 34 PGAEWNIMCECECYDIECVCPKRE-----VGYTTPCCRNENECDCLIH 82
DB 248 PNGQMSNFPKRCIR-----ECAMVSSPEHGKVNALSGDMIEGATL-----RFSCDS----- 293
QY 83 PGCTIFENCKSCR--NGSWGTL----- 103
DB 294 PYYLIGETLTCQNGQNGQIPQCKNLVPCPDLDPVNAHAKVKGVEQKYGQFPQGTB 353
QY 104 -----DDFYKGFYCAECR--AGWYGG--DCMR-----CGQVLR-- 133
DB 354 VTYTSGNRYLMPDITLKNPDSGWSGSPSCYKVAVDREVDCKAVDFLDVGEPRRIH 413
QY 134 APKQIILLES-----YPLNAHCWTIHA--KGFVI----- 162
DB 414 CPACGSLTAGTGWGTATAYHELSSVCRAIHAIGKLPNSGGAHVHVNNGPYDFLGSDLNGI 473
QY 163 ---QLRVMTLSLEFDY-----CQYDVEYRD-----GDNRDGQIHKRYCGN--E 202
DB 474 KSEBLKSLASFPRDYVSSSTAGKSGCPDGMFEVDENCYVYTSKORAMERAOQVCTMAA 533
QY 203 RPAIIGS--IGSSLHVLHFDG--SKNPDGFH-----AIYEITACSS 241
DB 534 RLAVLDKDVLPNSLTETLRGKGLTTWIGLHRLDAEKPFIMELMDRNVNLDWLTWAS 593
QY 242 SPCHDGTCLV---DKAGS--YKACIAGYTGRCENLEERN--CSPDGPVNGYQKI 293
DB 594 GEPENETNCVYMDIQDQSGVMTKSCFQPSFACMDLSDRNKAKCDDPSLENGHATL 653
QY 294 TGGEGILINGHAKIGTVSPFCNNSYVLSGNEKRTCOQNGEMSGKOPICIK--ACREPKI 351
DB 654 HGGS--IDGFYA--GSSIRYSCEVLHVLSTETVCTTNGTWSAPKRCIKVITCQNPV 709
QY 352 SDVRRRRLVPMQVQSRERPLHOLYSAFSSKOKLQ---SAPTKKRALPFGD----- 398
DB 710 PSYGSVEIKP--PSKRTNSISRVSFPRLRPLPLARAKAPPRKRSOSPSTVDLASK 766
QY 399 --LPMGYOHLHTOLQYECISPFYRLGSSRRCTCLRTGKMSGRAPSCIPICGKIENITAP- 455
DB 767 VKLPEGHYRVGSRAIYTCESRYVELLSQGRCDNSNGMWSGRPASCIPIVGRSDSPSPF 826
QY 456 -----KTQGLRWPMQAAIYRRTSGVHDSGLHKAMFLVCSGALVNERTVVAACVTDLG 510
DB 827 IWNGNSTELIQMPQAGISRWLA-----DHNMMFLOCGGSLINEKMIYVAACVTVSA 879
QY 511 KVTMIKTADLKVVVIGKPYRDDDEKTIQSLQISAILIHPNYPDILLADAIILKLDKA 570
DB 880 TAEIIDPNQFMVIGKTYRDSRDDVQVREALEIHVNEPYDPGNLFDALIQLTPTV 939
QY 571 RISTRVOPICLAASRLDLSFQESH-----TVAGNVLADVRSPEGKNDTLRSGVSV 624
DB 940 TLTRVQPICLPT--DITT---REHLKEGTLAVVTGWC---INENNTYSETIQOAVLPV 990
QY 625 VDSLCEQHEHDHGIPIVSVDNMFCAWEPTAPSDICTAETGGLAAVSFPGRASPEPRRH 684
DB 991 VAASTCEEGYKEADPLFTVTENMFCAGYK--KGRYDACSGLSDG--PLVFADSRTERRV 1047
QY 685 LMGLVSWGYDKTCSH--RLSTAFTKYLPRKWIIR 717
DB 1048 LEGIVSWGSPSGCGKANOYGGTAKVNVFLSWIRQ 1081

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RESULT 11
US-09-626-795-2
Sequence 2, Application US/09626795
Patent No. 6719973

GENERAL INFORMATION:
APPLICANT: DING, Jeak Ling
APPLICANT: HO, Bow
TITLE OF INVENTION: Use of Recombinant Factor C to Induce Bacteriostasis
FILE REFERENCE: 4810-61737
CURRENT APPLICATION NUMBER: US/09/626,795
CURRENT FILING DATE: 2000-07-26
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 1083
TYPE: PR1
ORGANISM: Carcinoscopus rotundicauda
US-09-626-795-2

16.9%; Score 665; DB 4; Length 1083;

Query Match
Best Local Similarity 25.4%; Pred. No. 1.8e-46;
Matches 222; Conservative 118; Mismatches 304; Indels 230; Gaps 37;

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QY 34 PGAEWNIMCECECYDIECVCPKRE-----VGYTTPCCRNENECDCLIH 82
DB 248 PNGQMSNFPKRCIR-----ECAMVSSPEHGKVNALSGDMIEGATL-----RFSCDS----- 293
QY 83 PGCTIFENCKSCR--NGSWGTL----- 103
DB 294 PYYLIGETLTCQNGQNGQIPQCKNLVPCPDLDPVNAHAKVKGVEQKYGQFPQGTB 353
QY 104 -----DDFYKGFYCAECR--AGWYGG--DCMR-----CGQVLR-- 133
DB 354 VTYTSGNRYLMPDITLKNPDSGWSGSPSCYKVAVDREVDCKAVDFLDVGEPRRIH 413
QY 134 APKQIILLES-----YPLNAHCWTIHA--KGFVI----- 162
DB 414 CPACGSLTAGTGWGTATAYHELSSVCRAIHAIGKLPNSGGAHVHVNNGPYDFLGSDLNGI 473
QY 163 ---QLRVMTLSLEFDY-----CQYDVEYRD-----GDNRDGQIHKRYCGN--E 202
DB 474 KSEBLKSLASFPRDYVSSSTAGKSGCPDGMFEVDENCYVYTSKORAMERAOQVCTMAA 533
QY 203 RPAIIGS--IGSSLHVLHFDG--SKNPDGFH-----AIYEITACSS 241
DB 534 RLAVLDKDVLPNSLTETLRGKGLTTWIGLHRLDAEKPFIMELMDRNVNLDWLTWAS 593
QY 242 SPCHDGTCLV---DKAGS--YKACIAGYTGRCENLEERN--CSPDGPVNGYQKI 293
DB 594 GEPENETNCVYMDIQDQSGVMTKSCFQPSFACMDLSDRNKAKCDDPSLENGHATL 653
QY 294 TGGEGILINGHAKIGTVSPFCNNSYVLSGNEKRTCOQNGEMSGKOPICIK--ACREPKI 351
DB 654 HGGS--IDGFYA--GSSIRYSCEVLHVLSTETVCTTNGTWSAPKRCIKVITCQNPV 709
QY 352 SDVRRRRLVPMQVQSRERPLHOLYSAFSSKOKLQ---SAPTKKRALPFGD----- 398
DB 710 PSYGSVEIKP--PSKRTNSISRVSFPRLRPLPLARAKAPPRKRSOSPSTVDLASK 766
QY 399 --LPMGYOHLHTOLQYECISPFYRLGSSRRCTCLRTGKMSGRAPSCIPICGKIENITAP- 455
DB 767 VKLPEGHYRVGSRAIYTCESRYVELLSQGRCDNSNGMWSGRPASCIPIVGRSDSPSPF 826
QY 456 -----KTQGLRWPMQAAIYRRTSGVHDSGLHKAMFLVCSGALVNERTVVAACVTDLG 510
DB 827 IWNGNSTELIQMPQAGISRWLA-----DHNMMFLOCGGSLINEKMIYVAACVTVSA 879
QY 511 KVTMIKTADLKVVVIGKPYRDDDEKTIQSLQISAILIHPNYPDILLADAIILKLDKA 570
DB 880 TAEIIDPNQFMVIGKTYRDSRDDVQVREALEIHVNEPYDPGNLFDALIQLTPTV 939
QY 571 RISTRVOPICLAASRLDLSFQESH-----TVAGNVLADVRSPEGKNDTLRSGVSV 624
DB 940 TLTRVQPICLPT--DITT---REHLKEGTLAVVTGWC---INENNTYSETIQOAVLPV 990
QY 625 VDSLCEQHEHDHGIPIVSVDNMFCAWEPTAPSDICTAETGGLAAVSFPGRASPEPRRH 684

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Db 991 VAASTCEBEGYKADLPVLTETNNPCAGYK-KGRYDACSDDSGG--PLVADDSRTERRNV 1047
 Qy 685 LMGVMSYDXTCSH-RLSTAFKVLPPKDWIER 717
 Db 1048 LEGIVSMGSPGCGKANQYGGFTKNVFLSWIRQ 1081

RESULT 12
 US-09-949-016-6138
 ; Sequence 6138, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 6138
 ; LENGTH: 699
 ; TYPE: PRT
 ; ORGANISM: Human
 ; US-09-949-016-6138

Query Match 12.2%; Score 482; DB 4; Length 699;
 Best Local Similarity 24.9%; Pred. No. 1,7e-31;
 Matches 178; Conservative 93; Mismatches 215; Indels 228; Gaps 39;

Qy 69 CENEBCDCLHPGCTIFENCKSCRNCSWGTLDDFYVKGFCYACBAGWY---GGD 124
 Db 143 CEREBEELSCDH-----CHN-----YIGGYCS-CRFGYLTHTDNT 180
 Qy 125 C-MRCGQVLRAKQQLL-----ESYPLNACEMTHAKRGVYQLRFVMLSLEPDY- 176
 Db 181 CVCESDNLFTORTGVTSPDPNPYPKSECLYTIIEEGFMVNLQFEDI---FDIQH 237
 Qy 177 ----COYDVEVRDGNRQGIIRKVCGERAPAPISIGSSLHVLFHSDGSKNPFDFHAI 232
 Db 238 PEVPCPYDIKIKVGP---KVLGPPCGEKABEPISIOHSHVILFHSNDSGBNRGRL- 292
 Qy 233 YEETACSSSPCFHDTGCVLDKAGSYKACLAGYTGORCENLLEBRNCSDPGGPVNGYOK 292
 Db 293 -----STRAA-----GNECPRL-----QP--PVH----- 309
 Qy 293 ITGGPGLINGRAKIGTVSFF-----CNSY-VLSGNERK-----TCOONGESGKQ 339
 Db 310 -----GKIEPSQAKY-----FFKDQVLVSCDTGYKVLKONVEMDTFOIECLKDGTWSNKT 359
 Qy 340 PIC-ICACBEPKISDLVRRRLVPMOVOSRETPHOLYSAFSAFKQKLSAPTKKRALPFQD 398
 Db 360 PTCKIVDCRAP-----SYRAA-----GNECPRL-----QP--PVH----- 372
 Qy 399 LPMGYOHLHT-----OLOYECISPFYRLGSSR--RTCLRTGKWS---GRA-PSC 442
 Db 373 LEHGLITFTSRNNLTYYKSEIKYSCEPYYKMLNNNTGYITCSAQGVMMNKVLGRSLPTC 432
 Qy 443 IPICG-----KIENITAPKTOGLRMPQOAIYRRTSGVHDSLHKGMFLVCSGA 492
 Db 433 LPTCGLPKFSRKLMAIFN-GRPAQGT-PTWIML-----SHLNGQPF--CGGS 478
 Qy 493 LVNERVVVAARV---TDLGKVT---MIKTADLVKLVGKPYRDDDEKTIQSLQIS 544
 Db 479 LIGSSWIVAAHCLHSLDPGDPDLTSLSPDSKIIIGKMR--LSDSEDEOHLGVK 536
 Qy 545 AIIHBNYDPIILDADIAIILKLDKARISRVQPCIAASRDISTFQE-SHITVAGMNV 603

Db 537 HTLLHPVDPTNFENDVALVELLESPLVNAFWPILCEBGP-----QGANVYISGWK 591
 Qy 604 LADVSPGKNDTLRSGVSVDSLLCEBQHDHGPVSVTNDMCASWEPTAPSDICTA 663
 Db 592 QFLQRPF---ETLWEIELEPIVDHSTQKAYAP--LKKKVTYDMICAG-EKGGKDACG 644
 Qy 664 ETGIIAAVSFPGRASPERRMHLGLVMSYDXTCSHRLSTAFKVLPPKDWIER 717
 Db 645 DSGGMVTLNRRG---QWLVGVTVSMGDDGKKDRVG-VYSYIHNNDWIQR 693

RESULT 13
 US-09-949-016-11182
 ; Sequence 11182, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 11182
 ; LENGTH: 717
 ; TYPE: PRT
 ; ORGANISM: Human
 ; US-09-949-016-11182

Query Match 12.0%; Score 475; DB 4; Length 717;
 Best Local Similarity 24.6%; Pred. No. 6.9e-31;
 Matches 176; Conservative 93; Mismatches 217; Indels 228; Gaps 38;

Qy 69 CENEBCDCLHPGCTIFENCKSCRNCSWGTLDDFYVKGFCYACBAGWY---GGD 124
 Db 161 CEREBEELSCDH-----CHN-----YIGGYCS-CRFGYLTHTDNT 198
 Qy 125 C-MRCGQVLRAKQQLL-----ESYPLNACEMTHAKRGVYQLRFVMLSLEPDY- 174
 Db 199 CVCESDNLFTORTGVTSPDPNPYPKSECLYTIIEEGFMVNLQFEDI---FDIEDH 255
 Qy 175 --YMOYDVEVRDGNRQGIIRKVCGERAPAPISIGSSLHVLFHSDGSKNPFDFHAI 232
 Db 256 PEVPCPYDIKIKVGP---KVLGPPCGEKABEPISIOHSHVILFHSNDSGBNRGRL- 310
 Qy 233 YEETACSSSPCFHDTGCVLDKAGSYKACLAGYTGORCENLLEBRNCSDPGGPVNGYOK 292
 Db 311 -----SYRAA-----GNECPRL-----QP--PVH----- 327
 Qy 293 ITGGPGLINGRAKIGTVSFF-----CNSY-VLSGNERK-----TCOONGESGKQ 339
 Db 328 -----GKIEPSQAKY-----FFKDQVLVSCDTGYKVLKONVEMDTFOIECLKDGTWSNKT 377
 Qy 340 PIC-ICACBEPKISDLVRRRLVPMOVOSRETPHOLYSAFSAFKQKLSAPTKKRALPFQD 398
 Db 378 PTCKIVDCRAP-----SYRAA-----GNECPRL-----QP--PVH----- 390
 Qy 399 LPMGYOHLHT-----OLOYECISPFYRLGSSR--RTCLRTGKWS---GRA-PSC 442
 Db 391 LEHGLITFTSRNNLTYYKSEIKYSCEPYYKMLNNNTGYITCSAQGVMMNKVLGRSLPTC 450
 Qy 443 IPICG-----KIENITAPKTOGLRMPQOAIYRRTSGVHDSLHKGMFLVCSGA 492
 Db 451 LPTCGLPKFSRKLMAIFN-GRPAQGT-PTWIML-----SHLNGQPF--CGGS 496

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QY 493 LUNERTVVAANCV-----TDLGKVTMIKTADLKVLGKFRYRDDDEKTIQSLQIS 544
DB 497 LSSSMWIVNAHCHLOSLDEPDLTDRSDSPSDFEIIIGKMR--LSDENEQHLGK 554
QY 545 AILHNVPDPIILDADIAIKLKDARISTRVOPICLAASRLDSTFSOE-SHTVAGMNV 603
DB 555 HTLLHQYDPTRENDVALVELLESFVLNAFVMPICLPEBPQ-----QEGAMIVSGMK 609
QY 604 LADVRSPGFKNDTLRSGVSVVDSLLCEEQEDHGIPIVSTDNMFCASWEPTAPSDICTA 663
DB 610 QFQRRP---ETLMEIEIPIVDHSTCQKAYAP--LKKKVTDRMICAG--EKEGKDACAG 662
QY 664 ETGCIAAVSPFGASPEPRNHLMGVSWSDKTSNRLSTAFKVLPRFDMIR 717
DB 663 DSGGPMVTLNRRG---QWYLVGVSWGDDCKKDRYG--VVSYIHNNDWIOR 711

RESULT 14
US-09-949-016-7775
; Sequence 7775, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7775
; LENGTH: 691
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-7775

Query Match 10.1%; Score 399.5; DB 4; Length 691;
Best Local Similarity 22.6%; Pred. No. 1.3e-24;
Matches 173; Conservative 79; Mismatches 243; Indels 269; Gaps 34;

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DB 76 LCEYDFPKLSSG---AKVLATLCQGESDTERAPGQDTFYSIGSSLDIFRSDYSEK 131
QY 226 FDFGHAII--EETTAGSSP---CFHDTCVLDKAGSYKACACLAGYTOR---CENL 274
DB 132 FTGFEAFYAEDIDECQVAGEAPTCDH--CHNHGFGFYCSCRAGYVLRHKKRTCSAL 188
QY 275 -----LLE----- 277
DB 189 CSGOVLTORSGELSSPEYPRPYKLSCTYSISLEBSVILDRVESFDEVTHTPELTCPY 248
QY 278 -----RNCSDP 283
DB 249 DFLKIQTDREHREHFGCKTLPHRIETKSNVTITFTVDESGDHTGMKIHVTSQAQPCPY 308
QY 284 GGPVNGYQKTTGGEGGLNGHAK--IGTVVSFFCNNSY-VLSG---NEKRTCOQNGEW 335
DB 309 MABPNGH-----VSPVQAKYILKDSFSIFCETGTEYELLOGLPLKSFVAVCOQKGSW 359
QY 336 SGQSPIC-ICAKREPKISDLVRRVRLPM-QVQSEFTPLHOLYGAAPSKOLQSAPTKPA 393
DB 360 DRPMFACISIVDCGPD-----YLPGRVVEYITGGVTTYKAV----- 396
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QY 448 KIENITAPKTOGLR-----WPMQAIYRRTSGVHDGSLHKAMFLVSGALVNERTVV 501
DB 441 LSARTTGRITYGQAKKRPDPFMOVLLIGIT-----AAGALLYDNWVLT 485
QY 502 AAHCYTDLQKVTMIKTADLKVLGKFRYRDDDEKTIQSLQ-----ISAIIHENV-D 553
DB 486 AAHAAYE---QKHASALDIRWG-----TLKRLSPHYQAWSEAVYIHEGYTH 530
QY 554 PILLDADIAIKLKDARISTRVOPICLAASRLDSTFSQESHITYAGMNVADVRSPGK 613
DB 531 DAGFNDIALIKLNNKVININSNITPICLPRKEASEFMRTDITGASGWG---LTORGFL 586
QY 614 NDTLRSGVSVVDSLLCEEQEDHGIPIVSTDNMFCASWEPTAPSDICTAETGCIAAVS 672
DB 587 ANNLMYVDIPYDHQKCTAAYEKPRYPRGSVYANMLCAGLE--SGGKDSRGDSGG--ALV 643
QY 673 FGRASPEPRNHLMGVSWSDKTSNRLSTAFKVLPRFDMIR 716
DB 644 F--LDSETERMFVGIVSGWSMNCBAGQGYVYTKVINYIPIWE 685
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RESULT 15
US-09-027-337-2
; Sequence 2, Application US/09027337B
; Patent No. 5972616
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Tanimoto, Hirotsoshi
; TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease Overexpressed in
; TITLE OF INVENTION: Breast and Ovarian Carcinomas
; FILE REFERENCE: D6064
; CURRENT APPLICATION NUMBER: US/09/027,337B
; CURRENT FILING DATE: 1998-02-20
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 2
; LENGTH: 855
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of TADG-15 encoded by nucleotides
; OTHER INFORMATION: 23 to 2589 of Sequence 1
; Patent No. 5972616
; US-09-027-337-2

Query Match 8.3%; Score 327; DB 2; Length 855;
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QY 235 EITAGSSSPCFHDTGTC-----VLDKAGSYKACIAGY----- 266
DB 445 -LSYSDSDPCPGQFTCRGCIKELRCGMADCTHSDELNCSCDAGHOFCKNFKCP 503
QY 267 -----TGRCENLLEERKSDPGRGVNGYQKTTGGEGGLNGHAKIGTVVSFFCNNSYV 320
DB 504 LFWVCDSVNDGDNDSDEQSCSP-----AQTRCSNGKC 537
QY 321 LSG---NEKRTCOQNGEWGKOPICIKAREPKISDLVRRVRLPMQVQSEFTPLHQLYS 376
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QY 474 GYHDGSLHKGAMFLVCSGALVNBRTVVVAAHCVTDLGKVTMIKTADLKVVLGKFRYRDDR 533
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GenCore version 5.1.6
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OM protein - protein search, using BW model

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(without alignments)
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Searched: 1726218 seqs, 38631768 residues

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and is derived by analysis of the total score distribution.

SUMMARIES

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744	3921.5	99.4	737	16	US-10-408-765A-1796
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746	3500.5	88.7	649	15	US-10-333-574-17
747	3089.5	78.3	567	14	US-10-004-551-2
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753	665	16.9	1019	14	US-10-183-992-8	Sequence 8, Appl
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864	308	7.8	419	14	US-10-182-263-4	Sequence 4, App1	1022	278	7.0	113	15	US-10-464-366-78	Sequence 78, App1
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866	299.5	7.6	467	15	US-10-406-031-2	Sequence 2, App1	1024	276.5	7.0	466	10	US-09-951-121A-1	Sequence 1, App1
867	298	7.6	397	15	US-10-104-047-3904	Sequence 3904, App	1025	276.5	7.0	466	10	US-09-848-107-1	Sequence 1, App1
868	296	7.5	229	15	US-10-051-874-101	Sequence 101, App	1026	276.5	7.0	466	14	US-10-295-682-1	Sequence 1, App1
869	296	7.5	230	10	US-09-981-151A-87	Sequence 87, App1	1027	276.5	7.0	655	14	US-10-172-712-28	Sequence 28, App1
870	296	7.5	230	10	US-09-981-151A-96	Sequence 96, App1	1028	276	7.0	249	9	US-09-961-721-5	Sequence 5, App1
871	296	7.5	230	14	US-10-032-189-66	Sequence 66, App1	1029	276	7.0	249	14	US-10-170-789-46	Sequence 46, App1
872	296	7.5	230	15	US-10-074-978A-221	Sequence 221, App	1030	276	7.0	251	9	US-09-961-721-4	Sequence 4, App1
873	296	7.5	230	15	US-10-074-978A-222	Sequence 222, App	1031	276	7.0	251	14	US-10-170-789-45	Sequence 45, App1
874	296	7.5	230	15	US-10-055-569A-96	Sequence 96, App1	1032	276	7.0	259	15	US-10-107-782-214	Sequence 214, App
875	296	7.5	230	15	US-10-042-865-155	Sequence 155, App	1033	276	7.0	259	15	US-10-038-854-100	Sequence 100, App
876	296	7.5	230	15	US-10-072-012-804	Sequence 804, App	1034	276	7.0	366	16	US-10-700-778-1	Sequence 1, App1
877	296	7.5	230	15	US-10-072-012-804	Sequence 812, App	1035	275.5	7.0	405	15	US-10-360-101-225	Sequence 225, App
878	296	7.5	230	15	US-10-037-417-135	Sequence 135, App	1036	275.5	7.0	406	10	US-09-782-587B-1	Sequence 1, App1
879	293	7.4	986	14	US-10-114-153-3	Sequence 50, App1	1037	275.5	7.0	406	14	US-09-782-587B-3	Sequence 3, App1
880	291.5	7.4	516	17	US-10-741-600-909	Sequence 909, App	1038	275.5	7.0	406	14	US-10-109-498-1	Sequence 1, App1
881	291	7.4	376	15	US-10-406-031-31	Sequence 31, App1	1039	275.5	7.0	406	14	US-10-255-032-1	Sequence 1, App1
882	289.5	7.3	658	10	US-09-776-191-10	Sequence 10, App1	1040	275.5	7.0	406	14	US-10-281-721-1	Sequence 1, App1
883	289.5	7.3	658	15	US-10-156-214A-10	Sequence 10, App1	1041	275.5	7.0	406	15	US-10-386-898-7	Sequence 7, App1
884	289.5	7.3	802	10	US-09-776-191-8	Sequence 8, App1	1042	275.5	7.0	406	15	US-10-383-898-1	Sequence 1, App1
885	289.5	7.3	802	15	US-10-156-214A-8	Sequence 8, App1	1043	275.5	7.0	406	15	US-10-617-500-1	Sequence 1, App1
886	288.5	7.3	802	9	US-09-888-615-113	Sequence 113, App	1044	275.5	7.0	406	15	US-10-263-205B-2	Sequence 2, App1
891	288.5	7.3	802	14	US-10-167-749-169	Sequence 169, App	1045	275.5	7.0	406	16	US-10-617-619-1	Sequence 1, App1
921	288.5	7.3	802	15	US-10-170-481A-169	Sequence 169, App	1046	275.5	7.0	406	16	US-10-701-294-1	Sequence 1, App1
957	288.5	7.3	802	15	US-10-210-028-169	Sequence 169, App	1047	275.5	7.0	406	16	US-10-669-537-1	Sequence 1, App1
959	288.5	7.3	802	15	US-10-162-521A-169	Sequence 169, App	1048	275.5	7.0	406	16	US-10-738-777-2	Sequence 2, App1
964	288.5	7.3	802	17	US-10-918-851-169	Sequence 169, App	1049	275.5	7.0	406	17	US-10-900-490-1	Sequence 1, App1
976	288.5	7.3	802	17	US-10-805-667-169	Sequence 169, App	1050	275.5	7.0	406	17	US-10-725-843-3	Sequence 3, App1
977	288.5	7.3	802	17	US-10-893-359-169	Sequence 169, App	1051	275.5	7.0	406	17	US-10-609-701A-1	Sequence 1, App1
978	288.5	7.3	802	17	US-10-893-359-169	Sequence 169, App	1052	275.5	7.0	444	15	US-10-411-037-8	Sequence 8, App1
979	288.5	7.3	802	17	US-10-893-359-169	Sequence 169, App	1053	275.5	7.0	444	15	US-10-382-248-34	Sequence 34, App1
980	288.5	7.3	802	17	US-10-897-360-169	Sequence 169, App							

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1055	275.5	7.0	444	15	US-10-410-962-8	Sequence 8, Appl1	1128	263	6.7	431	15	US-10-411-049-34	Sequence 34, Appl1
1056	275.5	7.0	444	15	US-10-411-049-8	Sequence 8, Appl1	1129	263	6.7	431	15	US-10-410-930-34	Sequence 34, Appl1
1057	275.5	7.0	444	15	US-10-263-205B-3	Sequence 3, Appl1	1130	263	6.7	431	16	US-10-410-997-34	Sequence 34, Appl1
1058	275.5	7.0	444	15	US-10-410-930-8	Sequence 8, Appl1	1131	263	6.7	431	16	US-10-411-012-34	Sequence 34, Appl1
1059	275.5	7.0	444	16	US-10-10-997-8	Sequence 8, Appl1	1132	263	6.7	431	16	US-10-287-994-34	Sequence 34, Appl1
1060	275.5	7.0	444	16	US-10-411-012-8	Sequence 8, Appl1	1133	263	6.7	431	16	US-10-410-913-34	Sequence 34, Appl1
1061	275.5	7.0	444	16	US-10-287-994-8	Sequence 8, Appl1	1134	263	6.7	431	17	US-10-741-600-1265	Sequence 1265, Ap
1062	275.5	7.0	444	16	US-10-410-913-8	Sequence 8, Appl1	1135	263	6.7	431	17	US-10-741-600-1266	Sequence 21, Appl1
1063	275.5	7.0	444	16	US-10-738-777-3	Sequence 3, Appl1	1136	263	6.7	431	17	US-10-901-417-21	Sequence 34, Appl1
1064	275.5	7.0	444	17	US-10-410-980-8	Sequence 8, Appl1	1137	263	6.7	431	17	US-10-410-980-34	Sequence 34, Appl1
1065	275.5	7.0	444	17	US-10-410-897-8	Sequence 8, Appl1	1138	263	6.7	431	17	US-10-645-785-38	Sequence 38, Appl1
1066	275.5	7.0	444	17	US-10-492-261-8	Sequence 8, Appl1	1139	263	6.7	431	17	US-10-410-897-34	Sequence 34, Appl1
1067	275.5	7.0	459	16	US-10-741-601-503	Sequence 503, App	1140	263	6.7	431	17	US-10-492-261-34	Sequence 34, Appl1
1068	275.5	7.0	459	16	US-10-741-601-504	Sequence 504, App	1141	263	6.7	437	13	US-10-087-192-594	Sequence 594, App
1069	275.5	7.0	641	16	US-10-617-619-8	Sequence 8, Appl1	1142	262.5	6.7	415	16	US-10-466-998A-2	Sequence 2, Appl1
1070	275.5	7.0	611	16	US-10-841-250-6	Sequence 6, Appl1	1143	262.5	6.7	433	16	US-10-466-671-1	Sequence 1, Appl1
1071	275.5	7.0	679	16	US-10-617-619-11	Sequence 11, Appl1	1144	262.5	6.7	456	15	US-10-038-854-95	Sequence 95, Appl1
1072	275	7.0	1113	17	US-10-926-083-4	Sequence 4, Appl1	1145	262.5	6.7	456	15	US-10-038-854-96	Sequence 96, Appl1
1073	273	6.9	560	9	US-09-912-559-3	Sequence 3, Appl1	1146	262.5	6.7	461	9	US-09-884-901-3	Sequence 3, Appl1
1074	273	6.9	560	14	US-10-172-712-132	Sequence 32, Appl1	1147	262.5	6.7	461	14	US-10-132-829-5	Sequence 5, Appl1
1075	273	6.9	560	15	US-10-391-215-5	Sequence 5, Appl1	1148	262.5	6.7	461	14	US-10-234-406-6	Sequence 6, Appl1
1076	273	6.9	560	15	US-10-391-215-6	Sequence 6, Appl1	1149	262.5	6.7	461	14	US-10-234-406-8	Sequence 8, Appl1
1077	273	6.9	560	15	US-10-391-215-7	Sequence 7, Appl1	1150	262.5	6.7	461	14	US-10-133-907-5	Sequence 5, Appl1
1078	273	6.9	560	15	US-10-391-215-8	Sequence 8, Appl1	1151	262.5	6.7	461	15	US-10-038-854-92	Sequence 92, Appl1
1079	273	6.9	560	15	US-10-391-215-9	Sequence 9, Appl1	1152	262.5	6.7	461	15	US-10-038-854-93	Sequence 93, Appl1
1080	273	6.9	560	16	US-10-719-993-854	Sequence 854, App	1153	262.5	6.7	461	15	US-10-038-854-94	Sequence 94, Appl1
1081	273	6.9	560	17	US-10-930-754-3	Sequence 3, Appl1	1154	262.5	6.7	461	15	US-10-239-498A-5	Sequence 5, Appl1
1082	273	6.9	560	17	US-10-930-754-4	Sequence 4, Appl1	1155	262.5	6.7	461	17	US-10-741-600-832	Sequence 832, App
1083	272.5	6.9	266	14	US-10-148-671-17	Sequence 17, Appl1	1156	262.5	6.7	696	17	US-10-841-250-8	Sequence 8, Appl1
1084	272	6.9	488	15	US-10-712-332-1	Sequence 1, Appl1	1157	262.5	6.7	1042	15	US-09-776-191-62	Sequence 62, Appl1
1085	271.5	6.9	244	14	US-10-097-340-169	Sequence 169, App	1158	262.5	6.7	1042	15	US-10-156-218A-99	Sequence 29, Appl1
1086	271.5	6.9	244	14	US-10-282-907-2	Sequence 2, Appl1	1159	262.5	6.7	1042	17	US-10-865-978-2	Sequence 2, Appl1
1087	271.5	6.9	244	14	US-10-301-822-97	Sequence 97, Appl1	1160	262.5	6.7	1042	17	US-10-926-008-2	Sequence 2, Appl1
1088	271.5	6.9	244	15	US-10-293-027-530	Sequence 530, App	1161	262.5	6.7	1042	17	US-10-865-978-9	Sequence 9, Appl1
1089	271.5	6.9	244	15	US-10-173-999-131	Sequence 131, App	1162	262.5	6.7	1076	15	US-10-276-774-2345	Sequence 2345, Ap
1090	271.5	6.9	244	15	US-10-344-394-25	Sequence 25, Appl1	1163	262	6.6	280	14	US-10-148-671-26	Sequence 26, Appl1
1091	271.5	6.9	244	16	US-10-757-262-28	Sequence 28, Appl1	1164	261.5	6.6	415	9	US-09-118-748-2	Sequence 2, Appl1
1092	271.5	6.9	244	17	US-10-868-490A-9	Sequence 9, Appl1	1165	261.5	6.6	443	17	US-10-741-600-830	Sequence 830, App
1093	271.5	6.9	244	17	US-10-868-490A-11	Sequence 11, Appl1	1166	261	6.6	431	14	US-10-193-656-4	Sequence 4, Appl1
1094	271.5	6.9	244	17	US-10-868-490A-13	Sequence 13, Appl1	1167	260.5	6.6	431	16	US-10-723-860-870	Sequence 870, App
1095	271.5	6.9	244	17	US-10-868-490A-15	Sequence 15, Appl1	1168	260.5	6.6	437	15	US-10-712-332-2	Sequence 814, App
1096	271.5	6.9	1006	15	US-10-210-037-62	Sequence 62, Appl1	1169	260.5	6.6	1032	16	US-10-719-993-814	Sequence 562, App
1097	271.5	6.9	1006	15	US-10-401-077-1	Sequence 1, Appl1	1170	260	6.6	431	15	US-10-282-174-562	Sequence 562, App
1098	269	6.8	462	16	US-10-416-952-2	Sequence 2, Appl1	1171	260	6.6	931	17	US-10-600-009-562	Sequence 562, App
1099	269	6.8	462	16	US-09-808-602-103	Sequence 103, App	1172	259.5	6.6	931	17	US-10-865-978-34	Sequence 34, Appl1
1100	269	6.8	643	9	US-09-800-198-86	Sequence 86, Appl1	1173	259	6.6	227	13	US-10-045-367A-4	Sequence 4, Appl1
1101	269	6.8	643	15	US-10-099-322-113	Sequence 113, App	1174	259	6.6	227	14	US-10-170-789-54	Sequence 54, Appl1
1102	269	6.8	643	15	US-10-044-564-113	Sequence 113, App	1175	258.5	6.6	411	15	US-09-880-503-3	Sequence 3, Appl1
1103	267	6.8	462	15	US-10-411-037-10	Sequence 10, Appl1	1176	258.5	6.6	411	15	US-10-407-821-2	Sequence 2, Appl1
1104	267	6.8	462	15	US-10-411-026-10	Sequence 10, Appl1	1177	258.5	6.6	412	16	US-10-825-911-2	Sequence 17, Appl1
1105	267	6.8	462	15	US-10-410-962-10	Sequence 10, Appl1	1178	257.5	6.5	551	17	US-10-865-978-17	Sequence 17, Appl1
1106	267	6.8	462	15	US-10-411-049-10	Sequence 10, Appl1	1179	257	6.5	215	15	US-10-051-874-108	Sequence 102, App
1107	267	6.8	462	16	US-10-410-930-10	Sequence 10, Appl1	1180	257	6.5	217	15	US-09-981-157A-97	Sequence 88, Appl1
1108	267	6.8	462	16	US-10-410-997-10	Sequence 10, Appl1	1181	257	6.5	217	14	US-09-981-157A-97	Sequence 97, Appl1
1109	267	6.8	462	16	US-10-411-012-10	Sequence 10, Appl1	1182	257	6.5	217	14	US-10-032-189-67	Sequence 67, Appl1
1110	267	6.8	462	16	US-10-287-994-10	Sequence 10, Appl1	1183	257	6.5	217	15	US-10-074-978A-233	Sequence 223, App
1111	267	6.8	462	16	US-10-410-913-10	Sequence 10, Appl1	1184	257	6.5	217	15	US-10-055-568A-97	Sequence 97, Appl1
1112	267	6.8	462	17	US-10-410-980-10	Sequence 10, Appl1	1185	257	6.5	217	15	US-10-042-865-156	Sequence 156, App
1113	267	6.8	462	17	US-10-410-897-10	Sequence 10, Appl1	1186	257	6.5	217	15	US-10-072-012-805	Sequence 805, App
1114	267	6.8	462	17	US-10-492-261-10	Sequence 10, Appl1	1187	257	6.5	217	15	US-10-072-012-813	Sequence 813, App
1115	265	6.7	419	15	US-10-382-248-36	Sequence 36, Appl1	1188	257	6.5	217	15	US-10-037-417-136	Sequence 136, App
1116	264.5	6.7	900	17	US-10-865-978-15	Sequence 15, Appl1	1189	257	6.5	529	16	US-10-398-037-2	Sequence 2, Appl1
1117	264	6.7	431	14	US-10-247-671-149	Sequence 149, App	1190	257	6.5	1039	17	US-10-865-978-30	Sequence 30, Appl1
1118	263.5	6.7	431	16	US-10-744-927-1	Sequence 1, Appl1	1191	256	6.5	207	15	US-10-004-378A-147	Sequence 147, App
1119	263	6.7	431	16	US-10-076-421-2	Sequence 2, Appl1	1192	255.5	6.5	244	9	US-09-796-294-11	Sequence 11, Appl1
1120	263	6.7	431	14	US-10-171-311-184	Sequence 184, App	1193	255.5	6.5	244	14	US-10-461-787-11	Sequence 829, App
1121	263	6.7	431	14	US-10-301-822-161	Sequence 161, App	1194	255.5	6.5	441	17	US-10-741-600-839	Sequence 829, App
1122	263	6.7	431	14	US-10-131-985-21	Sequence 21, App	1195	254.5	6.5	437	15	US-10-712-337-3	Sequence 1, Appl1
1123	263	6.7	431	15	US-10-295-027-414	Sequence 414, App	1196	254	6.4	431	9	US-09-264-468B-1	Sequence 95, Appl1
1124	263	6.7	431	15	US-10-395-027-414	Sequence 1275, Ap	1197	253.5	6.4	464	9	US-09-808-602-95	Sequence 93, Appl1
1125	263	6.7	431	15	US-10-411-037-34	Sequence 34, Appl1	1198	253.5	6.4	487	9	US-09-808-602-93	Sequence 80, Appl1
1126	263	6.7	431	15	US-10-411-026-34	Sequence 34, Appl1	1199	253.5	6.4	487	10	US-09-800-198-80	Sequence 80, Appl1

1200	253.5	6.4	1043	15	US-10-016-248-48	Sequence 48, Appl	1273	244.5	6.2	259	9	US-09-981-123-2	Sequence 2, Appl1
1201	253.5	6.4	1048	15	US-10-016-248-49	Sequence 49, Appl	1274	244.5	6.2	260	14	US-10-148-671-23	Sequence 23, Appl
1202	253	6.4	273	14	US-10-148-671-25	Sequence 25, Appl	1275	244.5	6.2	262	14	US-10-029-388-31995	Sequence 31995, A
1203	252.5	6.4	452	9	US-09-808-602-21	Sequence 21, Appl	1276	244	6.2	322	15	US-10-051-874-96	Sequence 96, Appl
1204	252	6.4	719	17	US-10-865-978-16	Sequence 16, Appl	1277	244	6.2	477	17	US-10-494-004-2	Sequence 2, Appl1
1205	252	6.4	889	17	US-10-865-978-22	Sequence 22, Appl	1278	244	6.2	638	15	US-10-099-322-114	Sequence 114, App
1206	251.5	6.4	487	9	US-09-808-602-17	Sequence 17, Appl	1279	244	6.2	638	15	US-10-044-564-114	Sequence 114, App
1207	251.5	6.4	487	9	US-09-808-602-19	Sequence 19, Appl	1280	244	6.2	638	15	US-10-287-222-672	Sequence 672, App
1208	251.5	6.4	487	10	US-09-800-198-17	Sequence 17, Appl	1281	243	6.2	273	15	US-10-028-248A-63	Sequence 63, Appl
1209	251.5	6.4	487	10	US-09-800-198-19	Sequence 19, Appl	1282	243	6.2	273	15	US-10-107-782-63	Sequence 63, Appl
1210	251	6.4	433	16	US-10-372-966-5	Sequence 5, Appl1	1283	243	6.2	282	15	US-10-051-874-97	Sequence 97, Appl
1211	249.5	6.3	403	9	US-09-880-503-6	Sequence 6, Appl1	1284	242.5	6.1	232	15	US-10-156-214A-276	Sequence 276, App
1212	249.5	6.3	822	9	US-09-147-947-6	Sequence 6, Appl1	1285	242.5	6.1	336	17	US-10-865-978-37	Sequence 37, Appl
1213	249.5	6.3	875	16	US-10-757-862-34	Sequence 34, Appl	1286	242.5	6.1	1019	15	US-10-016-248-99	Sequence 99, Appl
1214	249.5	6.3	875	16	US-10-723-860-4046	Sequence 4046, Ap	1287	242.5	6.1	3571	16	US-10-603-283-2	Sequence 2, Appl1
1215	249.5	6.3	875	17	US-10-843-299-2	Sequence 2, Appl1	1288	242	6.1	332	15	US-10-114-270-134	Sequence 134, App
1216	249.5	6.3	986	9	US-09-285-385C-19	Sequence 19, Appl	1289	242	6.1	730	9	US-09-850-048B-2	Sequence 2, Appl1
1217	249	6.3	235	10	US-09-776-191-6	Sequence 6, Appl1	1290	241.5	6.1	416	9	US-09-815-876-2	Sequence 2, Appl1
1218	249	6.3	235	15	US-10-156-214A-6	Sequence 6, Appl1	1291	241.5	6.1	416	17	US-10-239-032-8	Sequence 8, Appl1
1219	249	6.3	235	15	US-09-789-210-47	Sequence 47, Appl	1292	241.5	6.1	823	15	US-10-016-248-98	Sequence 98, Appl
1220	249	6.3	263	9	US-09-888-615-96	Sequence 96, Appl	1293	241	6.1	346	9	US-09-977-577-8	Sequence 8, Appl1
1221	248.5	6.3	250	10	US-09-898-837A-45	Sequence 45, Appl	1294	241	6.1	346	17	US-10-885-784-8	Sequence 8, Appl1
1222	248.5	6.3	250	11	US-09-789-210-51	Sequence 51, Appl	1295	240.5	6.1	966	9	US-09-850-048B-4	Sequence 4, Appl1
1223	248.5	6.3	251	10	US-09-898-837A-41	Sequence 41, Appl	1296	240.5	6.1	278	10	US-09-813-432-12	Sequence 12, Appl
1224	248	6.3	230	11	US-09-789-210-62	Sequence 62, Appl	1297	240.5	6.1	278	15	US-09-813-432-43	Sequence 43, Appl
1225	248	6.3	231	15	US-10-600-187-6	Sequence 6, Appl1	1298	240.5	6.1	278	15	US-10-174-364-12	Sequence 12, Appl
1226	248	6.3	263	16	US-10-733-969A-74	Sequence 74, Appl	1299	240.5	6.1	278	15	US-10-174-364-43	Sequence 43, Appl
1227	248	6.3	638	9	US-09-808-602-102	Sequence 102, App	1300	240.5	6.1	278	15	US-10-246-583-12	Sequence 12, Appl
1228	248	6.3	638	10	US-09-800-198-85	Sequence 85, Appl	1301	240.5	6.1	278	15	US-10-246-583-43	Sequence 43, Appl
1229	248	6.3	638	15	US-10-099-322-111	Sequence 111, App	1302	240.5	6.1	278	16	US-10-689-832-12	Sequence 12, Appl
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1231	248	6.3	638	15	US-10-403-161-50	Sequence 50, Appl	1304	240.5	6.1	430	16	US-10-372-966-4	Sequence 4, Appl1
1232	248	6.3	638	15	US-10-287-226-400	Sequence 400, App	1305	240.5	6.1	970	15	US-10-016-248-42	Sequence 42, Appl
1233	248	6.3	638	15	US-10-287-226-658	Sequence 658, App	1306	240.5	6.1	3571	9	US-09-911-842-2	Sequence 2, Appl1
1234	248	6.3	638	16	US-10-741-601-303	Sequence 303, App	1307	240.5	6.1	3571	13	US-10-150-821-2	Sequence 2, Appl1
1235	248	6.3	638	17	US-10-741-600-854	Sequence 854, App	1308	240	6.1	242	17	US-10-926-083-34	Sequence 34, Appl
1236	247.5	6.3	635	16	US-10-741-601-304	Sequence 304, App	1309	240	6.1	1128	9	US-09-888-615-97	Sequence 97, Appl
1237	247.5	6.3	635	17	US-10-741-600-855	Sequence 855, App	1310	239.5	6.1	406	9	US-10-399-645-8	Sequence 8, Appl1
1238	247	6.3	455	17	US-10-865-978-18	Sequence 18, Appl	1311	239.5	6.1	406	16	US-10-764-649-6	Sequence 6, Appl1
1239	247	6.3	619	15	US-10-403-161-52	Sequence 52, Appl	1312	239.5	6.1	406	16	US-10-723-860-811	Sequence 811, App
1240	247	6.3	619	15	US-10-287-226-404	Sequence 404, App	1313	239.5	6.1	406	16	US-10-723-860-811	Sequence 2, Appl1
1241	247	6.3	623	15	US-10-403-161-48	Sequence 48, Appl	1314	239.5	6.1	406	16	US-10-885-784-2	Sequence 13, Appl
1242	247	6.3	638	15	US-10-099-322-30	Sequence 30, Appl	1315	239.5	6.1	416	9	US-09-804-156-13	Sequence 13, Appl
1243	247	6.3	638	15	US-10-044-564-30	Sequence 30, Appl	1316	239.5	6.1	416	13	US-10-067-761-13	Sequence 13, Appl
1244	247	6.3	638	15	US-10-403-161-46	Sequence 46, Appl	1317	239.5	6.1	416	14	US-10-519-519-13	Sequence 13, Appl
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1247	247	6.3	764	15	US-10-236-031B-44	Sequence 44, Appl	1320	239.5	6.1	1015	16	US-10-101-993-644	Sequence 644, App
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1249	247	6.3	986	10	US-09-918-715-242	Sequence 242, App	1322	239.5	6.1	3557	15	US-10-295-027-1297	Sequence 1297, Ap
1250	247	6.3	986	15	US-10-366-345-33	Sequence 33, Appl	1323	239.5	6.1	3567	15	US-10-028-248A-47	Sequence 47, Appl
1251	247	6.3	986	16	US-10-474-794-342	Sequence 242, App	1324	239.5	6.1	3567	15	US-10-028-248A-47	Sequence 47, Appl1
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1253	247	6.3	986	18	US-10-979-159-242	Sequence 242, App	1326	239.5	6.1	3594	13	US-10-150-821-4	Sequence 4, Appl1
1254	246.5	6.2	259	11	US-09-789-210-52	Sequence 52, Appl	1327	239	6.1	328	9	US-09-888-615-91	Sequence 91, Appl
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1257	246.5	6.2	295	16	US-10-761-886-2	Sequence 2, Appl1	1330	238	6.0	237	18	US-10-846-341-3	Sequence 3, Appl1
1258	246.5	6.2	347	9	US-09-977-577-3	Sequence 3, Appl1	1331	238	6.0	263	10	US-10-094-886-128	Sequence 128, App
1259	246.5	6.2	347	14	US-10-885-784-3	Sequence 8, Appl1	1332	238	6.0	335	10	US-09-987-457-13	Sequence 13, Appl
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1351	236.5	6.0	339	10	US-09-987-457-12	Sequence 12, Appl	1424	229.5	5.8	624	15	US-10-004-378A-145	Sequence 145, App
1352	236.5	6.0	339	10	US-09-987-455-13	Sequence 13, Appl	1425	229.5	5.8	624	15	US-10-817-248-145	Sequence 3, Appl1
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1354	236.5	6.0	354	10	US-09-987-455-15	Sequence 15, Appl	1427	229	5.8	845	15	US-10-072-012-415	Sequence 415, App
1355	236.5	6.0	354	10	US-09-987-457-16	Sequence 16, Appl	1428	228.5	5.8	235	9	US-09-988-975A-6	Sequence 6, Appl1
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1372	234.5	5.9	556	9	US-09-729-674-92	Sequence 92, Appl	1445	227.5	5.8	305	14	US-10-885-441-57	Sequence 57, Appl
1373	234.5	5.9	556	17	US-10-913-553-92	Sequence 92, Appl	1446	227.5	5.8	305	14	US-10-239-663-56	Sequence 56, Appl
1374	234.5	5.9	620	15	US-10-004-378A-143	Sequence 143, App	1447	227.5	5.8	305	14	US-10-424-836-57	Sequence 57, Appl
1375	234	5.9	620	15	US-10-072-012-98	Sequence 90, Appl	1448	227.5	5.8	334	9	US-09-885-441-56	Sequence 56, Appl
1376	234	5.9	296	11	US-10-051-874-99	Sequence 99, Appl	1449	227.5	5.8	334	15	US-10-424-836-56	Sequence 50, Appl
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DE	Human PRO polypeptide #85.					
PN	US2003027272-A1.					
PD	06-FEB-2003.					
Query Match	100.0%;	Score 720;	DB 6;	Length 720;		
Best Local Similarity	100.0%;	Pred. No. 0;				
RESULT 7						
ID	ABU88032	standard;	protein;	720	AA.	
DE	Novel human secreted and transmembrane protein PRO1344.					
PN	US2003032127-A1.					
PD	13-FEB-2003.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 720;	DB 6;	Length 720;		
Best Local Similarity	100.0%;	Pred. No. 0;				
RESULT 8						
ID	ABU84347	standard;	protein;	720	AA.	
DE	Human secreted/transmembrane protein (PRO) #85.					
PN	US2003032112-A1.					
PD	13-FEB-2003.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 720;	DB 6;	Length 720;		
Best Local Similarity	100.0%;	Pred. No. 0;				
RESULT 9						
ID	ABR66221	standard;	protein;	720	AA.	
DE	Human secreted polypeptide PRO1344, SEQ ID NO:170.					
PN	US2003027278-A1.					
PD	06-FEB-2003.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 720;	DB 6;	Length 720;		
Best Local Similarity	100.0%;	Pred. No. 0;				
RESULT 10						
ID	ABR65611	standard;	protein;	720	AA.	
DE	Human secreted polypeptide PRO1344, SEQ ID NO:170.					
PN	US2003036159-A1.					
PD	20-FEB-2003.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 720;	DB 6;	Length 720;		
Best Local Similarity	100.0%;	Pred. No. 0;				
RESULT 11						
ID	ABU99551	standard;	protein;	720	AA.	
DE	Human secreted/transmembrane protein (PRO) #85.					
PN	US2003040070-A1.					
PD	27-FEB-2003.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 720;	DB 6;	Length 720;		
Best Local Similarity	100.0%;	Pred. No. 0;				
RESULT 12						
ID	ABU58033	standard;	protein;	720	AA.	
DE	Human PRO polypeptide #65.					
PN	US2003027165-A1.					
PD	06-FEB-2003.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 720;	DB 6;	Length 720;		
Best Local Similarity	100.0%;	Pred. No. 0;				
RESULT 13						
ID	ABU59111	standard;	protein;	720	AA.	
DE	Novel human secreted or transmembrane protein PRO1344.					
PN	US2002132252-A1.					
PD	19-SEP-2002.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 720;	DB 6;	Length 720;		
Best Local Similarity	100.0%;	Pred. No. 0;				
RESULT 14						
ID	ABU82623	standard;	protein;	720	AA.	
DE	Human secreted/transmembrane protein PRO1344.					
PN	US2003032023-A1.					
PD	13-FEB-2003.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 720;	DB 6;	Length 720;		
Best Local Similarity	100.0%;	Pred. No. 0;				
RESULT 15						
ID	ABU82790	standard;	protein;	720	AA.	
DE	Human PRO polypeptide #85.					
PN	US2003032113-A1.					
PD	13-FEB-2003.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 720;	DB 6;	Length 720;		
Best Local Similarity	100.0%;	Pred. No. 0;				
RESULT 16						
ID	ABU89911	standard;	protein;	720	AA.	
DE	Novel human secreted and transmembrane protein PRO1344.					
PN	US2003036147-A1.					
PD	20-FEB-2003.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 720;	DB 6;	Length 720;		
Best Local Similarity	100.0%;	Pred. No. 0;				

RESULT 17
ID ABR68160 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US200302764-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 18
ID ABU60542 standard; protein; 720 AA.
DE Human secreted/transmembrane protein; #94.
PN US2002160384-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 19
ID ABU96213 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003036144-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 20
ID ABU92644 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036149-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 21
ID ABO08721 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003044923-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 22
ID ABO02773 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003040062-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 23
ID ABR74927 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040056-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 24
ID ABR94689 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003044926-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 25
ID ABU13924 standard; protein; 720 AA.
DE Human PRO1344 polypeptide.
PN US2002103125-A1.
PD 01-AUG-2002.
PA (GETH) GENENTECH LTD.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 26
ID ABU85662 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003036140-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;

RESULT 27
ID AEU98622 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003013153-A1.
PD 16-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 28
ID AEU98037 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003017544-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 29
ID AEU91743 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003027277-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 30
ID AEU9436 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003036141-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 31
ID AEU67490 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 32
ID AEU67490 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 33
ID AEU80518 standard; protein; 720 AA.
DE Human PRO protein #85.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 34
ID AEU72509 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US200303531-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 35
ID AEU90894 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003018173-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 36
ID ABO33953 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003009013-A1.
PD 09-JAN-2003.

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PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 37
ID ABR99436 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040063-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 38
ID ABR98826 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 39
ID ABO16349 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003027267-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 40
ID ABR92249 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036160-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 41
ID ABO18890 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003044925-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 42
ID ABR78311 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054474-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 43
ID ABO19195 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003018183-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 44
ID ABO11213 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 45
ID ABO00186 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 46
ID ABO1518 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 47
ID ABO02163 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 48
ID ABO8737 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003036133-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 49
ID ABO83432 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036134-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 50
ID ABO06233 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003032294-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 51
ID ABR59269 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 52
ID ABO09331 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 53
ID ABO19195 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 54
ID ABO11213 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 55
ID ABR66831 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 56
ID ABO16044 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003040060-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
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RESULT 57
ID ABO13750 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 58
ID ABU71524 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344.
PN US2003013855-A1.
PD 16-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 59
ID ABU65653 standard; protein; 720 AA.
DE Human secreted/transmembrane protein, SEQ ID 170.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 60
ID ABO07501 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 61
ID ABO03688 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 62
ID ABR67136 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 63
ID ABO15739 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 64
ID ABUS6020 standard; protein; 720 AA.
DE Human secreted/transmembrane protein, PRO1344.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 65
ID ABU72305 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2002182638-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 66
ID ABU65348 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003032102-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;

RESULT 67
ID ABU95293 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 68
ID ABU71196 standard; protein; 720 AA.
DE Human PRO1344 protein.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 69
ID ABO07806 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 70
ID ABR70047 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 71
ID ABR69380 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 72
ID ABO01521 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 73
ID ABU81323 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 74
ID ABR60120 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003032137-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 75
ID ABU90978 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003018168-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 76
ID ABR67855 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027269-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;

RESULT 77
ID ABR65243 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027268-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 78
ID ABR6465 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027274-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 79
ID ABR7167 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 80
ID ABUS9258 standard; protein; 720 AA.
DE Human secreted/transmembrane protein, #94.
PN US2003027162-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 81
ID ABUS357 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 82
ID ABUS9047 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 83
ID ABUS3127 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003032105-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 84
ID ABUS94983 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 85
ID ABUS9531 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 86
ID ABUS4042 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 87
ID ABUS93693 standard; protein; 720 AA.

DE Novel human secreted and transmembrane protein PRO1344.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 88
ID ABO25955 standard; protein; 720 AA.
DE Human PRO1344 polypeptide.
PN US2002127576-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 89
ID ABR64938 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 90
ID ABO27299 standard; protein; 720 AA.
DE Human secreted/transmembrane polypeptide PRO1344.
PN US2003009012-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 91
ID ABR68770 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 92
ID ABO06586 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 93
ID ABR99131 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040068-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 94
ID ABUS7015 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003027280-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 95
ID ABUS85967 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003022300-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 96
ID ABUS2254 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003036136-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 97
ID ABUS7265 standard; protein; 720 AA.

DE Human PRO polypeptide #85.
PN US2003036138-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 98
ID ABR83737 standard; protein; 720 AA.
DE Human secreted/cranmembrane protein (PRO) #85.
PN US2003032109-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 99
ID ABO08111 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 100
ID ABO92494 standard; protein; 720 AA.
DE Human secreted/cranmembrane protein PRO1344.
PN US2003045684-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 101
ID ABR81822 standard; protein; 720 AA.
DE Novel human secreted and cranmembrane protein PRO1344.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 102
ID ABR65986 standard; protein; 720 AA.
DE Novel human secreted and cranmembrane protein PRO1344.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 103
ID ABR81164 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344.
PN US2003027212-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 104
ID ABR59815 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 105
ID ABR94003 standard; protein; 720 AA.
DE Novel human secreted and cranmembrane protein PRO1344.
PN US2003036155-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 106
ID ABR99856 standard; protein; 720 AA.
DE Novel human secreted and cranmembrane protein PRO1344.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 107
ID ABR66526 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.

PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 108
ID ABR90944 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 109
ID ABO53279 standard; protein; 720 AA.
DE Novel human secreted and cranmembrane protein PRO1344.
PN US2003027986-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 110
ID ABR58964 standard; protein; 720 AA.
DE Human secreted/cranmembrane protein, #94.
PN US2002142961-A1.
PD 03-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 111
ID ABR94371 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 112
ID ABR79253 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 113
ID ABR86582 standard; protein; 720 AA.
DE Human secreted/cranmembrane protein (PRO) #85.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 114
ID ABR86887 standard; protein; 720 AA.
DE Novel human secreted and cranmembrane protein PRO1344.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 115
ID ABR94676 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 116
ID ABO04603 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003032107-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 117
ID ABR70352 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.

PN US2003032139-A1.
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Query Match
RESULT 118
ID ABU92342 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003022187-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 119
ID ABU98517 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003022301-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 120
ID ABR65916 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036165-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 121
ID ABR64633 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027262-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 122
ID ABU59407 standard; protein; 720 AA.
DE Novel human secreted or transmembrane protein PRO1109.
PN US2003027985-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 123
ID ABU79558 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 124
ID ABU92949 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 125
ID ABU95908 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 126
ID ABU91128 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 127
ID ABU90221 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003036153-A1.
PD 20-FEB-2003.

Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 128
ID ABO09636 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 129
ID ABO10908 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 130
ID ABR70962 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040069-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 131
ID ABU98281 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2002183493-A1.
PD 05-DEC-2002.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 132
ID ABU87570 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003022293-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 133
ID ABU91438 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 134
ID ABU89286 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003036634-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 135
ID ABU84652 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 136
ID ABR69742 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 137
ID ABU80119 standard; protein; 720 AA.
DE Human PRO protein #85.
PN US2003036139-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;

Best Local Similarity 100.0%; Pred. No. 0;
RESULT 138
ID AB082493 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2002183494-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 139
ID AB092173 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003017476-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 140
ID AB093388 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003017541-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 141
ID AB009941 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003017543-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 142
ID AB009026 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036152-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 143
ID AB096457 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003027993-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 144
ID AB010879 standard; protein; 720 AA.
DE Human PRO polypeptide #65.
PN US2002123463-A1.
PD 05-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 145
ID AB010594 standard; protein; 720 AA.
DE Human secreted/transmembrane protein #85.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 146
ID AB081631 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2002177164-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 147
ID AB072127 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003023042-A1.

PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 148
ID AB095603 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003032115-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 149
ID AB096812 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003032140-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 150
ID AB070657 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 151
ID AB005008 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 152
ID AB008416 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003044922-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 153
ID AB085570 standard; protein; 720 AA.
DE Human secreted and transmembrane polypeptide PRO1344.
PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 154
ID AB034084 standard; protein; 720 AA.
DE Human PRO1344 polypeptide.
PN US2003017981-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 155
ID AB005623 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003032118-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 156
ID AB074012 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036135-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 157
ID AB095604 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.

PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 158
ID ABR80901 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 159
ID ABR81206 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 160
ID ABR00902 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 161
ID ABR8504 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 162
ID ABR77325 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 163
ID ABR02809 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068685-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 164
ID ABR031554 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 165
ID ABR07971 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 166
ID ABR040451 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068682-A1.

PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 167
ID ABR035876 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 168
ID ABR044015 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 169
ID ADA77922 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 170
ID ABR24810 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104539-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 171
ID ABR03078 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036131-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 172
ID ABR90334 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040075-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 173
ID ABR17248 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 174
ID ABR94994 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003044930-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 175
ID ABR95299 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 176

ID ADB17095 standard; protein; 720 AA.
PD Human transmembrane PRO polypeptide (Seqid 38).
PN US2003050462-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 177
ID ABO21537 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 178
ID ABR97801 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064452-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 179
ID ABR87589 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 180
ID ABR7630 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 181
ID ABR27860 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064440-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 182
ID ABR06141 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 183
ID ABR03647 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068722-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 184
ID ABR35098 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 185
ID ABR26335 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.

PN US2003104549-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 186
ID ABO48117 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049749-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 187
ID ABR92859 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064462-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 188
ID ABO24620 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003065159-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 189
ID ADA37742 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003008297-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 190
ID ABR11631 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064447-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 191
ID ABR02732 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073184-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 192
ID ABR16028 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064463-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 193
ID ABO27589 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 194
ID ABR29080 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068721-A1.

PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 195
ID ABO07056 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068699-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 196
ID ABO21150 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068707-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 197
ID ABO09496 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073175-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 198
ID ABO41366 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068695-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 199
ID ABO36181 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003068703-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 200
ID ABO43710 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003068732-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 201
ID ABO16959 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054470-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 202
ID ABO76106 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104548-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 203
ID ABO25725 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104542-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;

Best Local Similarity 100.0%; Pred. No. 0;
RESULT 204
ID ABO26030 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104543-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 205
ID ADA21428 standard; protein; 720 AA.
DE Human secreted/transmembrane polypeptide PRO1344.
PN US2003054404-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 206
ID ABO03383 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036127-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 207
ID ABO02468 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003040061-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 208
ID ABO44257 standard; protein; 720 AA.
DE Human secreted/transmembrane polypeptide PRO 1344.
PN US2003018172-A1.
PD 23-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 209
ID ABR90639 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036130-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 210
ID ABR73707 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054468-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 211
ID ABO16959 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 212
ID ABR94384 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049317-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 213
ID ABR75891 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003044929-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;

Best Local Similarity 100.0%; Pred. No. 0;
RESULT 214
ID ABR71267 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003059880-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 215
ID ABR93164 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064465-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 216
ID ABR93469 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054478-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 217
ID ADA10215 standard; protein; 720 AA.
DE Human secreted/transmembrane protein, PRO1344.
PN US2003059831-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 218
ID ABR87894 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068718-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 219
ID ABO27894 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003064454-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 220
ID ABO30029 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003064461-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 221
ID ABO33338 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 222
ID ABO04926 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 223
ID ABO23705 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 224
ID ABO36486 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 225
ID ABO35571 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003068758-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 226
ID ABO39536 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 227
ID ABO10411 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 228
ID ABO11936 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 229
ID ABO52082 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 230
ID ABO52387 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 231
ID ADA19900 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003069394-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 232
ID ABO23705 standard; protein; 720 AA.

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DE Human secreted/transmembrane protein (PRO) #85.
PN US2003032134-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 233
ID ADB17283 standard; protein; 720 AA.
DE Human transmembrane PRO polypeptide (SeqID 38).
PN US2003050465-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 234
ID ADAL17759 standard; protein; 720 AA.
DE Human PRO1344 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 235
ID ABR97191 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 236
ID ABR86979 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 237
ID ABM11021 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 238
ID ABM28165 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 239
ID ABO32164 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 240
ID ABM15291 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 241
ID ABM06446 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068709-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 242
ID ABM04257 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 243
ID ABM22370 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 244
ID ABM07666 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068751-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 245
ID ABO40756 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 246
ID ABM35403 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 247
ID ABM33166 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003087374-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 248
ID ABO52692 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 249
ID ABO50252 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 250
ID ABU99246 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003040055-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
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DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US200305986-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 271
ID ABR86369 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049758-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 272
ID ABR86674 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 273
ID ABR16638 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064448-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 274
ID ABR23690 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064456-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 275
ID ABO23114 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 276
ID ABR23895 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 277
ID ABR23285 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 278
ID ABR22065 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 279
ID ABO37706 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.

PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 280
ID ABR28470 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003082715-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 281
ID ABR28775 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003082716-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 282
ID ABR66419 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068737-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 283
ID ABR75801 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 284
ID ABR34081 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003096359-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 285
ID ABR34386 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003100061-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 286
ID ABO20317 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003032125-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 287
ID ABO21232 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003054454-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;
RESULT 288
ID ABO22147 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003054477-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Pred. No. 0;

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RESULT 289
ID ADA20072 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US200305522-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 290
ID ABO34185 standard; protein; 720 AA.
DE Human secreted/transmembrane polypeptide PRO 1344.
PN US2003060601-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 291
ID ABR96581 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 292
ID ADA94447 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003059832-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 293
ID ABR85759 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 294
ID ABR9741 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 295
ID ABR00597 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 296
ID ABR00292 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 297
ID ABO29724 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 298
ID ABR23590 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 299
ID ABR23985 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068679-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 300
ID ABO38316 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 301
ID ABO45616 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 302
ID ABR20540 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 303
ID ADA81441 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 304
ID ABO1654 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003027276-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 305
ID ABO18280 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003044920-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 306
ID ABO22707 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003027285-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 307
ID ABO23012 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
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RESULT 308
ID ABR92554 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064446-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 309
ID ABR81511 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 310
ID ABM77935 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 311
ID ABR89724 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073171-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 312
ID ABM26640 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003032121-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 313
ID ABM13766 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 314
ID ABO28504 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003064460-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 315
ID ABO30334 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 316
ID ABM07361 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 317
ID ABM03952 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 318
ID ABO37096 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 319
ID ABO41671 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 320
ID ABO35266 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 321
ID ABM25115 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104540-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 322
ID ABO47507 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 323
ID ABO47812 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 324
ID ABO48422 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 325
ID ABO51472 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003049786-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 326
ID ABO51777 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003049767-A1.
PD 13-MAR-2003.
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PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 327
ID ABO50557 standard; protein; 720 AA.
DE Human secreted/cranmembrane protein (PRO) #85.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 328
ID ABR79681 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040059-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 329
ID ABM16943 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040078-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 330
ID ABO17975 standard; protein; 720 AA.
DE Human secreted/cranmembrane protein (PRO) #85.
PN US2003044918-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 331
ID ABO20927 standard; protein; 720 AA.
DE Human secreted/cranmembrane protein (PRO) #85.
PN US2003032132-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 332
ID ABR96886 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054462-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 333
ID ADA38672 standard; protein; 720 AA.
DE Human secreted/cranmembrane protein PRO1344.
PN US2003059780-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 334
ID ABM12241 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064445-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 335
ID ABM16333 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064449-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 336
ID ABM24200 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068730-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 337
ID ABM14681 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068656-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 338
ID ABM04562 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 339
ID ABM06751 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068730-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 340
ID ABM09191 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073174-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 341
ID ABO39231 standard; protein; 720 AA.
DE Human secreted/cranmembrane protein (PRO) #85.
PN US2003068775-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 342
ID ABM75496 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104545-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 343
ID ABM25420 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104541-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 344
ID ABM19930 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104554-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 345
ID ABO46836 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003049762-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.

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Query Match          100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 346
ID ABO47141 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 347
ID ADA83239 standard; protein; 720 AA.
DE Human secreted/cranmembrane protein (PRO) #85.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 348
ID ABR71572 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003032133-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 349
ID ABR72182 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003032136-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 350
ID ABR9521 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036129-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 351
ID ABO06891 standard; protein; 720 AA.
DE Human secreted/cranmembrane protein (PRO) #85.
PN US2003040053-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 352
ID ABR84844 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040057-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 353
ID ABR73402 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054467-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 354
ID ABR76496 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003044932-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 355
ID ABR73097 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027270-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 356
ID ABR16163 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 357
ID ABO20622 standard; protein; 720 AA.
DE Human secreted/cranmembrane protein (PRO) #85.
PN US2003032126-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 358
ID ABO25365 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 359
ID ABO25670 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 360
ID ABR94079 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 361
ID ADA92793 standard; protein; 720 AA.
DE Human secreted/cranmembrane protein PRO1344.
PN US2003060407-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 362
ID ABR79986 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003060407-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 363
ID ABR11326 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064469-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 364
ID ABO32933 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 365
ID ABO30639 standard; protein; 720 AA.
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DE Human secreted/transmembrane protein (PRO) #85.
PN US2003064466-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 366
ID ABO30944 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003064468-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 367
ID ABW27250 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068760-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 368
ID ABW29995 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068769-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 369
ID ABW05531 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003045700-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 370
ID ABW15596 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068698-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 371
ID ABW08581 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068759-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 372
ID ABO42281 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049748-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 373
ID ABO38011 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068765-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 374
ID ABO45921 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003049754-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 375
ID ABM66724 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068688-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 376
ID ADB20282 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003082767-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 377
ID ABM19625 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104552-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 378
ID ABO49337 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049774-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 379
ID ABO49642 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049775-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 380
ID ADA78534 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003073181-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 381
ID ABR88199 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068720-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 382
ID ADA00369 standard; protein; 720 AA.
DE Human secreted/transmembrane polypeptide PRO 1344.
PN US2003027992-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
RESULT 383
ID ABW26945 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068739-A1.
PD 10-APR-2003.

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PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 384
ID ABO03342 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068763-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 385
ID ABO39841 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068689-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 386
ID ABO49947 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049776-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 387
ID ABO50862 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049780-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 388
ID ABO05318 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036126-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 389
ID ABR74622 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003044924-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 390
ID ABR77101 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003044927-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 391
ID ABM17858 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040072-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 392
ID ABR95909 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040073-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 393
ID ABO21842 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 394
ID ABO20012 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003032124-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 395
ID ABO24315 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003064467-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 396
ID ABR86064 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049759-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 397
ID ABM10716 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064455-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 398
ID ABM76715 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 399
ID ABR89419 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073170-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 400
ID ABM12546 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073176-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 401
ID ABM05836 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068717-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 402
ID ABO34961 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003068728-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
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Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 403
ID ABO03037 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068764-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 404
ID ABO19015 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104550-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 405
ID ABO19320 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104551-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 406
ID ABO46531 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003049761-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 407
ID ABO49032 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049757-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 408
ID ABO69075 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027273-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 409
ID ABR89114 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036119-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 410
ID ABR72487 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036120-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 411
ID ABR74317 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036161-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 412
ID ABO16585 standard; protein; 720 AA.

DE Human secreted/transmembrane protein (PRO) #85.
PN US2003044921-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 413
ID ABR80291 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049739-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 414
ID ABO01512 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003059882-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 415
ID ABO02122 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003059884-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 416
ID ABR87284 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068687-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 417
ID ABO12851 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073186-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 418
ID ABO30605 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064443-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 419
ID ABO24505 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064444-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 420
ID ABO29419 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068697-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 421
ID ABO31249 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068710-A1.

PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 422
ID ABR14376 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US200306868-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 423
ID ABR09801 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073178-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 424
ID ABR038926 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068774-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 425
ID ABR34691 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104538-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 426
ID ABR051167 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049781-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 427
ID ABR03993 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US200306158-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 428
ID ABR010463 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003036151-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 429
ID ABR053170 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003044806-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 430
ID ABR77706 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040067-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 431
ID ABR78916 standard; protein; 720 AA.

DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054456-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 432
ID ABR024010 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003054482-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 433
ID ABR93774 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054457-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 434
ID ABR01817 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003059883-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 435
ID ABR78240 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049764-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 436
ID ABR90029 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073177-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 437
ID ADA22354 standard; protein; 720 AA.
DE Human secreted/transmembrane polypeptide PRO1344.
PN US2003040473-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 438
ID ABR27555 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064442-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 439
ID ABR13156 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064450-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 440
ID ABR031859 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068731-A1.
PD 10-APR-2003.

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PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 441
ID ABR14071 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068683-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 442
ID ABR08276 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068754-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 443
ID ABO40146 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068681-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 444
ID ABR74581 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003096351-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 445
ID ABR33776 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003096358-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 446
ID ABR20235 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104556-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 447
ID ABO48727 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049756-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 448
ID ABO22540 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003017982-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 449
ID ABR72792 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036122-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 450
ID ABO15434 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036121-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 451
ID ABR85149 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040065-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 452
ID ABO15129 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003044919-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 453
ID ABO17264 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003040077-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 454
ID ABR17553 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003044928-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 455
ID ADA06520 standard; protein; 720 AA.
DE Human secreted/transmembrane PRO polypeptide #65.
PN US2003049638-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 456
ID ADA39213 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003059782-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 457
ID ABR85454 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049746-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 458
ID ABR77020 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054464-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 459
ID ABO28199 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003064459-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 460
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ID AEM22980 standard; protein; 720 AA. SEQ ID NO:170.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068757-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 461
ID AEM30300 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068723-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 462
ID AEM21760 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068741-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 463
ID AEM21455 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068744-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 464
ID AEM14986 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068766-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 465
ID ABO41061 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068694-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 466
ID ABO36791 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068715-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 467
ID ABO37401 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068726-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 468
ID AEM75191 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104544-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 469
ID AEM33471 standard; protein; 720 AA.

DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068357-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 470
ID ABO46226 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003049760-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 471
ID ADA82605 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049755-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 472
ID ADB85611 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003049735-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 473
ID ADB96239 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003054403-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 474
ID AEM31825 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068680-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 475
ID AEM31215 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068762-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 476
ID ADB85913 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003054472-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 477
ID AEM32130 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068708-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 478
ID AEM32435 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068713-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 479
ID ADB68290 standard; protein; 720 AA.
DE Human PRO1344 protein.
PN US2003065161-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 480
ID ADB68097 standard; protein; 720 AA.
DE Human PRO1344 protein.
PN US2003060600-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 481
ID AEM31520 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068761-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 482
ID AEM30910 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068771-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 483
ID ADB90914 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003083473-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 484
ID ADC57711 standard; protein; 720 AA.
DE Human PRO polypeptide #65.
PN US2003027754-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 485
ID ADC55075 standard; protein; 720 AA.
DE Human PRO polypeptide #65.
PN US2003045463-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 486
ID ADC11942 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003049681-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 487
ID ADC06994 standard; protein; 720 AA.
DE Human PRO1344 protein.
PN US2003060602-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 488

ID ADC56364 standard; protein; 720 AA.
DE Human PRO polypeptide #65.
PN US2003064375-A1.
PD 03-APR-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 489
ID ADC17173 standard; protein; 720 AA.
DE Mammalian PRO polypeptide (Seqid 38).
PN US2003065143-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 490
ID ADC07419 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003068647-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 491
ID ADC11409 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003069403-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 492
ID ADC14871 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003073208-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 493
ID ADC52366 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003138882-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 494
ID ADC14531 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003082546-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 495
ID ADB08063 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003068623-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 496
ID ADC8188 standard; protein; 720 AA.
DE Human PRO polypeptide #65.
PN US2003083461-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 497
ID ADB07530 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2002193299-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 498

RESULT 498
ID ADC82421 standard; protein; 720 AA.
DE Human PRO polypeptide #65.
PN US2003059833-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 499
ID ADD05643 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003087376-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 500
ID ADD06601 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003073090-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 501
ID ADD06650 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2002193300-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 502
ID ADC83097 standard; protein; 720 AA.
DE Human PRO polypeptide #65.
PN US2003059783-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 503
ID ADD55204 standard; protein; 720 AA.
DE Human PRO polypeptide #65.
PN US2003077593-A1.
PD 24-APR-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 504
ID ADD36042 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003105298-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 505
ID ADD56162 standard; protein; 720 AA.
DE Human PRO polypeptide #65.
PN US2003077594-A1.
PD 24-APR-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 506
ID ADD54600 standard; protein; 720 AA.
DE Human PRO polypeptide #65.
PN US2002133253-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 507
ID ADE26754 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003087304-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;

Best Local Similarity 100.0%; Pred. No. 0;
RESULT 508
ID ADE26221 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003087305-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 509
ID ADF67158 standard; protein; 720 AA.
DE Human PRO1344 amino acid sequence SEQ ID NO:231.
PN US2002198148-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 510
ID ADG01043 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003078387-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 511
ID ADG08596 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180793-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 512
ID ADG02638 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003207397-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 513
ID ADG01345 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003207399-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 514
ID ADF95520 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003207398-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 515
ID ADF95217 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180795-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 516
ID ADG12335 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003207392-A1.
PD 06-NOV-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 517
ID ADH24070 standard; protein; 720 AA.

DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180918-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 518
ID ADH34096 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180858-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 519
ID ADH29929 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180859-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 520
ID ADH23990 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180919-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 521
ID ADH08995 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003207395-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 522
ID ADG65304 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180904-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 523
ID ADH24580 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180907-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 524
ID ADH37436 standard; protein; 720 AA.
DE Human secreted and transmembrane protein PRO1344 CDNA.
PN US2003181646-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 525
ID ADH02025 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003180837-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 526
ID ADH37606 standard; protein; 720 AA.
DE Human secreted and transmembrane protein PRO1344 CDNA.
PN US2003181648-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 527
ID ADG85644 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180905-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 528
ID ADH24240 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180914-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 529
ID ADH38534 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181643-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 530
ID ADG83655 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003180794-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 531
ID ADH29463 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180860-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 532
ID ADH27579 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180906-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 533
ID ADH37776 standard; protein; 720 AA.
DE Human secreted and transmembrane protein PRO1344 CDNA.
PN US2003181647-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 534
ID ADH37953 standard; protein; 720 AA.
DE Human secreted and transmembrane protein PRO1344 CDNA.
PN US2003181649-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 535
ID ADH57373 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180920-A1.

PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 536
ID ADH53515 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181636-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 537
ID ADH53685 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181641-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 538
ID ADH52021 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181638-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 539
ID ADH4976 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181639-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 540
ID ADI2386 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181696-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 541
ID ADH90179 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181698-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 542
ID ADI2556 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181669-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 543
ID ADH97730 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181672-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 544
ID ADI35412 standard; protein; 720 AA.
DE Human PRO polypeptide #65.
PN US2003050457-A1.
PD 13-MAR-2003.

Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 545
ID ADI03578 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181656-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 546
ID ADI11935 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181686-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 547
ID ADH90009 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181697-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 548
ID ADH99904 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003049682-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 549
ID ADH98410 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181707-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 550
ID ADI11085 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181682-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 551
ID ADI11595 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181684-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 552
ID ADH98240 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181709-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 553
ID ADH98580 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181708-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 554
ID ADI35412 standard; protein; 720 AA.
DE Human PRO polypeptide #65.
PN US2003050457-A1.
PD 13-MAR-2003.

RESULT 554
ID ADH98070 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181673-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 555
ID AD105058 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180848-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 556
ID AD103408 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181654-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 557
ID AD104803 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181657-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 558
ID ADH78257 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181658-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 559
ID AD119601 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181676-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 560
ID ADH90349 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181659-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 561
ID AD103068 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181653-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 562
ID ADH77917 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181666-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 563
ID AD119431 standard; protein; 720 AA.

ID ADH97900 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181674-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 564
ID AD101285 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003190669-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 565
ID AD101980 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181652-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 566
ID AD103238 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181655-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 567
ID AD111425 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181681-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 568
ID AD102327 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181650-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 569
ID AD11765 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181685-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 570
ID AD105402 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003190716-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 571
ID ADH79474 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003191290-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 572
ID AD119431 standard; protein; 720 AA.

DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181675-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 573
ID ADI0532 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181677-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 574
ID ADH79644 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003191288-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 575
ID ADI01470 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181678-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 576
ID ADI01640 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181679-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 577
ID ADI01810 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181680-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 578
ID ADH79814 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003191289-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 579
ID ADI04632 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003171550-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 580
ID ADI02768 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181651-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 581
ID ADH78087 standard; protein; 720 AA.
DE Human PRO polypeptide #19.

PN US2003181667-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 582
ID ADI25726 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181670-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 583
ID ADI25896 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181671-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 584
ID ADK65408 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003073821-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 585
ID ADH98750 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003191284-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 586
ID ADH79991 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003191287-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 587
ID ADI32776 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003207396-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 588
ID ADM30310 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003073813-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 589
ID ADL93722 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003040013-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 590
ID ADC52176 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003130483-A1.

PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 591
ID ADE74307 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003211572-A1.
PD 13-NOV-2003.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 592
ID ADE74919 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003211574-A1.
PD 13-NOV-2003.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 593
ID ADF35357 standard; protein; 720 AA.
DE Human PRO1344 polypeptide.
PN US2003194760-A1.
PD 16-OCT-2003.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 594
ID ADG11607 standard; protein; 720 AA.
DE Human PRO1344 polypeptide.
PN US2003228655-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 595
ID ADP96132 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003215909-A1.
PD 20-NOV-2003.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 596
ID ADG04403 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003215912-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 597
ID ADG00563 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003215911-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 598
ID ADH06608 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180852-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 599
ID ADH06438 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180853-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 600

ID ADG68859 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180855-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 601
ID ADH27749 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180912-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 602
ID ADH25690 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180913-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 603
ID ADH33722 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181645-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 604
ID ADG82819 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003215910-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 605
ID ADH02365 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003180839-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 606
ID ADH07972 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180845-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 607
ID ADG69369 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180846-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 608
ID ADH39190 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180917-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 609
ID ADH26100 standard; protein; 720 AA.

DE Novel human secreted and transmembrane protein PRO1344.
PN US2003068770-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 8; Length 720;
Pred. No. 0;
RESULT 610
ID ADG83930 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003180842-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 8; Length 720;
Pred. No. 0;
RESULT 611
ID ADH19477 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003228656-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 8; Length 720;
Pred. No. 0;
RESULT 612
ID ADG85474 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003166848-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 8; Length 720;
Pred. No. 0;
RESULT 613
ID ADH06268 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180854-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 8; Length 720;
Pred. No. 0;
RESULT 614
ID ADH30098 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180856-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 8; Length 720;
Pred. No. 0;
RESULT 615
ID ADH24410 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180910-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 8; Length 720;
Pred. No. 0;
RESULT 616
ID ADH33069 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003068768-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 8; Length 720;
Pred. No. 0;
RESULT 617
ID ADG69539 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180844-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 8; Length 720;
Pred. No. 0;
RESULT 618
ID ADH07802 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.

PN US2003180851-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 8; Length 720;
Pred. No. 0;
RESULT 619
ID ADG85614 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180861-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 8; Length 720;
Pred. No. 0;
RESULT 620
ID ADH39360 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180916-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 8; Length 720;
Pred. No. 0;
RESULT 621
ID ADH33552 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181637-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 8; Length 720;
Pred. No. 0;
RESULT 622
ID ADH33892 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181644-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 8; Length 720;
Pred. No. 0;
RESULT 623
ID ADH01102 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003180838-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 8; Length 720;
Pred. No. 0;
RESULT 624
ID ADG69709 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180843-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 8; Length 720;
Pred. No. 0;
RESULT 625
ID ADH20970 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003224358-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 8; Length 720;
Pred. No. 0;
RESULT 626
ID ADH02195 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003180841-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 8; Length 720;
Pred. No. 0;
RESULT 627
ID ADG69199 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180847-A1.
PD 25-SEP-2003.

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PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 628
ID ADG58984 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180862-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 629
ID ADH24920 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180909-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 630
ID ADH39537 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180915-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 631
ID ADH20010 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US200319856-A1.
PD 27-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 632
ID ADH02535 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003180840-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 633
ID ADG69029 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180849-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 634
ID ADH07632 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180850-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 635
ID ADG6154 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180863-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 636
ID ADH24750 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180908-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 637
ID ADH25798 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180911-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 638
ID ADH38364 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180922-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 639
ID ADH57203 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181642-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 640
ID ADH52191 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180921-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 641
ID ADH49557 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180857-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 642
ID ADH90519 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181700-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 643
ID ADI11255 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181683-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 644
ID ADH98920 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003190698-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 645
ID ADI02150 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003190699-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
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Best Local Similarity 100.0%; Pred. No. 0;
RESULT 646
ID ADH90689 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181701-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 8; Length 720;
RESULT 647
ID ADH54608 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2004023321-A1.
PD 05-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 8; Length 720;
RESULT 648
ID ADH98564 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003187197-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 8; Length 720;
RESULT 649
ID ADH98734 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003187228-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 8; Length 720;
RESULT 650
ID ADH78893 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181703-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 8; Length 720;
RESULT 651
ID ADH99127 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003186408-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 8; Length 720;
RESULT 652
ID ADH99297 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003187196-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 8; Length 720;
RESULT 653
ID ADH98915 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003187242-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 8; Length 720;
RESULT 654
ID ADH79063 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181702-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 8; Length 720;
RESULT 655
ID ADH79063 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181702-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 8; Length 720;

RESULT 655
ID ADK00923 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003186407-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 8; Length 720;
RESULT 656
ID ADK14444 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003187229-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 8; Length 720;
RESULT 657
ID ADH64579 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2004038337-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 8; Length 720;
RESULT 658
ID ADM31475 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2004048334-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 8; Length 720;
RESULT 659
ID ADM36522 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2004053358-A1.
PD 18-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 8; Length 720;
RESULT 660
ID ADM40327 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2004048335-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 8; Length 720;
RESULT 661
ID ADM80893 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2004058411-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 8; Length 720;
RESULT 662
ID ADN37935 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2004091959-A1.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 8; Length 720;
RESULT 663
ID AAB70531 standard; protein; 567 AA.
DE Human PRO1 protein sequence SEQ ID NO:2.
PN WO200110902-A2.
PD 15-FEB-2001.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 100.0%; Score 556; DB 4; Length 567;
RESULT 664

ID AA88280 standard; protein; 720 AA.
DE Human TANGO 215 protein.
PN WO200018904-A2.
PD 06-APR-2000.
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
Query Match 71.9%; Score 518; DB 3; Length 720;
Best Local Similarity 99.7%; Pred. No. 0;
RESULT 665
ID AAB70532 standard; protein; 720 AA.
DE Human PRO2 protein sequence SEQ ID NO:4.
PN WO200110902-A2.
PD 15-FEB-2001.
PA (CURA-) CURAGEN CORP.
Query Match 71.9%; Score 518; DB 4; Length 720;
Best Local Similarity 99.7%; Pred. No. 0;
RESULT 666
ID AAU00401 standard; protein; 720 AA.
DE Human secreted protein, POLY13.
PN WO200119856-A2.
PD 22-MAR-2001.
PA (CURA-) CURAGEN CORP.
Query Match 71.9%; Score 518; DB 4; Length 720;
Best Local Similarity 99.7%; Pred. No. 0;
RESULT 667
ID ADH89028 standard; protein; 720 AA.
DE Human POLYX polypeptide #11.
PN US200319858-A1.
PD 23-OCT-2003.
PA (SHIM/) SHIMKETS R. A.
PA (PERN/) PERMANDES E.
PA (HERR/) HERRMANN J L.
PA (LIUX/) LIU X.
PA (YANG/) YANG M.
PA (BOLD/) BOLDOS F L.
PA (SMIT/) SMITHSON G.
PA (RAST/) RASTELLI L.
Query Match 71.9%; Score 518; DB 8; Length 720;
Best Local Similarity 99.7%; Pred. No. 0;
RESULT 668
ID AAM41706 standard; protein; 499 AA.
DE Human polypeptide SEQ ID NO 6637.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 61.9%; Score 446; DB 4; Length 499;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 669
ID AAB85891 standard; protein; 737 AA.
DE Human serine protease-like protein (hC-PLACE1009992).
PN WO200109349-A1.
PD 08-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 61.9%; Score 446; DB 4; Length 737;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 670
ID AAB93670 standard; protein; 737 AA.
DE Human protein sequence SEQ ID NO:13202.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 61.9%; Score 446; DB 4; Length 737;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 671
ID ADU69990 standard; protein; 737 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID1796.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 61.9%; Score 446; DB 7; Length 737;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 672
ID ADN04640 standard; protein; 737 AA.

DE Antiporiatic protein sequence #505.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 61.9%; Score 446; DB 8; Length 737;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 673
ID AD885034 standard; protein; 737 AA.
DE Human atopic dermatitis-related protein sequence SeqID36.
PN WO2004033386-A1.
PD 15-APR-2004.
PA (GENO-) GENOX RES INC.
PA (UYJU-) UNIV JUNTENDO.
Query Match 61.9%; Score 446; DB 8; Length 737;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 674
ID AD85022 standard; protein; 737 AA.
DE Human atopic dermatitis-related protein sequence SeqID24.
PN WO2004033386-A1.
PD 15-APR-2004.
PA (GENO-) GENOX RES INC.
PA (UYJU-) UNIV JUNTENDO.
Query Match 61.9%; Score 446; DB 8; Length 737;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 675
ID AAB85893 standard; protein; 762 AA.
DE Human serine protease-like protein (hC-PLACE1009992).
PN WO200109349-A1.
PD 08-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 61.9%; Score 446; DB 4; Length 762;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 676
ID ADL06662 standard; protein; 417 AA.
DE Human 3T3 cell conversion promoter FP938.
PN CN1403477-A.
PD 19-MAR-2003.
PA (SHAN-) SHANGHAI XINSHIJI GENE TECHN DEV CO LTD.
Query Match 53.6%; Score 386; DB 7; Length 417;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 677
ID AAE19180 standard; protein; 649 AA.
DE Human protease, PRIS-17 protein.
PN WO200208396-A2.
PD 31-JAN-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 52.1%; Score 375; DB 5; Length 649;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 678
ID AAM39920 standard; protein; 359 AA.
DE Human polypeptide SEQ ID NO 3065.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 49.9%; Score 359; DB 4; Length 359;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 679
ID AAM39957 standard; protein; 359 AA.
DE Human polypeptide SEQ ID NO 3102.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 49.9%; Score 359; DB 4; Length 359;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 680
ID AAB49533 standard; protein; 570 AA.
DE Clone HPEY75.
PN WO200061774-A2.
PD 19-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 49.3%; Score 355; DB 3; Length 570;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 681

ID AAB20817 standard; protein; 455 AA.
DE Human gene 5 encoded secreted protein HSLG75, SEQ ID NO:79.
PN WO200218435-A1.
PD 07-MAR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 38.5%; Score 277; DB 5; Length 455;
Best Local Similarity 100.0%; Pred. No. 4.5e-261;
RESULT 682
ID AAG64652 standard; protein; 455 AA.
DE Human albumin fusion protein #1327.
PN WO200172137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 38.5%; Score 277; DB 5; Length 455;
Best Local Similarity 100.0%; Pred. No. 4.5e-261;
RESULT 683
ID ADL77919 standard; protein; 455 AA.
DE Albumin fusion protein related therapeutic protein X, SEQ ID NO 1401.
PN US2004010134-A1.
PD 15-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (HASE/) HASELTINE W A.
Query Match 38.5%; Score 277; DB 8; Length 455;
Best Local Similarity 100.0%; Pred. No. 4.5e-261;
RESULT 684
ID ADR41485 standard; protein; 551 AA.
DE Human CD-like molecule HSLG41, SEQ ID NO:284.
PN WO200226830-A2.
PD 04-APR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 38.5%; Score 277; DB 5; Length 551;
Best Local Similarity 100.0%; Pred. No. 5.4e-261;
RESULT 685
ID AAE20797 standard; protein; 323 AA.
DE Human gene 5 encoded secreted protein HSLG75, SEQ ID NO:59.
PN WO200218435-A1.
PD 07-MAR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 38.3%; Score 276; DB 5; Length 323;
Best Local Similarity 100.0%; Pred. No. 3.2e-260;
RESULT 686
ID AAG64653 standard; protein; 323 AA.
DE Human albumin fusion protein #1328.
PN WO200172137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 38.3%; Score 276; DB 5; Length 323;
Best Local Similarity 100.0%; Pred. No. 3.2e-260;
RESULT 687
ID ADL77920 standard; protein; 323 AA.
DE Albumin fusion protein related therapeutic protein X, SEQ ID NO 1402.
PN US2004010134-A1.
PD 15-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (HASE/) HASELTINE W A.
Query Match 38.3%; Score 276; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 3.2e-260;
RESULT 688
ID AAM24485 standard; protein; 234 AA.
DE Human EST encoded protein SEQ ID NO: 2010.
PN WO200154477-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 25.4%; Score 183; DB 4; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-169;
RESULT 689
ID AAM41743 standard; protein; 146 AA.
DE Human polypeptide SEQ ID NO 6674.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 15.8%; Score 114; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 2.2e-102;

RESULT 690
ID AAB09927 standard; protein; 719 AA.
DE Murine TAMCO 215 protein.
PN WO200018904-A2.
PD 06-APR-2000.
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
Query Match 8.5%; Score 61; DB 3; Length 719;
Best Local Similarity 100.0%; Pred. No. 5.2e-50;
RESULT 691
ID AAB85892 standard; protein; 720 AA.
DE Mouse serine protease-like protein (mc-PLACE1009992).
PN WO200109349-A1.
PD 08-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 8.5%; Score 61; DB 4; Length 720;
Best Local Similarity 100.0%; Pred. No. 5.2e-50;
RESULT 692
ID AAY11743 standard; protein; 103 AA.
DE Human 5' EST secreted protein SEQ ID NO: 343.
PN WO9906550-A2.
PD 11-FEB-1999.
PA (GEST-) GENSET.
Query Match 5.3%; Score 38; DB 2; Length 103;
Best Local Similarity 100.0%; Pred. No. 2.5e-28;
RESULT 693
ID AAY11763 standard; protein; 34 AA.
DE Human 5' EST secreted protein SEQ ID NO: 363.
PN WO9906550-A2.
PD 11-FEB-1999.
PA (GEST-) GENSET.
Query Match 2.1%; Score 15; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 2.6e-06;
RESULT 694
ID AAB49539 standard; peptide; 12 AA.
DE Clone HEPHY75 peptide fragment.
PN WO200061774-A2.
PD 19-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.7%; Score 12; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00086;
RESULT 695
ID AAY72114 standard; peptide; 12 AA.
DE Human serine protease epidermal growth factor (EGF)-like domain.
PN WO200068247-A2.
PD 16-NOV-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.7%; Score 12; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00086;
RESULT 696
ID AAR93594 standard; peptide; 30 AA.
DE UK c-pA hybrid peptide CS14 residues 276-306.
PN WO9509908-A1.
PD 13-APR-1995.
PA (SUMU-) SUMITOMO PHARM CO LTD.
Query Match 1.2%; Score 9; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.7;
RESULT 697
ID AAR76945 standard; peptide; 30 AA.
DE UK c-pA hybrid peptide CS13 (residues 276-306).
PN WO9509908-A1.
PD 13-APR-1995.
PA (SUMU-) SUMITOMO PHARM CO LTD.
Query Match 1.2%; Score 9; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.7;
RESULT 698
ID AAR93590 standard; peptide; 30 AA.
DE UK c-pA hybrid peptide CS20 residues 276-306.
PN WO9509908-A1.
PD 13-APR-1995.
PA (SUMU-) SUMITOMO PHARM CO LTD.
Query Match 1.2%; Score 9; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.7;
RESULT 699

ID AAR93593 standard; peptide: 30 AA.
DE UK t-PA hybrid peptide CS11 residues 276-306.
PN WO9509908-A1.
PD 13-APR-1995.
PA (SUMU) SUMITOMO PHARM CO LTD.
Query Match 1.2%; Score 9; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.7;
RESULT 700
ID AAR93588 standard; peptide: 30 AA.
DE UK t-PA hybrid peptide CS18 residues 276-306.
PN WO9509908-A1.
PD 13-APR-1995.
PA (SUMU) SUMITOMO PHARM CO LTD.
Query Match 1.2%; Score 9; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.7;
RESULT 701
ID AAY82896 standard; protein: 101 AA.
DE CUB domain from murine BMP-1.
PN WO200009691-A2.
PD 24-FEB-2000.
PA (UROG-) UROGENESYS INC.
PA (AFAR-) AFAR D E.
PA (HUBE-) HUBERT R S.
PA (LEON-) LEONG K.
PA (RAIT-) RAITANO A B.
PA (SAFE-) SAFFRAN D C.
PA (JAKO-) JAKOBOVITS A.
Query Match 1.2%; Score 9; DB 3; Length 101;
Best Local Similarity 100.0%; Pred. No. 5.1;
RESULT 702
ID AAY27043 standard; protein: 110 AA.
DE Amino acid sequence of human Bmp-1 CUB1 domain.
PN WO9937757-A1.
PD 29-JUL-1999.
PA (TULA) TULANE EDUCATIONAL FUND.
PA (INRM) INST NAT SANTE & RECH MEDICALE.
Query Match 1.2%; Score 9; DB 2; Length 110;
Best Local Similarity 100.0%; Pred. No. 5.5;
RESULT 703
ID ABM84572 standard; protein: 622 AA.
DE Human diagnostic and therapeutic protein SEQ ID NO:4821.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 1.2%; Score 9; DB 8; Length 622;
Best Local Similarity 100.0%; Pred. No. 27;
RESULT 704
ID ABM80969 standard; protein: 622 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO81651, SEQ:2500.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GERTH) GENENTECH INC.
Query Match 1.2%; Score 9; DB 8; Length 622;
Best Local Similarity 100.0%; Pred. No. 27;
RESULT 705
ID AAP0618 standard; protein: 730 AA.
DE Human Bone Morphogenic Protein-1 of lambda U20S-1.
PN WO8800205-A.
PD 14-JAN-1988.
PA (GEMT) GENETICS INST INC.
Query Match 1.2%; Score 9; DB 1; Length 730;
Best Local Similarity 100.0%; Pred. No. 31;
RESULT 706
ID AAW13669 standard; protein: 730 AA.
DE C-proteinase encoded by clone pcP-1.
PN WO9706242-A1.
PD 20-FEB-1997.
PA (UYXE-) UNIV JEFFERSON THOMAS.
Query Match 1.2%; Score 9; DB 2; Length 730;
Best Local Similarity 100.0%; Pred. No. 31;
RESULT 707
ID ADP65217 standard; protein: 730 AA.
DE Human bone morphogenetic protein 1, isoform 1, precursor, PCP.

PN WO2003072827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Query Match 1.2%; Score 9; DB 7; Length 730;
Best Local Similarity 100.0%; Pred. No. 31;
RESULT 708
ID ABM80967 standard; protein: 730 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO2042, SEQ:2496.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GERTH) GENENTECH INC.
Query Match 1.2%; Score 9; DB 8; Length 730;
Best Local Similarity 100.0%; Pred. No. 31;
RESULT 709
ID AAW75919 standard; protein: 788 AA.
DE C-proteinase sequence used to cleave procollagene.
PN US5807981-A.
PD 15-SEP-1998.
PA (FIBR-) FIBROGEN INC.
Query Match 1.2%; Score 9; DB 2; Length 788;
Best Local Similarity 100.0%; Pred. No. 33;
RESULT 710
ID ADH41541 standard; protein: 821 AA.
DE Novel human protein NOV8e.
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 1.2%; Score 9; DB 8; Length 821;
Best Local Similarity 100.0%; Pred. No. 34;
RESULT 711
ID ADH41549 standard; protein: 821 AA.
DE Novel human protein NOV8i.
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 1.2%; Score 9; DB 8; Length 821;
Best Local Similarity 100.0%; Pred. No. 34;
RESULT 712
ID ADH41533 standard; protein: 821 AA.
DE Novel human protein NOV8a.
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 1.2%; Score 9; DB 8; Length 821;
Best Local Similarity 100.0%; Pred. No. 34;
RESULT 713
ID ADH41543 standard; protein: 821 AA.
DE Novel human protein NOV8f.
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 1.2%; Score 9; DB 8; Length 821;
Best Local Similarity 100.0%; Pred. No. 34;
RESULT 714
ID ADH41545 standard; protein: 821 AA.
DE Novel human protein NOV8g.
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 1.2%; Score 9; DB 8; Length 821;
Best Local Similarity 100.0%; Pred. No. 34;
RESULT 715
ID ADH41547 standard; protein: 821 AA.
DE Novel human protein NOV8h.
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 1.2%; Score 9; DB 8; Length 821;
Best Local Similarity 100.0%; Pred. No. 34;
RESULT 716
ID ADM87216 standard; protein: 823 AA.
DE Human protein SEQ ID NO:309.
PN WO2004009834-A2.

PD 29-JAN-2004.
PA (NUVE-) NUVELO INC.
Query Match 1.2%; Score 9; DB 8; Length 823;
Best Local Similarity 100.0%; Pred. No. 34;
RESULT 717
ID ABM80968 standard; protein; 823 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO81650, SEQ:2498.
PN W02004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 1.2%; Score 9; DB 8; Length 823;
Best Local Similarity 100.0%; Pred. No. 34;
RESULT 718
ID ABG79188 standard; protein; 970 AA.
DE Human colloid-like 2-like protein #2.
PN W0200264791-A2.
PD 22-AUG-2002.
PA (CURA-) CURAGEN CORP.
Query Match 1.2%; Score 9; DB 5; Length 970;
Best Local Similarity 100.0%; Pred. No. 40;
RESULT 719
ID ADH41539 standard; protein; 970 AA.
DE Novel human protein NOV8d.
PN W02003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 1.2%; Score 9; DB 8; Length 970;
Best Local Similarity 100.0%; Pred. No. 40;
RESULT 720
ID AAW13670 standard; protein; 986 AA.
DE C-proteinase encoded by clone pcp-2.
PN W09706242-A1.
PD 20-FEB-1997.
PA (UYJE-) UNIV JEFFERSON THOMAS.
Query Match 1.2%; Score 9; DB 2; Length 986;
Best Local Similarity 100.0%; Pred. No. 41;
RESULT 721
ID AB990755 standard; protein; 986 AA.
DE Human Tumour Endothelial Marker polypeptide SEQ ID NO 242.
PN W0200210217-A2.
PD 07-FEB-2002.
PA (UYJO) UNIV JOHNS HOPKINS.
Query Match 1.2%; Score 9; DB 5; Length 986;
Best Local Similarity 100.0%; Pred. No. 41;
RESULT 722
ID ABUS4462 standard; protein; 986 AA.
DE Human tumour endothelial marker TEM 25.
PN W0200283874-A2.
PD 24-OCT-2002.
PA (UYJO) UNIV JOHNS HOPKINS.
Query Match 1.2%; Score 9; DB 6; Length 986;
Best Local Similarity 100.0%; Pred. No. 41;
RESULT 723
ID ADH11578 standard; protein; 986 AA.
DE Human bone morphogenic protein (BMP) polypeptide #6.
PN US2003224501-A1.
PD 04-DEC-2003.
PA (YOUN) YOUNG P E.
PA (RUBE) RUBEN S M.
Query Match 1.2%; Score 9; DB 8; Length 986;
Best Local Similarity 100.0%; Pred. No. 41;
RESULT 724
ID AD018558 standard; protein; 986 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 1377.
PN W02004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 1.2%; Score 9; DB 8; Length 986;
Best Local Similarity 100.0%; Pred. No. 41;
RESULT 725
ID ABG79187 standard; protein; 992 AA.
DE Human colloid-like 2-like protein #1.
PN W0200264791-A2.
PD 22-AUG-2002.
PA (CURA-) CURAGEN CORP.
Query Match 1.2%; Score 9; DB 5; Length 992;
Best Local Similarity 100.0%; Pred. No. 41;
RESULT 726
ID ADH41535 standard; protein; 992 AA.
DE Novel human protein NOV8d.
PN W02003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 1.2%; Score 9; DB 8; Length 992;
Best Local Similarity 100.0%; Pred. No. 41;
RESULT 727
ID AAY32240 standard; protein; 1015 AA.
DE Human colloid-like protein mtl1-2.
PN W09951730-A2.
PD 14-OCT-1999.
PA (WISC) WISCONSIN ALUMNI RES FOUND.
Query Match 1.2%; Score 9; DB 3; Length 1015;
Best Local Similarity 100.0%; Pred. No. 42;
RESULT 728
ID ADH41537 standard; protein; 1015 AA.
DE Novel human protein NOV8c.
PN W02003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 1.2%; Score 9; DB 8; Length 1015;
Best Local Similarity 100.0%; Pred. No. 42;
RESULT 729
ID AB871111 standard; protein; 1464 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 40125.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 1.2%; Score 9; DB 4; Length 1464;
Best Local Similarity 100.0%; Pred. No. 58;
RESULT 730
ID AB877068 standard; peptide; 11 AA.
DE AC2885 antibody light chain hypervariable region CDR1.
PN W0200216436-A2.
PD 28-FEB-2002.
PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERM GES MBH.
Query Match 1.1%; Score 8; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 64;
RESULT 731
ID ADH17899 standard; peptide; 11 AA.
DE Human ISH12/19D12 CDR (complementarity determining region)-L1 peptide.
PN W02003100008-A2.
PD 04-DEC-2003.
PA (SCHE) SCHERING CORP.
Query Match 1.1%; Score 8; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 64;
RESULT 732
ID ADM41606 standard; peptide; 11 AA.
DE Interleukin-1 receptor type 1 antibody light chain variable region CDR1.
PN W020040422718-A2.
PD 18-MAR-2004.
PA (AMGE-) AMGEN INC.
Query Match 1.1%; Score 8; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 64;
RESULT 733
ID AAE36802 standard; protein; 50 AA.
DE Human epigen BGF-like domain.
PN W02003014159-A1.
PD 20-FEB-2003.
PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
PA (BIOM-) BIOCROMOLECULAR RES INST LTD.
PA (HALI-) HALI INST MEDICAL RES VALTER & ELIZA.
PA (LUDW-) LUDWIG INST CANCER RES.
Query Match 1.1%; Score 8; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 25;
RESULT 734

	ID	ADP07347	standard; protein; 95 AA.	
	DE	Human antibody A26 light chain variable region.		
	PD	22-APR-2004.		
	PA	(INTE-) INTEGRIGEN INC.		
	Query Match	1.1%; Score 8; DB 8; Length 95;		
	Best Local Similarity	100.0%; Pred. No. 46;		
	RESULT 750			
	ID	AD007348	standard; protein; 95 AA.	
	DE	Human antibody A10 light chain variable region.		
	PD	22-APR-2004.		
	PA	(INTE-) INTEGRIGEN INC.		
	Query Match	1.1%; Score 8; DB 8; Length 95;		
	Best Local Similarity	100.0%; Pred. No. 46;		
	RESULT 751			
	ID	AAB35905	standard; protein; 96 AA.	
	DE	Human A10/A26 antibody light chain germline protein.		
	PD	EPI262193-A1.		
	PA	(PTZ) PRIZER PROD INC.		
	Query Match	1.1%; Score 8; DB 6; Length 96;		
	Best Local Similarity	100.0%; Pred. No. 46;		
	RESULT 752			
	ID	AD007305	standard; protein; 107 AA.	
	DE	Human proteolytic A26-OX1 light chain, used in catalytic antibody		

PN WO2004033658-A2.
PD 22-APR-2004.
PA (INTE-) INTEGRIGEN INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 51;
RESULT 753
ID APO07307 standard; protein; 107 AA.
DE Human proteolytic A10-JK1 light chain, used in catalytic antibody.
PN WO2004033658-A2.
PD 22-APR-2004.
PA (INTE-) INTEGRIGEN INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 51;
RESULT 754
ID ABB03399 standard; protein; 124 AA.
DE Human musculoskeletal system related polypeptide SEQ ID NO 1346.
PN WO200155367-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 58;
RESULT 755
ID ABB12693 standard; protein; 124 AA.
DE Novel human musculoskeletal system antigen #313.
PN US2002147140-A1.
PD 10-OCT-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match
Best Local Similarity 100.0%; Pred. No. 58;
RESULT 756
ID ADJ28719 standard; protein; 124 AA.
DE Human musculoskeletal system-associated protein - SEQ ID 1346.
PN US2004009488-A1.
PD 15-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 58;
RESULT 757
ID ABB77064 standard; protein; 126 AA.
DE ACZ885 antibody light chain variable region.
PN WO200216436-A2.
PD 28-FEB-2002.
PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GBS MBH.
Query Match
Best Local Similarity 100.0%; Pred. No. 59;
RESULT 758
ID ADM41553 standard; protein; 126 AA.
DE Anti-interleukin-1 receptor type 1 antibody kappa chain variable region.
PN WO2004022718-A2.
PD 18-MAR-2004.
PA (AMGE-) AMGEN INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 59;
RESULT 759
ID APP57370 standard; protein; 127 AA.
DE Anti-TRAIL-R antibody related clone KMTR1 protein SEQ ID NO:35.
PN WO200294880-A1.
PD 28-NOV-2002.
PA (KIRI) KIRIN BEER KK.
Query Match
Best Local Similarity 100.0%; Pred. No. 60;
RESULT 760
ID AAY56718 standard; protein; 128 AA.
DE Amino acid sequence of chimpanzee V kappa CDNA clone 46-4.
PN WO9955369-A1.
PD 04-NOV-1999.
PA (SMIK) SMITHKLINE BEECHAM CORP.
Query Match
Best Local Similarity 100.0%; Pred. No. 60;
RESULT 761

ID ADH17963 standard; protein; 128 AA.
DE Human modified 15H12/19D12 light chain C (LCC) protein.
PN WO2003100008-A2.
PD 04-DEC-2003.
PA (SCHE) SCHERING CORP.
Query Match
Best Local Similarity 100.0%; Pred. No. 60;
RESULT 762
ID ADH17967 standard; protein; 128 AA.
DE Human modified 15H12/19D12 light chain E (LCE) protein.
PN WO2003100008-A2.
PD 04-DEC-2003.
PA (SCHE) SCHERING CORP.
Query Match
Best Local Similarity 100.0%; Pred. No. 60;
RESULT 763
ID ADH17969 standard; protein; 128 AA.
DE Human modified 15H12/19D12 light chain F (LCF) protein.
PN WO2003100008-A2.
PD 04-DEC-2003.
PA (SCHE) SCHERING CORP.
Query Match
Best Local Similarity 100.0%; Pred. No. 60;
RESULT 764
ID ADH17932 standard; protein; 128 AA.
DE Human 15H12/19D12 light chain A (LCA) protein.
PN WO2003100008-A2.
PD 04-DEC-2003.
PA (SCHE) SCHERING CORP.
Query Match
Best Local Similarity 100.0%; Pred. No. 60;
RESULT 765
ID ADH17965 standard; protein; 128 AA.
DE Human modified 15H12/19D12 light chain D (LCD) protein.
PN WO2003100008-A2.
PD 04-DEC-2003.
PA (SCHE) SCHERING CORP.
Query Match
Best Local Similarity 100.0%; Pred. No. 60;
RESULT 766
ID ADH17934 standard; protein; 128 AA.
DE Human 15H12/19D12 light chain B (LCB) protein.
PN WO2003100008-A2.
PD 04-DEC-2003.
PA (SCHE) SCHERING CORP.
Query Match
Best Local Similarity 100.0%; Pred. No. 60;
RESULT 767
ID ADH17893 standard; protein; 128 AA.
DE Human 15H12/19D12 light chain variable region protein.
PN WO2003100008-A2.
PD 04-DEC-2003.
PA (SCHE) SCHERING CORP.
Query Match
Best Local Similarity 100.0%; Pred. No. 60;
RESULT 768
ID AAY76009 standard; protein; 152 AA.
DE Murine TGF-alpha homologue mUTR1, SEQ ID 187.
PN WO9355865-A1.
PD 04-NOV-1999.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match
Best Local Similarity 100.0%; Pred. No. 70;
RESULT 769
ID AAB55948 standard; protein; 152 AA.
DE Skin cell protein, SEQ ID NO: 187.
PN WO200069884-A2.
PD 23-NOV-2000.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match
Best Local Similarity 100.0%; Pred. No. 70;
RESULT 770
ID ABB72148 standard; protein; 152 AA.

	DE	Murine protein isolated from skin cells SEQ ID NO: 187.
P1	MOJ00190357-A1.	
P2	29-NOV-2001.	
PA	(GENE-) GENESIS RES & DEV CORP LTD.	
Query Match	1.1%; Score 8;	DB 5; Length 152;
Best Local Similarity	100.0%; Pred. No. 70;	
RESULT 771		
ID	AAY93714 standard; protein; 155 AA.	
DE	The kappa chain of immunoglobulin clone 2.1.3.	
P1	WO200037504-A2.	
P2	29-JUN-2000.	
PA	(PEIZ) PFIZER INC.	
PA	(ABGE-) ABGENIX INC.	
Query Match	1.1%; Score 8;	DB 3; Length 155;
Best Local Similarity	100.0%; Pred. No. 71;	
RESULT 772		
ID	AAE35906 standard; protein; 155 AA.	
DE	Human 2.1.3 anti-CTLA-4 antibody kappa chain.	
P1	EPI362193-A1.	
P2	04-DEC-2002.	
PA	(PTIZ) PFIZER PROD INC.	
Query Match	1.1%; Score 8;	DB 6; Length 155;
Best Local Similarity	100.0%; Pred. No. 71;	
RESULT 773		
ID	ADKS2330 standard; protein; 157 AA.	
DE	Human anti-MCP-1 variable region light chain #9.	
P1	WO2004016769-A2.	
P2	26-FEB-2004.	
PA	(ABGE-) ABGENIX INC.	
Query Match	1.1%; Score 8;	DB 8; Length 157;
Best Local Similarity	100.0%; Pred. No. 72;	
RESULT 774		
ID	ADM41575 standard; protein; 233 AA.	
DE	Anti-Interleukin-1 receptor type 1 antibody light chain.	
P1	WO2004022718-A2.	
P2	18-MAR-2004.	
PA	(AMGE-) AMGEN INC.	
Query Match	1.1%; Score 8;	DB 8; Length 233;
Best Local Similarity	100.0%; Pred. No. 1e+02;	
RESULT 775		
ID	ABU70774 standard; protein; 235 AA.	
DE	Human adipocyte Selected Interacting domain, SID, #405.	
P1	WO2000286132-A2.	
P2	31-OCT-2002.	
PA	(HVRB-) HVBREGENICS.	
Query Match	1.1%; Score 8;	DB 6; Length 235;
Best Local Similarity	100.0%; Pred. No. 1e+02;	
RESULT 776		
ID	ADN24003 standard; protein; 302 AA.	
DE	Bacterial polypeptide #6656.	
P1	US200333675-A1.	
P2	18-DEC-2003.	
PA	(CAOV/) CAO Y.	
PA	(HINK/) HINKLE S J.	
PA	(SLAT/) SLATER S C.	
PA	(CHEN/) CHEN X.	
PA	(GOLD/) GOLDMAN B S.	
Query Match	1.1%; Score 8;	DB 8; Length 302;
Best Local Similarity	100.0%; Pred. No. 1.3e+02;	
RESULT 777		
ID	AAI79332 standard; protein; 467 AA.	
DE	Human EGF repeat-containing protein EGF-Hy1.	
P1	WO200017357-A1.	
P2	30-MAR-2000.	
PA	(HYSE-) HYSEQ INC.	
Query Match	1.1%; Score 8;	DB 3; Length 467;
Best Local Similarity	100.0%; Pred. No. 1.9e+02;	
RESULT 778		
ID	ABU22131 standard; protein; 596 AA.	
DE	Protein encoded by Prokaryotic essential gene #7658.	
P1	WO2000277183-A2.	
P2	03-OCT-2002.	
PA	(ELUT-) ELUTRA PHARM INC.	

Query Match	1.1%;	Score 8;	DB 6;	Length 596;
Best Local Similarity	100.0%;	Pred. No. 2.4e+02;		
RESULT 779				
ID ADG93413 standard; protein; 807 AA.				
DE Maize lipoxygenase (LOX) polypeptide #22.				
PN US2003166855-A1.				
PD 04-SEP-2003.				
PA (PION-) PIONEER HI-BRED INT INC.				
Query Match	1.1%;	Score 8;	DB 7;	Length 807;
Best Local Similarity	100.0%;	Pred. No. 3.2e+02;		
RESULT 780				
ID ADG93411 standard; protein; 807 AA.				
DE Maize lipoxygenase (LOX) polypeptide #21.				
PN US2003166855-A1.				
PD 04-SEP-2003.				
PA (PION-) PIONEER HI-BRED INT INC.				
Query Match	1.1%;	Score 8;	DB 7;	Length 807;
Best Local Similarity	100.0%;	Pred. No. 3.2e+02;		
RESULT 781				
ID ABP69935 standard; protein; 859 AA.				
DE Human polypeptide SEQ ID NO 982.				
PN WO200270539-A2.				
PD 12-SEP-2002.				
PA (HYSE-) HYSEQ INC.				
Query Match	1.1%;	Score 8;	DB 5;	Length 859;
Best Local Similarity	100.0%;	Pred. No. 3.4e+02;		
RESULT 782				
ID AAW43394 standard; protein; 1019 AA.				
DE Singapore horseshoe crab factor C protezyme (CrFC 21).				
PN SG42456-A1.				
PD 15-AUG-1997.				
PA (UTSI-) UNIV SINGAPORE NAT.				
Query Match	1.1%;	Score 8;	DB 2;	Length 1019;
Best Local Similarity	100.0%;	Pred. No. 4e+02;		
RESULT 783				
ID AAY05750 standard; protein; 1019 AA.				
DE Horseshoe crab Factor C.				
PN MO9915676-A1.				
PD 01-APR-1999.				
PA (UTSI-) UNIV SINGAPORE NAT.				
Query Match	1.1%;	Score 8;	DB 2;	Length 1019;
Best Local Similarity	100.0%;	Pred. No. 4e+02;		
RESULT 784				
ID AAW94302 standard; protein; 1019 AA.				
DE Horseshoe crab Factor C protein #2.				
PN US5858706-A.				
PD 12-JAN-1999.				
PA (UTSI-) UNIV SINGAPORE NAT.				
Query Match	1.1%;	Score 8;	DB 2;	Length 1019;
Best Local Similarity	100.0%;	Pred. No. 4e+02;		
RESULT 785				
ID AAY42490 standard; protein; 1019 AA.				
DE Recombinant N-terminally truncated Horseshoe crab Factor C protein				
PN US5985590-A.				
PD 16-NOV-1999.				
PA (UTSI-) UNIV SINGAPORE NAT.				
Query Match	1.1%;	Score 8;	DB 3;	Length 1019;
Best Local Similarity	100.0%;	Pred. No. 4e+02;		
RESULT 786				
ID AAB60935 standard; protein; 1019 AA.				
DE Horseshoe crab recombinant Factor C #2.				
PN WO200127289-A2.				
PD 19-APR-2001.				
PA (UTSI-) UNIV SINGAPORE NAT.				
Query Match	1.1%;	Score 8;	DB 4;	Length 1019;
Best Local Similarity	100.0%;	Pred. No. 4e+02;		
RESULT 787				
ID ABP72332 standard; protein; 1019 AA.				
DE Horseshoe crab Factor C.				
PN WO2003002976-A2.				
PD 09-JAN-2003.				
PA (WHIK) BIONEER INC.				
Query Match	1.1%;	Score 8;	DB 6;	Length 1019;

Best Local Similarity 100.0%; Pred. No. 4e+02;
RESULT 788
ID AAB72334 standard; protein; 1019 AA.
DE Horsehoe crab Factor C.
PN W02003002976-A2.
PD 09-JAN-2003.
PA (WHIK) BIOWHITTAKER INC.
Query Match 1.1%; Score 8; DB 6; Length 1019;
Best Local Similarity 100.0%; Pred. No. 4e+02;
RESULT 789
ID AAM43393 standard; protein; 1083 AA.
DE Singapore horsehoe crab factor C proenzyme (CrFC 26).
PN S642456-A1.
PD 15-AUG-1997.
PA (UYSI-) UNIV SINGAPORE NAT.
Query Match 1.1%; Score 8; DB 2; Length 1083;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
RESULT 790
ID AAY05749 standard; protein; 1083 AA.
DE Horsehoe crab Factor C.
PN W09915676-A1.
PD 01-APR-1999.
PA (UYSI-) UNIV SINGAPORE NAT.
Query Match 1.1%; Score 8; DB 2; Length 1083;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
RESULT 791
ID AAM94301 standard; protein; 1083 AA.
DE Horsehoe crab Factor C protein #1.
PN U55858706-A.
PD 12-JAN-1999.
PA (UYSI-) UNIV SINGAPORE NAT.
Query Match 1.1%; Score 8; DB 2; Length 1083;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
RESULT 792
ID AAY42489 standard; protein; 1083 AA.
DE Horsehoe crab recombinant Factor C protein.
PN U55985590-A.
PD 16-NOV-1999.
PA (UYSI-) UNIV SINGAPORE NAT.
Query Match 1.1%; Score 8; DB 3; Length 1083;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
RESULT 793
ID AAB60934 standard; protein; 1083 AA.
DE Horsehoe crab recombinant Factor C #1.
PN W0200127289-A2.
PD 19-APR-2001.
PA (UYSI-) UNIV SINGAPORE NAT.
Query Match 1.1%; Score 8; DB 4; Length 1083;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
RESULT 794
ID AAB72333 standard; protein; 1083 AA.
DE Horsehoe crab Factor C.
PN W02003002976-A2.
PD 09-JAN-2003.
PA (WHIK) BIOWHITTAKER INC.
Query Match 1.1%; Score 8; DB 6; Length 1083;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
RESULT 795
ID AAB62022 standard; protein; 1238 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 12858.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 1.1%; Score 8; DB 4; Length 1238;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
RESULT 796
ID AAB94754 standard; protein; 1316 AA.
DE Human protein sequence SEQ ID NO.15811.
PN EPI074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 1.1%; Score 8; DB 4; Length 1316;
Best Local Similarity 100.0%; Pred. No. 5e+02;

RESULT 797
ID ADF28695 standard; protein; 1484 AA.
DE Neurological therapy-related protein - SED ID 605.
PN W02003048326-A2.
PD 12-JUN-2003.
PA (HYSE-) HYSEQ INC.
Query Match 1.1%; Score 8; DB 7; Length 1484;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
RESULT 798
ID ADF28692 standard; protein; 1487 AA.
DE Human peroxidase-like protein - SED ID 602.
PN W02003048326-A2.
PD 12-JUN-2003.
PA (HYSE-) HYSEQ INC.
Query Match 1.1%; Score 8; DB 7; Length 1487;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
RESULT 799
ID ADS10671 standard; protein; 1507 AA.
DE Human therapeutic protein - SEQ ID 908.
PN W02004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Query Match 1.1%; Score 8; DB 8; Length 1507;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
RESULT 800
ID ADF28708 standard; protein; 1538 AA.
DE Peroxidase-like protein - SED ID 618.
PN W02003048326-A2.
PD 12-JUN-2003.
PA (HYSE-) HYSEQ INC.
Query Match 1.1%; Score 8; DB 7; Length 1538;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
RESULT 801
ID ADS10672 standard; protein; 1538 AA.
DE Human therapeutic protein - SEQ ID 909.
PN W02004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Query Match 1.1%; Score 8; DB 8; Length 1538;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
RESULT 802
ID ADN39112 standard; protein; 3557 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:430.
PN W02003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 1.1%; Score 8; DB 7; Length 3557;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
RESULT 803
ID ADN39979 standard; protein; 3557 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C349.
PN W02003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 1.1%; Score 8; DB 7; Length 3557;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
RESULT 804
ID AAB37944 standard; protein; 3570 AA.
DE Human GSD-33 protein.
PN W02003050253-A2.
PD 19-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 1.1%; Score 8; DB 7; Length 3570;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
RESULT 805
ID AAE20146 standard; protein; 3571 AA.
DE Human C3b/C4b complement receptor-like protein.
PN W0200210388-A2.
PD 07-FEB-2002.
PA (AMGB-) AMGEN INC.
Query Match 1.1%; Score 8; DB 5; Length 3571;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
RESULT 806

ID ADL22512 standard; protein; 3571 AA.
DE Human CNGH0004 antibody protein.
PN WO2004003147-A2.
PD 08-JAN-2004.
PA (CENZ) CENTOCOR INC.
Query Match 1.1%; Score 8; DB 8; Length 3571;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
RESULT 807
ID AD075791 standard; peptide; 10 AA.
DE Human 213P1F11 HLA motif bearing epitope #9890.
PN US2004019915-A1.
PD 29-JAN-2004.
PA (CHAL/) CHALILITA-EID P M.
PA (RAIT/) RAITANO A B.
PA (FARI/) FARIS M.
PA (HUBE/) HUBERT R S.
PA (MORR/) MORRISON R K.
PA (GEWW/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match 1.0%; Score 7; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 56;
RESULT 808
ID AD077622 standard; peptide; 15 AA.
DE Human 213P1F11 HLA motif bearing epitope #11721.
PN US2004019915-A1.
PD 29-JAN-2004.
PA (CHAL/) CHALILITA-EID P M.
PA (RAIT/) RAITANO A B.
PA (FARI/) FARIS M.
PA (HUBE/) HUBERT R S.
PA (MORR/) MORRISON R K.
PA (GEWW/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match 1.0%; Score 7; DB 8; Length 15;
Best Local Similarity 100.0%; Pred. No. 81;
RESULT 809
ID AAR71665 standard; peptide; 30 AA.
DE Modified urinary plasminogen activator residues 159-188.
PN JP07039374-A.
PD 10-FEB-1995.
PA (SUMU) SUMITOMO SEIYAKU KK.
Query Match 1.0%; Score 7; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
RESULT 810
ID ABP78761 standard; protein; 43 AA.
DE N. gonorrhoeae amino acid sequence SEQ ID 4052.
PN WO200279243-A2.
PD 10-OCT-2002.
PA (CHIR-) CHIRON SPA.
Query Match 1.0%; Score 7; DB 6; Length 43;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
RESULT 811
ID AAM23985 standard; protein; 49 AA.
DE Human EST encoded protein SEQ ID NO: 1380.
PN WO200154477-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 1.0%; Score 7; DB 4; Length 49;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
RESULT 812
ID ADC33279 standard; protein; 49 AA.
DE Human novel contig-encoded polypeptide sequence, SEQ ID NO:3361.
PN WO2003029271-A2.
PD 10-APR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 1.0%; Score 7; DB 7; Length 49;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
RESULT 813
ID AAM06451 standard; protein; 50 AA.
DE Human foetal protein, SEQ ID NO: 182.
PN WO200155339-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 1.0%; Score 7; DB 4; Length 50;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
RESULT 814
ID AAG91460 standard; protein; 54 AA.
DE C glutamicum protein fragment SEQ ID NO: 5214.
PN EP108790-A2.
PD 20-JUN-2001.
PA (KXOW) KYOWA HAKKO KOGYO KK.
Query Match 1.0%; Score 7; DB 4; Length 54;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
RESULT 815
ID AAY02522 standard; protein; 56 AA.
DE Clone selected after panning a NNK library of the invention.
PN WO9920749-A1.
PD 29-APR-1999.
PA (MED1-) MEDICAL RES COUNCIL.
Query Match 1.0%; Score 7; DB 2; Length 56;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
RESULT 816
ID ABW71426 standard; protein; 59 AA.
DE Staphylococcus aureus protein #666.
PN WO200294868-A2.
PD 28-NOV-2002.
PA (CHIR-) CHIRON SPA.
Query Match 1.0%; Score 7; DB 6; Length 59;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
RESULT 817
ID AAU48293 standard; protein; 62 AA.
DE Propionibacterium acnes immunogenic protein #9189.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (COR1-) CORIXA CORP.
Query Match 1.0%; Score 7; DB 4; Length 62;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
RESULT 818
ID ABW44812 standard; protein; 62 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #9488.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (COR1-) CORIXA CORP.
Query Match 1.0%; Score 7; DB 6; Length 62;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
RESULT 819
ID ABB42063 standard; peptide; 63 AA.
DE Peptide #9569 encoded by human foetal liver single exon probe.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 1.0%; Score 7; DB 4; Length 63;
Best Local Similarity 100.0%; Pred. No. 3e+02;
RESULT 820
ID AAM75756 standard; protein; 63 AA.
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 36062.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 1.0%; Score 7; DB 4; Length 63;
Best Local Similarity 100.0%; Pred. No. 3e+02;
RESULT 821
ID AAM62944 standard; protein; 63 AA.
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 35049.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 1.0%; Score 7; DB 4; Length 63;
Best Local Similarity 100.0%; Pred. No. 3e+02;
RESULT 822
ID ABG57494 standard; peptide; 63 AA.
DE Human liver peptide, SEQ ID NO 36142.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 1.0%; Score 7; DB 4; Length 63;

Best Local Similarity 100.0%; Pred. No. 3e+02;
RESULT 823
ID AAB35189 standard; protein; 74 AA.
DE Human deaminase-like ORF4162 protein, SEQ ID NO:8324.
PN W0200190366-A2.
PD 29-NOV-2001.
PA (CURA-) CURAGEN CORP.
Query Match 1.0%; Score 7; DB 5; Length 74;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
RESULT 824
ID AAV66472 standard; protein; 76 AA.
DE Propionibacterium acnes immunogenic protein #27368.
PN W0200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 1.0%; Score 7; DB 4; Length 76;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
RESULT 825
ID AAV67610 standard; protein; 76 AA.
DE Propionibacterium acnes immunogenic protein #28506.
PN W0200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 1.0%; Score 7; DB 4; Length 76;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
RESULT 826
ID AAM62991 standard; protein; 76 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #27667.
PN W02001903515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 1.0%; Score 7; DB 6; Length 76;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
RESULT 827
ID AAM64129 standard; protein; 76 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #28805.
PN W02001903515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 1.0%; Score 7; DB 6; Length 76;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
RESULT 828
ID AAE20816 standard; protein; 79 AA.
DE Human gene 5 encoded secreted protein HSLGU75, SEQ ID NO:78.
PN W0200218435-A1.
PD 07-MAR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.0%; Score 7; DB 5; Length 79;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
RESULT 829
ID AAG64651 standard; protein; 79 AA.
DE Human albumin fusion protein #1326.
PN W0200177137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.0%; Score 7; DB 5; Length 79;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
RESULT 830
ID AAV77918 standard; protein; 79 AA.
DE Albumin fusion protein related therapeutic protein X, SEQ ID NO 1400.
PN US2004010134-A1.
PD 15-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (HASE/) HASELTINE W A.
Query Match 1.0%; Score 7; DB 8; Length 79;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
RESULT 831
ID AAM64695 standard; protein; 81 AA.
DE Propionibacterium acnes immunogenic polypeptide #29371.
PN W02001903515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 1.0%; Score 7; DB 6; Length 81;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
RESULT 832
ID ADF05104 standard; protein; 83 AA.
DE Bacterial polypeptide #1217.
PN US6605709-B1.
PD 12-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 1.0%; Score 7; DB 7; Length 83;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
RESULT 833
ID AAG03800 standard; protein; 103 AA.
DE Human secreted protein, SEQ ID NO: 7881.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST-) GENSET.
Query Match 1.0%; Score 7; DB 3; Length 103;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
RESULT 834
ID AAV64590 standard; peptide; 105 AA.
DE Nonclassical cadherin extracellular domain SEQ ID NO:18.
PN W09957149-A2.
PD 11-NOV-1999.
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
Query Match 1.0%; Score 7; DB 3; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
RESULT 835
ID AAB06753 standard; protein; 107 AA.
DE Human ORFX protein sequence SEQ ID NO:13488.
PN W0200192523-A2.
PD 06-DEC-2001.
PA (CURA-) CURAGEN CORP.
Query Match 1.0%; Score 7; DB 5; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
RESULT 836
ID AAV27656 standard; protein; 108 AA.
DE Human protein AFP548753.
PN W020016748-A2.
PD 13-SEP-2001.
PA (ZYMO-) ZYMOGENETICS INC.
Query Match 1.0%; Score 7; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
RESULT 837
ID AAG32136 standard; protein; 108 AA.
DE Mutant B lichenformis secreted polypeptide SeqID 106.
PN W02003093453-A2.
PD 13-NOV-2003.
PA (NOVO-) NOVOZYMES AS.
Query Match 1.0%; Score 7; DB 8; Length 108;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
RESULT 838
ID AAM99113 standard; protein; 111 AA.
DE Bovine zeta 2 prethrombin 2.
PN W0985130-A1.
PD 10-DEC-1998.
PA (UYEM-) UNIV EMORY.
Query Match 1.0%; Score 7; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 5e+02;
RESULT 839
ID ABO74597 standard; protein; 111 AA.
DE Pseudomonas aeruginosa polypeptide #6772.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 1.0%; Score 7; DB 7; Length 111;
Best Local Similarity 100.0%; Pred. No. 5e+02;
RESULT 840
ID AAM99115 standard; protein; 116 AA.
DE Human zeta 2 prethrombin 2.
PN W0985130-A1.
PD 10-DEC-1998.
PA (UYEM-) UNIV EMORY.
Query Match 1.0%; Score 7; DB 2; Length 116;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;

RESULT 841
ID AAG26792 standard; protein; 117 AA.
DE Zea mays protein fragment SEQ ID NO: 31379.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 1.0%; Score 7; DB 3; Length 117;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
RESULT 842
ID AAG51373 standard; protein; 121 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 65194.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 1.0%; Score 7; DB 3; Length 121;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
RESULT 843
ID AAG26791 standard; protein; 121 AA.
DE Zea mays protein fragment SEQ ID NO: 31378.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 1.0%; Score 7; DB 3; Length 121;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
RESULT 844
ID ABO73690 standard; protein; 121 AA.
DE Pseudomonas aeruginosa polypeptide #5865.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 1.0%; Score 7; DB 7; Length 121;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
RESULT 845
ID AAG11631 standard; protein; 128 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 10420.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 1.0%; Score 7; DB 3; Length 128;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
RESULT 846
ID AAG51372 standard; protein; 128 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 65193.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 1.0%; Score 7; DB 3; Length 128;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
RESULT 847
ID AAG26790 standard; protein; 142 AA.
DE Zea mays protein fragment SEQ ID NO: 31377.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 1.0%; Score 7; DB 3; Length 142;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
RESULT 848
ID ABO63944 standard; protein; 142 AA.
DE Klebsiella pneumoniae polypeptide seqid 10461.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 1.0%; Score 7; DB 7; Length 142;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
RESULT 849
ID AAW41967 standard; protein; 144 AA.
DE Flea beetle protease SEQ ID NO: 81.
PN WO9740058-A1.
PD 30-OCT-1997.
PA (HESK-) HESKA CORP.
Query Match 1.0%; Score 7; DB 2; Length 144;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
RESULT 850
ID AAS50629 standard; protein; 144 AA.
DE US6150125-A.
PN 21-NOV-2000.
PA (HESK-) HESKA CORP.
Query Match 1.0%; Score 7; DB 4; Length 144;

Best Local Similarity 100.0%; Pred. No. 6.3e+02;
RESULT 851
ID AAU64494 standard; protein; 148 AA.
DE Propionibacterium acnes immunogenic protein #25390.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (COR-) CORIXA CORP.
Query Match 1.0%; Score 7; DB 4; Length 148;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
RESULT 852
ID AAM61013 standard; protein; 148 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #25689.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (COR-) CORIXA CORP.
Query Match 1.0%; Score 7; DB 6; Length 148;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
RESULT 853
ID AAG51371 standard; protein; 151 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 65192.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 1.0%; Score 7; DB 3; Length 151;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
RESULT 854
ID ADI45291 standard; protein; 164 AA.
DE Rice isoprenoid biosynthesis-associated protein #111.
PN US2004010815-A1.
PD 15-JAN-2004.
PA (LANG/) LANGE B M.
PA (GHAS/) GHASEMIAN M.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B J.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREBS J.
PA (MOUG/) MOUGHAMER T.
PA (PROV/) PROVART N.
PA (RICK/) RICKES D.
PA (ZHUT/) ZHU T.
Query Match 1.0%; Score 7; DB 8; Length 164;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
RESULT 855
ID AA334950 standard; protein; 172 AA.
DE Amino acid sequence of a Chlamydia pneumoniae protein.
PN WO9927105-A2.
PD 03-JUN-1999.
PA (GENST-) GENSET.
Query Match 1.0%; Score 7; DB 2; Length 172;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
RESULT 856
ID ABU39246 standard; protein; 172 AA.
DE Protein encoded by Prokaryotic essential gene #24773.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITPA PHARM INC.
Query Match 1.0%; Score 7; DB 6; Length 172;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
RESULT 857
ID AAG51370 standard; protein; 184 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 65190.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 1.0%; Score 7; DB 3; Length 184;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
RESULT 858
ID ADC97109 standard; protein; 187 AA.
DE E. faecium protein sequence SEQ ID 6736.
PN US6583275-B1.
PD 24-JUN-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 1.0%; Score 7; DB 7; Length 187;

Best Local Similarity 100.0%; Pred. No. 8e+02;
RESULT 859
ID AAU25597 standard; protein; 194 AA.
DE Human G Protein-Coupled Receptor (GPCR) polypeptide #44.
PN WC200162797-A2.
PD 30-AUG-2001.
PA (PHMA) PHARMACIA & UPJOHN CO.
Query Match 1.0%; Score 7; DB 4; Length 194;
Best Local Similarity 100.0%; Pred. No. 8.3e+02;
RESULT 860
ID AAU29491 standard; protein; 200 AA.
DE Human G protein-coupled receptor (GPCR) polypeptide #112.
PN WC200168858-A2.
PD 20-SEP-2001.
PA (PHAA) PHARMACIA & UPJOHN CO.
Query Match 1.0%; Score 7; DB 4; Length 200;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
RESULT 861
ID ABG60779 standard; protein; 200 AA.
DE Novel G protein coupled receptor (nGPCR-x) #112.
PN US2002058306-A1.
PD 16-MAY-2002.
PA (VOGE/) VOGELI G.
Query Match 1.0%; Score 7; DB 5; Length 200;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
RESULT 862
ID AB865610 standard; protein; 202 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 23622.
PN WC200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 1.0%; Score 7; DB 4; Length 202;
Best Local Similarity 100.0%; Pred. No. 8.6e+02;
RESULT 863
ID ADR09068 standard; protein; 202 AA.
DE Human protein useful for treating neurological disease Seq 2574.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 1.0%; Score 7; DB 8; Length 202;
Best Local Similarity 100.0%; Pred. No. 8.6e+02;
RESULT 864
ID AAU45202 standard; protein; 209 AA.
DE Propionibacterium acnes immunogenic protein #6098.
PN WC200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 1.0%; Score 7; DB 4; Length 209;
Best Local Similarity 100.0%; Pred. No. 8.9e+02;
RESULT 865
ID ABM41721 standard; protein; 209 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #6397.
PN WC2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 1.0%; Score 7; DB 6; Length 209;
Best Local Similarity 100.0%; Pred. No. 8.9e+02;
RESULT 866
ID AAY35451 standard; protein; 210 AA.
DE Chlamydia pneumoniae transmembrane protein sequence.
PN WC09927105-A2.
PD 03-JUN-1999.
PA (GEST) GENSET.
Query Match 1.0%; Score 7; DB 2; Length 210;
Best Local Similarity 100.0%; Pred. No. 8.9e+02;
RESULT 867
ID ABU27599 standard; protein; 210 AA.
DE Protein encoded by prokaryotic essential gene #13126.
PN WC200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 1.0%; Score 7; DB 6; Length 210;
Best Local Similarity 100.0%; Pred. No. 8.9e+02;
RESULT 868
ID ADS41665 standard; protein; 210 AA.
DE Bacterial polypeptide #20095.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOV/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 1.0%; Score 7; DB 8; Length 210;
Best Local Similarity 100.0%; Pred. No. 8.9e+02;
RESULT 869
ID ABU4962 standard; protein; 211 AA.
DE Protein encoded by prokaryotic essential gene #35489.
PN WC200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 1.0%; Score 7; DB 6; Length 211;
Best Local Similarity 100.0%; Pred. No. 9e+02;
RESULT 870
ID AAU34556 standard; protein; 212 AA.
DE E. coli cellular proliferation protein #137.
PN WC200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 1.0%; Score 7; DB 4; Length 212;
Best Local Similarity 100.0%; Pred. No. 9e+02;
RESULT 871
ID ABU31486 standard; protein; 212 AA.
DE Protein encoded by prokaryotic essential gene #17013.
PN WC200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 1.0%; Score 7; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 9e+02;
RESULT 872
ID ABU48063 standard; protein; 212 AA.
DE Protein encoded by prokaryotic essential gene #33590.
PN WC200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 1.0%; Score 7; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 9e+02;
RESULT 873
ID ABU15066 standard; protein; 212 AA.
DE Protein encoded by prokaryotic essential gene #593.
PN WC200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 1.0%; Score 7; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 9e+02;
RESULT 874
ID ABU45471 standard; protein; 212 AA.
DE Protein encoded by prokaryotic essential gene #30998.
PN WC200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 1.0%; Score 7; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 9e+02;
RESULT 875
ID ABB54972 standard; protein; 213 AA.
DE Lactococcus lactis protein kdga.
PN FR2807446-A1.
PD 12-OCT-2001.
PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
Query Match 1.0%; Score 7; DB 5; Length 213;
Best Local Similarity 100.0%; Pred. No. 9e+02;
RESULT 876
ID ABU40559 standard; protein; 213 AA.
DE Protein encoded by prokaryotic essential gene #26086.
PN WC200277183-A2.
PD 03-OCT-2002.

PA (ELIT-) ELITRA PHARM INC.
Query Match 1.0%; Score 7; DB 6; Length 213;
Best Local Similarity 100.0%; Pred. No. 9e+02;
RESULT 877
ID ADF04315 standard; protein; 214 AA.
DE Bacterial polypeptide #428.
PN US6605709-B1.
PD 12-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 1.0%; Score 7; DB 7; Length 214;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
RESULT 878
ID ABB65059 standard; protein; 221 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 21969.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 1.0%; Score 7; DB 4; Length 221;
Best Local Similarity 100.0%; Pred. No. 9.3e+02;
RESULT 879
ID ADR49443 standard; protein; 221 AA.
DE Drosophila small endoplasmic reticulum resident protein 3 (emerp3).
PN EP1447412-A1.
PD 18-AUG-2004.
PA (UTUT-) UNIV UTRECHT HOLDING BV.
Query Match 1.0%; Score 7; DB 8; Length 221;
Best Local Similarity 100.0%; Pred. No. 9.3e+02;
RESULT 880
ID ABO61145 standard; protein; 226 AA.
DE Klebsiella pneumoniae polypeptide seqid 7662.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 1.0%; Score 7; DB 7; Length 226;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
RESULT 881
ID AAG51369 standard; protein; 227 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 65189.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 1.0%; Score 7; DB 3; Length 227;
Best Local Similarity 100.0%; Pred. No. 9.6e+02;
RESULT 882
ID AAB92525 standard; protein; 227 AA.
DE Human protein sequence SEQ ID NO:10677.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 1.0%; Score 7; DB 4; Length 227;
Best Local Similarity 100.0%; Pred. No. 9.6e+02;
RESULT 883
ID ABU40124 standard; protein; 227 AA.
DE Protein encoded by Prokaryotic essential gene #25651.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 1.0%; Score 7; DB 6; Length 227;
Best Local Similarity 100.0%; Pred. No. 9.6e+02;
RESULT 884
ID AAG15809 standard; protein; 228 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 16207.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 1.0%; Score 7; DB 3; Length 228;
Best Local Similarity 100.0%; Pred. No. 9.6e+02;
RESULT 885
ID ABU41513 standard; protein; 228 AA.
DE Protein encoded by Prokaryotic essential gene #27040.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 1.0%; Score 7; DB 6; Length 228;
Best Local Similarity 100.0%; Pred. No. 9.6e+02;
RESULT 886
ID AAG33373 standard; protein; 230 AA.
DE Zea mays protein fragment SEQ ID NO: 40426.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 1.0%; Score 7; DB 3; Length 230;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
RESULT 887
ID ABU27062 standard; protein; 231 AA.
DE Protein encoded by Prokaryotic essential gene #12589.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 1.0%; Score 7; DB 6; Length 231;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
RESULT 888
ID AAU33655 standard; protein; 232 AA.
DE Pseudomonas aeruginosa cellular proliferation protein #99.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 1.0%; Score 7; DB 4; Length 232;
Best Local Similarity 100.0%; Pred. No. 9.8e+02;
RESULT 889
ID ABU15506 standard; protein; 232 AA.
DE Protein encoded by Prokaryotic essential gene #1033.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 1.0%; Score 7; DB 6; Length 232;
Best Local Similarity 100.0%; Pred. No. 9.8e+02;
RESULT 890
ID AAW41957 standard; protein; 233 AA.
DE Flea serine protease SEQ ID NO:27.
PN WO9740058-A1.
PD 30-OCT-1997.
PA (HESK-) HESKA CORP.
Query Match 1.0%; Score 7; DB 2; Length 233;
Best Local Similarity 100.0%; Pred. No. 9.8e+02;
RESULT 891
ID AAG51368 standard; protein; 234 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 65188.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 1.0%; Score 7; DB 3; Length 234;
Best Local Similarity 100.0%; Pred. No. 9.8e+02;
RESULT 892
ID AAG15808 standard; protein; 235 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 16206.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 1.0%; Score 7; DB 3; Length 235;
Best Local Similarity 100.0%; Pred. No. 9.9e+02;
RESULT 893
ID AAG33372 standard; protein; 237 AA.
DE Zea mays protein fragment SEQ ID NO: 40425.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 1.0%; Score 7; DB 3; Length 237;
Best Local Similarity 100.0%; Pred. No. 1e+03;
RESULT 894
ID ABU49459 standard; protein; 239 AA.
DE Protein encoded by Prokaryotic essential gene #34986.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 1.0%; Score 7; DB 6; Length 239;
Best Local Similarity 100.0%; Pred. No. 1e+03;
RESULT 895
ID AAG33371 standard; protein; 241 AA.
DE Zea mays protein fragment SEQ ID NO: 40424.
PN EP1033405-A2.
PD 06-SEP-2000.

Query Match 1.0%; Score 7; DB 3; Length 241;
Best Local Similarity 100.0%; Pred. No. 1e+03;
RESULT 896
ID ABO77745 standard; protein: 245 AA.
DE Pseudomonas aeruginosa polypeptide #9920.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 1.0%; Score 7; DB 7; Length 245;
Best Local Similarity 100.0%; Pred. No. 1e+03;
RESULT 897
ID ADC73285 standard; protein: 254 AA.
DE Human 187H_H protein - SEQ ID 11.
PN WO2003060765-A1.
PD 24-JUL-2003.
PA (AJIN) AJINOMOTO CO INC.
PA (UMEV) UMEVAMA H.
Query Match 1.0%; Score 7; DB 7; Length 254;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 898
ID ADK17097 standard; protein: 254 AA.
DE Nanocarchaeum equitans cancer-associated (CA) protein #524.
PN WO2003093434-A2.
PD 13-NOV-2003.
PA (DIVE-) DIVERSA CORP.
Query Match 1.0%; Score 7; DB 8; Length 254;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 899
ID ADL05143 standard; protein: 255 AA.
DE M. catarrhalis protein #909.
PN US6673910-B1.
PD 06-JAN-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 1.0%; Score 7; DB 8; Length 255;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 900
ID AAV38252 standard; protein: 257 AA.
DE Salmonella typhi cellular proliferation protein #143.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 1.0%; Score 7; DB 4; Length 257;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 901
ID ADA35762 standard; protein: 257 AA.
DE Acinetobacter baumannii protein #2923.
PN US6562958-B1.
PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 1.0%; Score 7; DB 6; Length 257;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 902
ID AAG15607 standard; protein: 258 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 16205.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 1.0%; Score 7; DB 3; Length 258;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 903
ID AAW1545 standard; protein: 259 AA.
DE Human thrombin Aen9 mutant.
PN WO9641868-A2.
PD 27-DEC-1996.
PA (IMMO) IMMO AG.
Query Match 1.0%; Score 7; DB 2; Length 259;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 904
ID ABB60565 standard; protein: 259 AA.
DE Human thrombin variant W215A/E217A B-chain.
PN WO2002100337-A2.
PD 19-DEC-2002.
PA (UYEM-) UNIV EMORY.
Query Match 1.0%; Score 7; DB 6; Length 259;

Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 905
ID ABB60563 standard; protein: 259 AA.
DE Human thrombin variant W215A B-chain.
PN WO2002100337-A2.
PD 19-DEC-2002.
PA (UYEM-) UNIV EMORY.
Query Match 1.0%; Score 7; DB 6; Length 259;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 906
ID AAW72891 standard; protein: 265 AA.
DE Mycobacterium tuberculosis antigen CFP29.
PN WO984419-A1.
PD 08-OCT-1998.
PA (STAT-) STATENS SERUM INST.
Query Match 1.0%; Score 7; DB 2; Length 265;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 907
ID AAY21908 standard; protein: 265 AA.
DE Amino acid sequence of antigen CFP29.
PN WO9924577-A1.
PD 20-MAY-1999.
PA (STAT-) STATENS SERUM INST.
Query Match 1.0%; Score 7; DB 2; Length 265;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 908
ID AAW1956 standard; protein: 266 AA.
DE Flea serine protease SEQ ID NO: 24.
PN WO9740058-A1.
PD 30-OCT-1997.
PA (HESK-) HESKA CORP.
Query Match 1.0%; Score 7; DB 2; Length 266;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 909
ID AAO17669 standard; protein: 266 AA.
DE B tropicalis allergen B10 3 protein SEQ ID NO: 4.
PN WO200230968-A1.
PD 18-APR-2002.
PA (UYSI-) UNIV SINGAPORE NAT.
Query Match 1.0%; Score 7; DB 5; Length 266;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 910
ID AAO17668 standard; protein: 266 AA.
DE B tropicalis allergen B10 3 protein SEQ ID NO: 2.
PN WO200230968-A1.
PD 18-APR-2002.
PA (UYSI-) UNIV SINGAPORE NAT.
Query Match 1.0%; Score 7; DB 5; Length 266;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 911
ID AAB62510 standard; protein: 268 AA.
DE Flea serine protease F1SP2_268.
PN US6204010-B1.
PD 20-MAR-2001.
PA (HESK-) HESKA CORP.
Query Match 1.0%; Score 7; DB 4; Length 268;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 912
ID ADB69394 standard; protein: 271 AA.
DE Human heat mitochondrial protein as a therapeutic target Segid1200.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
Query Match 1.0%; Score 7; DB 7; Length 271;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 913
ID ADO21743 standard; protein: 271 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 4563.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 1.0%; Score 7; DB 8; Length 271;

Best Local Similarity	100.0%;	Pred. No. 1.1e+03;
RESULT 914		
ID AAR61421 standard; protein; 280 AA.		
DE <i>Propionibacterium acnes</i> immunogenic protein #22317.		
PN WO200181581-A2.		
PD 01-NOV-2001.		
PA (CORI-) CORIXA CORP.		
Query Match	1.0%;	Score 7; DB 4; Length 280;
Best Local Similarity	100.0%;	Pred. No. 1.2e+03;
RESULT 915		
ID ABM57940 standard; protein; 280 AA.		
DE <i>Propionibacterium acnes</i> predicted ORF-encoded polypeptide		
PN WO2003033515-A1.		
PD 24-APR-2003.		
PA (CORI-) CORIXA CORP.		
Query Match	1.0%;	Score 7; DB 6; Length 280;
Best Local Similarity	100.0%;	Pred. No. 1.2e+03;
RESULT 916		
ID AAR82700 standard; protein; 284 AA.		
DE Tick derived serine protease protein sequence #1.		
PN JP2000083677-A.		
PD 28-MAR-2000.		
PA (FARB) BAYER KK.		
Query Match	1.0%;	Score 7; DB 3; Length 284;
Best Local Similarity	100.0%;	Pred. No. 1.2e+03;
RESULT 917		
ID AAR74778 standard; protein; 295 AA.		
DE Mutant thrombin E229F.		
PN WO9513385-A2.		
PD 18-MAY-1995.		
PA (GILE-) GILEAD SCT.		
Query Match	1.0%;	Score 7; DB 2; Length 295;
Best Local Similarity	100.0%;	Pred. No. 1.2e+03;
RESULT 918		
ID AAR76033 standard; protein; 295 AA.		
DE Mutant thrombin E229Y.		
PN WO9513385-A2.		
PD 18-MAY-1995.		
PA (GILE-) GILEAD SCT.		
Query Match	1.0%;	Score 7; DB 2; Length 295;
Best Local Similarity	100.0%;	Pred. No. 1.2e+03;
RESULT 919		
ID AAR74776 standard; protein; 295 AA.		
DE Mutant thrombin K52A, R233A.		
PN WO9513385-A2.		
PD 18-MAY-1995.		
PA (GILE-) GILEAD SCT.		
Query Match	1.0%;	Score 7; DB 2; Length 295;
Best Local Similarity	100.0%;	Pred. No. 1.2e+03;
RESULT 920		
ID AAR76038 standard; protein; 295 AA.		
DE Mutant thrombin K52C.		
PN WO9513385-A2.		
PD 18-MAY-1995.		
PA (GILE-) GILEAD SCT.		
Query Match	1.0%;	Score 7; DB 2; Length 295;
Best Local Similarity	100.0%;	Pred. No. 1.2e+03;
RESULT 921		
ID AAR76039 standard; protein; 295 AA.		
DE Mutant thrombin W50E.		
PN WO9513385-A2.		
PD 18-MAY-1995.		
PA (GILE-) GILEAD SCT.		
Query Match	1.0%;	Score 7; DB 2; Length 295;
Best Local Similarity	100.0%;	Pred. No. 1.2e+03;
RESULT 922		
ID AAR74779 standard; protein; 295 AA.		
DE Mutant thrombin E229S.		
PN WO9513385-A2.		
PD 18-MAY-1995.		
PA (GILE-) GILEAD SCT.		
Query Match	1.0%;	Score 7; DB 2; Length 295;
Best Local Similarity	100.0%;	Pred. No. 1.2e+03;
RESULT 923		
ID AAR74779 standard; protein; 295 AA.		
DE Mutant thrombin E229S.		
PN WO9513385-A2.		
PD 18-MAY-1995.		
PA (GILE-) GILEAD SCT.		
Query Match	1.0%;	Score 7; DB 2; Length 295;
Best Local Similarity	100.0%;	Pred. No. 1.2e+03;

RESULT 923	ID	AA76035 standard; protein; 295 AA.
	DE	Mutant thrombin R233D.
	PN	WO9513385-A2.
	PD	18-MAY-1995.
	PA	(GILE-) GILEAD SCI.
Query Match		1.0%; Score 7; DB 2; Length 295;
Best Local Similarity		100.0%; Pred. No. 1.2e+03;
RESULT 924	ID	AA74775 standard; protein; 295 AA.
	DE	wild-type thrombin.
	PN	WO9513385-A2.
	PD	18-MAY-1995.
	PA	(GILE-) GILEAD SCI.
Query Match		1.0%; Score 7; DB 2; Length 295;
Best Local Similarity		100.0%; Pred. No. 1.2e+03;
RESULT 925	ID	AA74780 standard; protein; 295 AA.
	DE	Mutant thrombin E223W.
	PN	WO9513385-A2.
	PD	18-MAY-1995.
	PA	(GILE-) GILEAD SCI.
Query Match		1.0%; Score 7; DB 2; Length 295;
Best Local Similarity		100.0%; Pred. No. 1.2e+03;
RESULT 926	ID	AA76036 standard; protein; 295 AA.
	DE	Mutant thrombin R233F.
	PN	WO9513385-A2.
	PD	18-MAY-1995.
	PA	(GILE-) GILEAD SCI.
Query Match		1.0%; Score 7; DB 2; Length 295;
Best Local Similarity		100.0%; Pred. No. 1.2e+03;
RESULT 927	ID	AA74777 standard; protein; 295 AA.
	DE	Mutant thrombin E223D.
	PN	WO9513385-A2.
	PD	18-MAY-1995.
	PA	(GILE-) GILEAD SCI.
Query Match		1.0%; Score 7; DB 2; Length 295;
Best Local Similarity		100.0%; Pred. No. 1.2e+03;
RESULT 928	ID	AA76034 standard; protein; 295 AA.
	DE	Mutant thrombin R233N.
	PN	WO9513385-A2.
	PD	18-MAY-1995.
	PA	(GILE-) GILEAD SCI.
Query Match		1.0%; Score 7; DB 2; Length 295;
Best Local Similarity		100.0%; Pred. No. 1.2e+03;
RESULT 929	ID	AA76040 standard; protein; 295 AA.
	DE	Mutant thrombin W50K.
	PN	WO9513385-A2.
	PD	18-MAY-1995.
	PA	(GILE-) GILEAD SCI.
Query Match		1.0%; Score 7; DB 2; Length 295;
Best Local Similarity		100.0%; Pred. No. 1.2e+03;
RESULT 930	ID	AA76037 standard; protein; 295 AA.
	DE	Mutant thrombin W50C.
	PN	WO9513385-A2.
	PD	18-MAY-1995.
	PA	(GILE-) GILEAD SCI.
Query Match		1.0%; Score 7; DB 2; Length 295;
Best Local Similarity		100.0%; Pred. No. 1.2e+03;
RESULT 931	ID	AAW2892 standard; protein; 295 AA.
	DE	Human mature thrombin mutant Gly274Ala.
	PN	DE19605126-A1.
	PD	14-AUG-1997.
	PA	(BADI-) BASF AG.
Query Match		1.0%; Score 7; DB 2; Length 295;
Best Local Similarity		100.0%; Pred. No. 1.2e+03;
RESULT 932	ID	AAW2892 standard; protein; 295 AA.
	DE	Mutant thrombin R233D.
	PN	WO9513385-A2.
	PD	18-MAY-1995.
	PA	(GILE-) GILEAD SCI.
Query Match		1.0%; Score 7; DB 2; Length 295;
Best Local Similarity		100.0%; Pred. No. 1.2e+03;
RESULT 933	ID	AAW2892 standard; protein; 295 AA.
	DE	Mutant thrombin R233D.
	PN	WO9513385-A2.
	PD	18-MAY-1995.
	PA	(GILE-) GILEAD SCI.
Query Match		1.0%; Score 7; DB 2; Length 295;
Best Local Similarity		100.0%; Pred. No. 1.2e+03;
RESULT 934	ID	AAW2892 standard; protein; 295 AA.
	DE	Mutant thrombin R233D.
	PN	WO9513385-A2.
	PD	18-MAY-1995.
	PA	(GILE-) GILEAD SCI.
Query Match		1.0%; Score 7; DB 2; Length 295;
Best Local Similarity		100.0%; Pred. No. 1.2e+03;
RESULT 935	ID	AAW2892 standard; protein; 295 AA.
	DE	Mutant thrombin R233D.
	PN	WO9513385-A2.
	PD	18-MAY-1995.
	PA	(GILE-) GILEAD SCI.
Query Match		1.0%; Score 7; DB 2; Length 295;
Best Local Similarity		100.0%; Pred. No. 1.2e+03;
RESULT 936	ID	AAW2892 standard; protein; 295 AA.
	DE	Mutant thrombin R233D.
	PN	WO9513385-A2.
	PD	18-MAY-1995.
	PA	(GILE-) GILEAD SCI.
Query Match		1.0%; Score 7; DB 2; Length 295;
Best Local Similarity		100.0%; Pred. No. 1.2e+03;
RESULT 937	ID	AAW2892 standard; protein; 295 AA.
	DE	Mutant thrombin R233D.
	PN	WO9513385-A2.
	PD	18-MAY-1995.
	PA	(GILE-) GILEAD SCI.
Query Match		1.0%; Score 7; DB 2; Length 295;
Best Local Similarity		100.0%; Pred. No. 1.2e+03;
RESULT 938	ID	AAW2892 standard; protein; 295 AA.
	DE	Mutant thrombin R233D.
	PN	WO9513385-A2.
	PD	18-MAY-1995.
	PA	(GILE-) GILEAD SCI.
Query Match		1.0%; Score 7; DB 2; Length 295;
Best Local Similarity		100.0%; Pred. No. 1.2e+03;
RESULT 939	ID	AAW2892 standard; protein; 295 AA.
	DE	Mutant thrombin R233D.
	PN	WO9513385-A2.
	PD	18-MAY-1995.
	PA	(GILE-) GILEAD SCI.
Query Match		1.0%; Score 7; DB 2; Length 295;
Best Local Similarity		100.0%; Pred. No. 1.2e+03;
RESULT 940	ID	AAW2892 standard; protein; 295 AA.
	DE	Mutant thrombin R233D.
	PN	WO9513385-A2.
	PD	18-MAY-1995.
	PA	(GILE-) GILEAD SCI.
Query Match		1.0%; Score 7; DB 2; Length 295;
Best Local Similarity		100.0%; Pred. No. 1.2e+03;
RESULT 941	ID	AAW2892 standard; protein;

ID AAB08633 standard; protein; 295 AA.
DE Amino acid sequence of a wild type human thrombin.
PN US6110721-A.
PD 29-AUG-2000.
PA (GILE-) GILEAD SCI INC.
Query Match 1.0%; Score 7; DB 3; Length 295;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
RESULT 933
ID AAB60562 standard; protein; 295 AA.
DE Human thrombin variant W215A.
PN WO2002100337-A2.
PD 19-DEC-2002.
PA (UYEM-) UNIV EMORY.
Query Match 1.0%; Score 7; DB 6; Length 295;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
RESULT 934
ID AAB60564 standard; protein; 295 AA.
DE Human thrombin variant W215A/E217A.
PN WO2002100337-A2.
PD 19-DEC-2002.
PA (UYEM-) UNIV EMORY.
Query Match 1.0%; Score 7; DB 6; Length 295;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
RESULT 935
ID ADS11062 standard; protein; 295 AA.
DE Human therapeutic protein - SEQ ID 1299.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Query Match 1.0%; Score 7; DB 8; Length 295;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
RESULT 936
ID AAO17678 standard; protein; 296 AA.
DE B tropicalis allergen Bloc 3 polymorphic variant protein SEQ ID NO: 40.
PN WO200230968-A1.
PD 18-APR-2002.
PA (UYSI-) UNIV SINGAPORE NAT.
Query Match 1.0%; Score 7; DB 5; Length 296;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
RESULT 937
ID AAO17676 standard; protein; 296 AA.
DE B tropicalis allergen Bloc 3 polymorphic variant protein SEQ ID NO: 38.
PN WO200230968-A1.
PD 18-APR-2002.
PA (UYSI-) UNIV SINGAPORE NAT.
Query Match 1.0%; Score 7; DB 5; Length 296;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
RESULT 938
ID AAO17677 standard; protein; 296 AA.
DE B tropicalis allergen Bloc 3 polymorphic variant protein SEQ ID NO: 39.
PN WO200230968-A1.
PD 18-APR-2002.
PA (UYSI-) UNIV SINGAPORE NAT.
Query Match 1.0%; Score 7; DB 5; Length 296;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
RESULT 939
ID AAM99107 standard; protein; 308 AA.
DE Bovine prethrombin 2.
PN WO9855130-A1.
PD 10-DEC-1998.
PA (UYEM-) UNIV EMORY.
Query Match 1.0%; Score 7; DB 2; Length 308;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
RESULT 940
ID AAM99109 standard; protein; 308 AA.
DE Human prethrombin 2.
PN WO9855130-A1.
PD 10-DEC-1998.
PA (UYEM-) UNIV EMORY.
Query Match 1.0%; Score 7; DB 2; Length 308;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
RESULT 941
ID AAB87820 standard; protein; 308 AA.

DE Mouse T2R26 amino acid sequence SEQ ID NO:155.
PN WO200118050-A2.
PD 15-MAR-2001.
PA (REGC) UNIV CALIFORNIA.
PA (USHS) US DEPT HEALTH & HUMAN SERVICES.
Query Match 1.0%; Score 7; DB 4; Length 308;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
RESULT 942
ID ADR29216 standard; protein; 308 AA.
DE Taste receptor modulation-related mouse T2R26 protein sequence SeqID155.
PN WO2004069191-A2.
PD 19-AUG-2004.
PA (SENO-) SENOMYX INC.
Query Match 1.0%; Score 7; DB 8; Length 308;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
RESULT 943
ID ADC94558 standard; protein; 310 AA.
DE E. faecium protein sequence SEQ ID 4185.
PN US6583275-B1.
PD 24-JUN-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 1.0%; Score 7; DB 7; Length 310;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
RESULT 944
ID ABR52886 standard; protein; 312 AA.
DE Protein sequence #SEQ ID 637.
PN EP1258494-A1.
PD 20-NOV-2002.
PA (CELL-) CELLSOME AG.
Query Match 1.0%; Score 7; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
RESULT 945
ID ADK62400 standard; protein; 312 AA.
DE Disease treating protein complex-derived protein #326.
PN EP1338608-A2.
PD 27-AUG-2003.
PA (CELL-) CELLSOME AG.
Query Match 1.0%; Score 7; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
RESULT 946
ID ADC73300 standard; protein; 313 AA.
DE Stereostucture-related IBTH protein.
PN WO2003060765-A1.
PD 24-JUL-2003.
PA (AJIN) AJINOMOTO CO INC.
PA (UMERY) UMERYAMA H.
Query Match 1.0%; Score 7; DB 7; Length 313;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
RESULT 947
ID AAB72885 standard; protein; 314 AA.
DE Murine ztrypl.
PN WO200112788-A2.
PD 22-FEB-2001.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 1.0%; Score 7; DB 4; Length 314;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
RESULT 948
ID ABU62253 standard; protein; 314 AA.
DE Mouse tryptase-like polypeptide Ztryp-1.
PN US6514741-B1.
PD 04-FEB-2003.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 1.0%; Score 7; DB 6; Length 314;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
RESULT 949
ID ABR62454 standard; protein; 314 AA.
DE Bovine recombinant prethrombin-2, expressed in Escherichia coli.
PN WO2003052059-A2.
PD 26-JUN-2003.
PA (ELIT) LILLY & CO ELI.
Query Match 1.0%; Score 7; DB 7; Length 314;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
RESULT 950

ID ABR62456 standard; protein; 314 AA.
DE Bovine Factor Xa activated recombinant prethrombin-2.
PN WO2003052059-A2.
PD 26-JUN-2003.
PA (ELIL) LILLY & CO ELI.
Query Match 1.0%; Score 7; DB 7; Length 314;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
RESULT 951
ID ABR62453 standard; protein; 314 AA.
DE Bovine thrombin.
PN WO2003052059-A2.
PD 26-JUN-2003.
PA (ELIL) LILLY & CO ELI.
Query Match 1.0%; Score 7; DB 7; Length 314;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
RESULT 952
ID ABR62450 standard; protein; 314 AA.
DE Bovine recombinant prethrombin-2, expressed in Escherichia coli.
PN WO2003052059-A2.
PD 26-JUN-2003.
PA (ELIL) LILLY & CO ELI.
Query Match 1.0%; Score 7; DB 7; Length 314;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
RESULT 953
ID ADCl7377 standard; protein; 314 AA.
DE Mouse serine protease ztlypl.
PN US2003119035-A1.
PD 26-JUN-2003.
PA (ZYMO-) ZYMOGENETICS INC.
Query Match 1.0%; Score 7; DB 7; Length 314;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
RESULT 954
ID ABP41695 standard; protein; 324 AA.
DE Human ovarian antigen HNTB23, SEQ ID NO:2827.
PN WO200200677-A1.
PD 03-JAN-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.0%; Score 7; DB 5; Length 324;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
RESULT 955
ID ADS27176 standard; protein; 330 AA.
DE Bacterial polypeptide #16209.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 1.0%; Score 7; DB 8; Length 330;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
RESULT 956
ID ADS26796 standard; protein; 330 AA.
DE Bacterial polypeptide #15829.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 1.0%; Score 7; DB 8; Length 330;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
RESULT 957
ID AAB87793 standard; protein; 332 AA.
DE Rat T2R13 amino acid sequence SEQ ID NO:101.
PN WO200118050-A2.
PD 15-MAR-2001.
PA (REGC) UNIV CALIFORNIA.
PA (USHS) US DEPT HEALTH & HUMAN SERVICES.
Query Match 1.0%; Score 7; DB 4; Length 332;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
RESULT 958

ID ADR29162 standard; protein; 332 AA.
DE Taste receptor modulation-related rat T2R13 protein sequence SeqId101.
PN WO2004069191-A2.
PD 19-AUG-2004.
PA (SENO-) SENOMYX INC.
Query Match 1.0%; Score 7; DB 8; Length 332;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
RESULT 959
ID ADS26428 standard; protein; 332 AA.
DE Bacterial polypeptide #15461.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 1.0%; Score 7; DB 8; Length 332;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
RESULT 960
ID ADJ49544 standard; protein; 336 AA.
DE Oil-associated gene related protein #1044.
PN US2004025202-A1.
PD 05-FEB-2004.
PA (LAUR/) LAURIE C C.
PA (RAVA/) RAVANELLO M.
PA (SAVA/) SAVAGE T.
PA (LEDE/) LEDEAUX J R.
PA (ROGE/) ROGERS J A.
Query Match 1.0%; Score 7; DB 8; Length 336;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
RESULT 961
ID ADJ49561 standard; protein; 338 AA.
DE Oil-associated gene related protein #1061.
PN US2004025202-A1.
PD 05-FEB-2004.
PA (LAUR/) LAURIE C C.
PA (RAVA/) RAVANELLO M.
PA (SAVA/) SAVAGE T.
PA (LEDE/) LEDEAUX J R.
PA (ROGE/) ROGERS J A.
Query Match 1.0%; Score 7; DB 8; Length 338;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
RESULT 962
ID ADC31358 standard; protein; 357 AA.
DE Human novel polypeptide sequence, SEQ ID NO:1440.
PN WO2003029271-A2.
PD 10-APR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 1.0%; Score 7; DB 7; Length 357;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
RESULT 963
ID ADR09339 standard; protein; 357 AA.
DE Human protein useful for treating neurological disease Seq 2845.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 1.0%; Score 7; DB 8; Length 357;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
RESULT 964
ID ABR62452 standard; protein; 362 AA.
DE Bovine recombinant prethrombin-2, expressed in CHO cells.
PN WO2003052059-A2.
PD 26-JUN-2003.
PA (ELIL) LILLY & CO ELI.
Query Match 1.0%; Score 7; DB 7; Length 362;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
RESULT 965
ID AAY38815 standard; protein; 375 AA.
DE Neisseria meningitidis strain A antigen encoded by ORF146.
PN WO9924578-A2.
PD 20-MAY-1999.
PA (CHIR-) CHIRON SPA.

Query Match 1.0%; Score 7; DB 2; Length 375;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
RESULT 966
ID AAY3814 standard; protein; 375 AA.
DE Neisseria meningitidis antigen encoded by ORF146.
PN W0924578-A2.
PD 20-MAY-1999.
PA (CHIR-) CHIRON SPA.
Query Match 1.0%; Score 7; DB 2; Length 375;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
RESULT 967
ID AAY3817 standard; protein; 375 AA.
DE Neisseria gonorrhoeae antigenic protein encoded by ORF146.
PN W0924578-A2.
PD 20-MAY-1999.
PA (CHIR-) CHIRON SPA.
Query Match 1.0%; Score 7; DB 2; Length 375;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
RESULT 968
ID AAY75445 standard; protein; 375 AA.
DE Neisseria gonorrhoeae ORF 706 protein sequence SEQ ID NO:2364.
PN W0924578-A2.
PD 11-NOV-1999.
PA (CHIR-) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
Query Match 1.0%; Score 7; DB 3; Length 375;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
RESULT 969
ID AAY75446 standard; protein; 375 AA.
DE Neisseria meningitidis ORF 706 protein sequence SEQ ID NO:2366.
PN W0924578-A2.
PD 11-NOV-1999.
PA (CHIR-) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
Query Match 1.0%; Score 7; DB 3; Length 375;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
RESULT 970
ID AAY75447 standard; protein; 375 AA.
DE Neisseria meningitidis ORF 706 protein sequence SEQ ID NO:2368.
PN W0924578-A2.
PD 11-NOV-1999.
PA (CHIR-) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
Query Match 1.0%; Score 7; DB 3; Length 375;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
RESULT 971
ID AAY72957 standard; protein; 375 AA.
DE Neisseria meningitidis virulence protein #47.
PN W0200185772-A2.
PD 15-NOV-2001.
PA (MICR-) MICROSCIENCE LTD.
Query Match 1.0%; Score 7; DB 5; Length 375;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
RESULT 972
ID AAR4197 standard; protein; 376 AA.
DE CD4/Thrombin fusion protein.
PN W09318162-A1.
PD 16-SEP-1993.
PA (CREA-) CREAGEN INC.
Query Match 1.0%; Score 7; DB 2; Length 376;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
RESULT 973
ID AAY42789 standard; protein; 376 AA.
DE Human CD4/thrombin fusion protein.
PN US5961973-A.
PD 05-OCT-1999.
PA (CREA/) CREA R.
Query Match 1.0%; Score 7; DB 2; Length 376;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
RESULT 974
ID AAU10703 standard; protein; 376 AA.
DE Human CD4-thrombin fusion protein.
PN US6287561-B1.

PD 11-SEP-2001.
PA (CREA/) CREA R.
Query Match 1.0%; Score 7; DB 5; Length 376;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
RESULT 975
ID AAG21667 standard; protein; 398 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 24304.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 1.0%; Score 7; DB 3; Length 398;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
RESULT 976
ID ABO80228 standard; protein; 399 AA.
DE Pseudomonas aeruginosa polypeptide #12403.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 1.0%; Score 7; DB 7; Length 399;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
RESULT 977
ID AAY3816 standard; protein; 409 AA.
DE Neisseria gonorrhoeae antigen encoded by partial ORF146.
PN W0924578-A2.
PD 20-MAY-1999.
PA (CHIR-) CHIRON SPA.
Query Match 1.0%; Score 7; DB 2; Length 409;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
RESULT 978
ID ABB0460 standard; protein; 409 AA.
DE N. gonorrhoeae amino acid sequence SEQ ID 7450.
PN W0200279243-A2.
PD 10-OCT-2002.
PA (CHIR-) CHIRON SPA.
Query Match 1.0%; Score 7; DB 6; Length 409;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
RESULT 979
ID ABB79601 standard; protein; 409 AA.
DE N. gonorrhoeae amino acid sequence SEQ ID 5732.
PN W0200279243-A2.
PD 10-OCT-2002.
PA (CHIR-) CHIRON SPA.
Query Match 1.0%; Score 7; DB 6; Length 409;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
RESULT 980
ID ABB37254 standard; protein; 409 AA.
DE Protein encoded by Prokaryotic essential gene #22781.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 1.0%; Score 7; DB 6; Length 409;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
RESULT 981
ID ADD1516 standard; protein; 420 AA.
DE Fruitfly odorant receptor protein (Seqid 68).
PN W02003020913-A2.
PD 13-MAR-2003.
PA (SENT-) SENTIGEN CORP.
Query Match 1.0%; Score 7; DB 7; Length 420;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
RESULT 982
ID ABO65926 standard; protein; 422 AA.
DE Klebsiella pneumoniae polypeptide seqid 12443.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 1.0%; Score 7; DB 7; Length 422;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
RESULT 983
ID AAB03444 standard; protein; 426 AA.
DE Candida albicans essential growth protein #2.
PN W0200034481-A2.
PD 15-JUN-2000.
PA (JANC) JANSSEN PHARM NV.

Query Match 1.0%; Score 7; DB 3; Length 426;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
RESULT 984
ID AB061095 standard; protein; 437 AA.
DE Klebsiella pneumoniae polypeptide seqid 7612.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 1.0%; Score 7; DB 7; Length 437;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
RESULT 985
ID A0134680 standard; protein; 443 AA.
DE Protein encoded by Prokaryotic essential gene #20207.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 1.0%; Score 7; DB 6; Length 443;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
RESULT 986
ID ABU17062 standard; protein; 444 AA.
DE Protein encoded by Prokaryotic essential gene #2589.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 1.0%; Score 7; DB 6; Length 444;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
RESULT 987
ID ADA34407 standard; protein; 448 AA.
DE Acinetobacter baumannii protein #1568.
PN US6562958-B1.
PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 1.0%; Score 7; DB 6; Length 448;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
RESULT 988
ID AAG21666 standard; protein; 452 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 24303.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 1.0%; Score 7; DB 3; Length 452;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
RESULT 989
ID AAE26435 standard; protein; 456 AA.
DE Drosophila melanogaster odorant receptor DOR28.
PN W0200050566-A2.
PD 31-AUG-2000.
PA (UNIV) UNIV COLUMBIA NEW YORK.
Query Match 1.0%; Score 7; DB 3; Length 456;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
RESULT 990
ID ABB64797 standard; protein; 456 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 21183.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 1.0%; Score 7; DB 4; Length 456;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
RESULT 991
ID ADJ32828 standard; protein; 459 AA.
DE Human prethrembin protein.
PN US200332414-A1.
PD 18-DEC-2003.
PA (MOOR/) MOORE M D.
Query Match 1.0%; Score 7; DB 8; Length 459;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
RESULT 992
ID AB033733 standard; protein; 461 AA.
DE Protein encoded by Prokaryotic essential gene #19260.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 1.0%; Score 7; DB 6; Length 461;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;

RESULT 993
ID AB036990 standard; protein; 461 AA.
DE Protein encoded by Prokaryotic essential gene #22517.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 1.0%; Score 7; DB 6; Length 461;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
RESULT 994
ID AAB60460 standard; protein; 463 AA.
DE Human cell cycle and proliferation protein CCYPR-8, SEQ ID NO:8.
PN W0200107471-A2.
PD 01-FEB-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 1.0%; Score 7; DB 4; Length 463;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
RESULT 995
ID ADP23764 standard; protein; 463 AA.
DE PRO polypeptide SEQ ID NO:942.
PN W02004041170-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 1.0%; Score 7; DB 8; Length 463;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
RESULT 996
ID ABW73357 standard; protein; 465 AA.
DE Staphylococcus aureus protein #2597.
PN W0200294868-A2.
PD 28-NOV-2002.
PA (CHIR-) CHIRON SPA.
Query Match 1.0%; Score 7; DB 6; Length 465;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
RESULT 997
ID ADJ50012 standard; protein; 465 AA.
DE Oil-associated gene related protein #1512.
PN US2004025202-A1.
PD 05-FEB-2004.
PA (LAUR/) LAURIE C C.
PA (RAVA/) RAVANELLO M.
PA (SAVA/) SAVAGE T.
PA (LEDE/) LEDEAUX J R.
PA (ROGE/) ROGERS J A.
Query Match 1.0%; Score 7; DB 8; Length 465;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
RESULT 998
ID ADN21085 standard; protein; 467 AA.
DE Bacterial polypeptide #3738.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 1.0%; Score 7; DB 8; Length 467;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
RESULT 999
ID AAG21665 standard; protein; 469 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 24302.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 1.0%; Score 7; DB 3; Length 469;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
RESULT 1000
ID ABW72219 standard; protein; 469 AA.
DE Staphylococcus aureus protein #1459.
PN W0200294868-A2.
PD 28-NOV-2002.
PA (CHIR-) CHIRON SPA.
Query Match 1.0%; Score 7; DB 6; Length 469;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
RESULT 1001
ID ADK41715 standard; protein; 470 AA.

DE Soybean amino acid transporter protein.
PN WO2003066879-A2.
PD 14-AUG-2003.
PA (MONS) MONSANTO TECHNOLOGY LLC.
Query Match
Best Local Similarity 1.0%; Score 7; DB 7; Length 470;
Pred. No. 1.9e+03;
RESULT 1002
ID AAY20047 standard; protein; 481 AA.
DE B. burgdorferi antigenic protein, t352.aa.
PN WO9859071-A1.
PD 30-DEC-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (MEDI-) MEDIMMUNE INC.
Query Match
Best Local Similarity 1.0%; Score 7; DB 2; Length 481;
Pred. No. 1.9e+03;
RESULT 1003
ID AAM68866 standard; protein; 492 AA.
DE Photorehabdus luminescens protein sequence #1963.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match
Best Local Similarity 1.0%; Score 7; DB 6; Length 492;
Pred. No. 1.9e+03;
RESULT 1004
ID ABO84661 standard; protein; 494 AA.
DE Mouse cancer-associated protein MP20-004.1.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match
Best Local Similarity 1.0%; Score 7; DB 8; Length 494;
Pred. No. 1.9e+03;
RESULT 1005
ID AAW72030 standard; protein; 497 AA.
DE HSV-2 strain SBS Contig ID 103 ORF#8 protein.
PN WO9820016-A1.
PD 14-MAY-1998.
PA (SMIK) SMITHKLINE BEECHAM CORP.
Query Match
Best Local Similarity 1.0%; Score 7; DB 2; Length 497;
Pred. No. 2e+03;
RESULT 1006
ID AAW72132 standard; protein; 497 AA.
DE HSV-2 strain SBS Contig ID 16 ORF#8 protein.
PN WO9820016-A1.
PD 14-MAY-1998.
PA (SMIK) SMITHKLINE BEECHAM CORP.
Query Match
Best Local Similarity 1.0%; Score 7; DB 2; Length 497;
Pred. No. 2e+03;
RESULT 1007
ID AAY20046 standard; protein; 497 AA.
DE B. burgdorferi antigenic protein, f352.aa.
PN WO9859071-A1.
PD 30-DEC-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (MEDI-) MEDIMMUNE INC.
Query Match
Best Local Similarity 1.0%; Score 7; DB 2; Length 497;
Pred. No. 2e+03;
RESULT 1008
ID AAB27287 standard; protein; 497 AA.
DE Streptococcus polypeptide SEQ ID NO 3750.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match
Best Local Similarity 1.0%; Score 7; DB 5; Length 497;
Pred. No. 2e+03;
RESULT 1009
ID ABO23531 standard; protein; 497 AA.
DE Borrelia burgdorferi outer protein #1.
PN US2003039963-A1.
PD 27-FEB-2003.
PA (BRAH/) BRAHMACHARI S K.
PA (RAMA/) RAMACHANDRAN S.

PA (NAND/) NANDI T.
PA (BHIM/) BHIMARAO C.
Query Match
Best Local Similarity 1.0%; Score 7; DB 7; Length 497;
Pred. No. 2e+03;
RESULT 1010
ID AAU16169 standard; protein; 498 AA.
DE Human novel secreted protein, Seq ID 1122.
PN WO200155322-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 1.0%; Score 7; DB 4; Length 498;
Pred. No. 2e+03;
RESULT 1011
ID ABU55238 standard; protein; 498 AA.
DE Human novel polypeptide #325.
PN US2002133753-A1.
PD 19-SEP-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match
Best Local Similarity 1.0%; Score 7; DB 6; Length 498;
Pred. No. 2e+03;
RESULT 1012
ID ADS41994 standard; protein; 500 AA.
DE Bacterial polypeptide #20424.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 1.0%; Score 7; DB 8; Length 500;
Pred. No. 2e+03;
RESULT 1013
ID ABU01365 standard; protein; 502 AA.
DE S. pneumoniae type 4 strain protein from coding region #940.
PN WO200277021-A2.
PD 03-OCT-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match
Best Local Similarity 1.0%; Score 7; DB 6; Length 502;
Pred. No. 2e+03;
RESULT 1014
ID ABB81378 standard; protein; 502 AA.
DE Streptococcus pneumoniae polypeptide SEQ ID NO 295.
PN WO200283855-A2.
PD 24-OCT-2002.
PA (AMCY) AMERICAN CYANAMID CO.
Query Match
Best Local Similarity 1.0%; Score 7; DB 6; Length 502;
Pred. No. 2e+03;
RESULT 1015
ID AAY00189 standard; protein; 503 AA.
DE Enterococcus faecalis antigenic polypeptide fragment EF094.
PN WO9850554-A2.
PD 12-NOV-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 1.0%; Score 7; DB 2; Length 503;
Pred. No. 2e+03;
RESULT 1016
ID ABB43408 standard; protein; 503 AA.
DE E. faecalis EF094 antigenic fragment.
PN US2002045737-A1.
PD 18-APR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 1.0%; Score 7; DB 5; Length 503;
Pred. No. 2e+03;
RESULT 1017
ID ABU88436 standard; protein; 503 AA.
DE E. faecalis novel protein #180.
PN US2003017495-A1.
PD 23-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.

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Query Match          1.0%; Score 7; DB 6; Length 503;
Best Local Similarity 100.0%; Pred. No. 2e+03;
RESULT 1018
ID ABU13687 standard; protein: 503 AA.
DE Enterococcus faecalis EF040 polypeptide #180.
PN US648043-B1.
PD 10-SEP-2002.
PA (HUMA-) HUMAN GENOME SCT INC.
Query Match
Best Local Similarity 1.0%; Score 7; DB 6; Length 503;
RESULT 1019
ID AAB68138 standard; protein: 504 AA.
DE Amino acid sequence of a partial murine SP64 polypeptide.
PN FR2798138-A1.
PD 09-MAR-2001.
PA (CNRS ) CNRS CENT NAT RECH SCI.
Query Match
Best Local Similarity 1.0%; Score 7; DB 4; Length 504;
RESULT 1020
ID AAG29530 standard; protein: 508 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 35152.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 1.0%; Score 7; DB 3; Length 508;
RESULT 1021
ID ABUS4588 standard; protein: 509 AA.
DE Human NOVX polypeptide #47.
PN WO200281498-A2.
PD 17-OCT-2002.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 1.0%; Score 7; DB 6; Length 509;
RESULT 1022
ID ADS22207 standard; protein: 513 AA.
DE Bacterial polypeptide #11240.
PN US200333675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 1.0%; Score 7; DB 8; Length 513;
RESULT 1023
ID AAE20968 standard; protein: 517 AA.
DE Staphylococcus aureus von Willebrand factor binding protein (vwb).
PN WO200228882-A1.
PD 11-APR-2002.
PA (BIOS-) BIOSTAPRO AB.
Query Match
Best Local Similarity 1.0%; Score 7; DB 5; Length 517;
RESULT 1024
ID ABUS5877 standard; protein: 518 AA.
DE Mouse notch ligand jagged 2 protein.
PN WO200277204-A2.
PD 03-OCT-2002.
PA (AXOR-) AXORDIA LTD.
Query Match
Best Local Similarity 1.0%; Score 7; DB 6; Length 518;
RESULT 1025
ID AAG34033 standard; protein: 518 AA.
DE Murine notch ligand jagged 2 protein.
PN WO200290992-A2.
PD 14-NOV-2002.
PA (AXOR-) AXORDIA LTD.
Query Match
Best Local Similarity 1.0%; Score 7; DB 6; Length 518;
RESULT 1026
ID ABO75124 standard; protein: 525 AA.
DE Pseudomonas aeruginosa polypeptide #7299.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 1.0%; Score 7; DB 7; Length 525;
RESULT 1027
ID ADO26850 standard; protein: 525 AA.
DE Human receptor and membrane-associated protein, REMAP-40.
PN WO2004044159-A2.
PD 27-MAY-2004.
PA (INCY-) INCYTE CORP.
Query Match
Best Local Similarity 1.0%; Score 7; DB 8; Length 525;
RESULT 1028
ID ABB58809 standard; protein: 542 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 3219.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE ) PE CORP NY.
Query Match
Best Local Similarity 1.0%; Score 7; DB 4; Length 542;
RESULT 1029
ID ADN21059 standard; protein: 543 AA.
DE Bacterial polypeptide #3712.
PN US200333675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 1.0%; Score 7; DB 8; Length 543;
RESULT 1030
ID AAU37798 standard; protein: 553 AA.
DE Streptococcus pneumoniae cellular proliferation protein #227.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 1.0%; Score 7; DB 4; Length 553;
RESULT 1031
ID AAM01018 standard; protein: 553 AA.
DE CFE 17 protein sequence.
PN WO200149721-A2.
PD 12-JUL-2001.
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.
Query Match
Best Local Similarity 1.0%; Score 7; DB 4; Length 553;
RESULT 1032
ID ABU00989 standard; protein: 553 AA.
DE S. pneumoniae type 4 strain protein from coding region #558.
PN WO200277021-A2.
PD 03-OCT-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match
Best Local Similarity 1.0%; Score 7; DB 6; Length 553;
RESULT 1033
ID ABU45930 standard; protein: 553 AA.
DE Protein encoded by Prokaryotic essential gene #31457.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 1.0%; Score 7; DB 6; Length 553;
RESULT 1034
ID ADK48791 standard; protein: 553 AA.
DE Streptococcus pneumoniae protein, Seq ID No 5306.
PN US6699703-B1.
PD 02-MAR-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 1.0%; Score 7; DB 8; Length 553;
PD 02-MAR-2004.
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RESULT 1035
ID AAG29529 standard; protein; 555 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 35151.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 1.0%; Score 7; DB 3; Length 555;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
RESULT 1036
ID AAU08803 standard; protein; 556 AA.
DE Human phosphatidyl glycerol phosphate (PGP) synthase.
PN W0200164895-A2.
PD 07-SEP-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 1.0%; Score 7; DB 4; Length 556;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
RESULT 1037
ID ADCL14217 standard; protein; 556 AA.
DE Human enzyme ENZM-23.
PN W02003042357-A2.
PD 22-MAY-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 1.0%; Score 7; DB 7; Length 556;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
RESULT 1038
ID ADJ57901 standard; protein; 556 AA.
DE Human 27411 PGP synthase protein.
PN US2004009553-A1.
PD 15-JAN-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 1.0%; Score 7; DB 8; Length 556;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
RESULT 1039
ID APB61060 standard; protein; 557 AA.
DE Lactobacillus rhamnosus HN001 polypeptide SEQ ID NO 120.
PN W0200244383-A1.
PD 06-JUN-2002.
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (VIAL-) VIALACTIA BIOSCIENCE NZ LTD.
Query Match 1.0%; Score 7; DB 5; Length 557;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
RESULT 1040
ID ADR95837 standard; protein; 558 AA.
DE Novel S. pneumoniae protein sequence, SEQ ID 4472.
PN US6800744-B1.
PD 05-OCT-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 1.0%; Score 7; DB 8; Length 558;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
RESULT 1041
ID ABP75529 standard; protein; 563 AA.
DE Human secretory polypeptide SPTM SEQ ID NO 713.
PN W0200283876-A2.
PD 24-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 1.0%; Score 7; DB 6; Length 563;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
RESULT 1042
ID ABU18645 standard; protein; 573 AA.
DE Protein encoded by prokaryotic essential gene #4172.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 1.0%; Score 7; DB 6; Length 573;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
RESULT 1043
ID AAR35763 standard; protein; 579 AA.
DE Prothrombin (PT).
PN W09309804-A1.
PD 27-MAY-1993.
PA (Scri) SCRIPPS RES INST.
Query Match 1.0%; Score 7; DB 2; Length 579;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
RESULT 1044

ID AAM11544 standard; protein; 579 AA.
DE Human prothrombin Asn419 mutant.
PN W09641868-A2.
PD 27-DEC-1996.
PA (IMMO) IMMUNO AG.
Query Match 1.0%; Score 7; DB 2; Length 579;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
RESULT 1045
ID AAM11546 standard; protein; 579 AA.
DE Human prothrombin mutant (generic sequence).
PN W09641868-A2.
PD 27-DEC-1996.
PA (IMMO) IMMUNO AG.
Query Match 1.0%; Score 7; DB 2; Length 579;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
RESULT 1046
ID AAM99108 standard; protein; 579 AA.
DE Human prothrombin.
PN W0985130-A1.
PD 10-DEC-1998.
PA (VYEM-) UNIV EMORY.
Query Match 1.0%; Score 7; DB 2; Length 579;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
RESULT 1047
ID AD133974 standard; protein; 579 AA.
DE Human meizothrombin analogue mature protein.
PN W02004007714-A1.
PD 22-JAN-2004.
PA (ASAH) ASAH KASEI KK.
Query Match 1.0%; Score 7; DB 8; Length 579;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
RESULT 1048
ID AAM99106 standard; protein; 582 AA.
DE Bovine prothrombin.
PN W0985130-A1.
PD 10-DEC-1998.
PA (VYEM-) UNIV EMORY.
Query Match 1.0%; Score 7; DB 2; Length 582;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
RESULT 1049
ID AAG29528 standard; protein; 582 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 35150.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 1.0%; Score 7; DB 3; Length 582;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
RESULT 1050
ID ABR62449 standard; protein; 583 AA.
DE Bovine recombinant prothrombin, expressed in Escherichia coli.
PN W02003052059-A2.
PD 26-JUN-2003.
PA (ELIT-) LILLY & CO ELI.
Query Match 1.0%; Score 7; DB 7; Length 583;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
RESULT 1051
ID ADS28808 standard; protein; 588 AA.
DE Bacterial polypeptide #17841.
PN US200233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 1.0%; Score 7; DB 8; Length 588;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
RESULT 1052
ID ABB66001 standard; protein; 603 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 24795.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 1.0%; Score 7; DB 4; Length 603;

Best Local Similarity 100.0%; Pred. No. 2.3e+03;
RESULT 1053
ID AAR38741 standard; protein; 615 AA.
DE Human prothrombin.
PN WO9313208-A1.
PD 08-JUL-1993.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 1.0%; Score 7; DB 2; Length 615;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
RESULT 1054
ID AAR90377 standard; protein; 615 AA.
DE Human prothrombin.
PN US5476777-A.
PD 19-DEC-1995.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 1.0%; Score 7; DB 2; Length 615;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
RESULT 1055
ID AAR96216 standard; protein; 615 AA.
DE Human prothrombin.
PN US5502034-A.
PD 26-MAR-1996.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 1.0%; Score 7; DB 2; Length 615;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
RESULT 1056
ID AAR68137 standard; protein; 616 AA.
DE Amino acid sequence of the human SPG4 polypeptide.
PN FR2798183-A1.
PD 09-MAR-2001.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 1.0%; Score 7; DB 4; Length 616;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
RESULT 1057
ID AAW11543 standard; protein; 622 AA.
DE Human preprothrombin (wild-type).
PN WO9641868-A2.
PD 27-DEC-1996.
PA (IMMO) IMMO AG.
Query Match 1.0%; Score 7; DB 2; Length 622;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
RESULT 1058
ID AAT49566 standard; protein; 622 AA.
DE Platelet membrane glycoprotein IIIa beta subunit protein sequence.
PN WO9590454-A2.
PD 07-OCT-1999.
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
Query Match 1.0%; Score 7; DB 2; Length 622;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
RESULT 1059
ID ABG74671 standard; protein; 622 AA.
DE Human F2 protein.
PN WO2003016494-A2.
PD 27-FEB-2003.
PA (VITI-) VITIVITY INC.
Query Match 1.0%; Score 7; DB 6; Length 622;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
RESULT 1060
ID ADB88551 standard; protein; 622 AA.
DE Human Factor 2, F2, protein, SEQ ID 2.
PN WO2003029493-A1.
PD 10-APR-2003.
PA (VITI-) VITIVITY INC.
Query Match 1.0%; Score 7; DB 7; Length 622;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
RESULT 1061
ID ADL18196 standard; protein; 622 AA.
DE Human coagulation factor II protein SEQ ID NO:116.
PN WO2003014381-A1.
PD 20-FEB-2003.
PA (AHRA-) AHRAW BIOSYSTEMS INC.
Query Match 1.0%; Score 7; DB 7; Length 622;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
RESULT 1062
ID ADI33975 standard; protein; 622 AA.
DE Human meizothrombin analogue full-length protein.
PN WO2004007714-A1.
PD 22-JAN-2004.
PA (ASAH) ASAH KASEI KK.
Query Match 1.0%; Score 7; DB 8; Length 622;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
RESULT 1063
ID ADQ30580 standard; protein; 622 AA.
DE Pancreas cancer marker - prothrombin precursor.
PN WO2004055519-A2.
PD 01-JUL-2004.
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
PA (SINO-) SINGENOMAX CO LTD CHINESE NAT HUMAN GEN.
Query Match 1.0%; Score 7; DB 8; Length 622;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
RESULT 1064
ID ABR62455 standard; protein; 625 AA.
DE Bovine preprothrombin.
PN WO2003052059-A2.
PD 26-JUN-2003.
PA (ELIL) LILLY & CO ELI.
Query Match 1.0%; Score 7; DB 7; Length 625;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
RESULT 1065
ID ABR62451 standard; protein; 635 AA.
DE Bovine recombinant prothrombin, expressed in CHO cells.
PN WO2003052059-A2.
PD 26-JUN-2003.
PA (ELIL) LILLY & CO ELI.
Query Match 1.0%; Score 7; DB 7; Length 635;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
RESULT 1066
ID ADI27332 standard; peptide; 638 AA.
DE Amino acid sequence of prethrombin(44S)3scfvalphaHA.
PN WO2004019878-A2.
PD 11-MAR-2004.
PA (COMP-) COMPOUND THERAPEUTICS INC.
PA (AFEV) AFEVAN N B.
Query Match 1.0%; Score 7; DB 8; Length 638;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
RESULT 1067
ID ADI27333 standard; peptide; 638 AA.
DE Amino acid sequence of schA(G4S)3prethrombin.
PN WO2004019878-A2.
PD 11-MAR-2004.
PA (COMP-) COMPOUND THERAPEUTICS INC.
PA (AFEV) AFEVAN N B.
Query Match 1.0%; Score 7; DB 8; Length 638;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
RESULT 1068
ID ABB93056 standard; protein; 658 AA.
DE Herbicidally active polypeptide SEQ ID NO 2267.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match 1.0%; Score 7; DB 5; Length 658;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
RESULT 1069
ID ABB58511 standard; protein; 683 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 2325.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 1.0%; Score 7; DB 4; Length 683;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
RESULT 1070
ID AAG30915 standard; protein; 684 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 37042.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 1.0%; Score 7; DB 3; Length 684;

Best Local Similarity 100.0%; Pred. No. 2.6e+03;
RESULT 1071
ID ABB03731 standard; protein; 696 AA.
DE Novel human diagnostic protein #3722.
PN W0200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
RESULT 1072
ID ABB22196 standard; protein; 713 AA.
DE Protein encoded by Prokaryotic essential gene #7723.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
RESULT 1073
ID ABB68587 standard; protein; 716 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 32553.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
RESULT 1074
ID AAB70937 standard; protein; 763 AA.
DE S. pombe potassium transporter TKGp protein.
PN DE19941766-A1.
PD 15-MAR-2001.
PA (LICH-) LICHTENBERG-FRATE H.
Query Match
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
RESULT 1075
ID ABB70253 standard; protein; 776 AA.
DE C. neoformans amino acid sequence SEQ ID NO:3297.
PN W02003052076-A2.
PD 26-JUN-2003.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 100.0%; Score 7; DB 7; Length 776;
RESULT 1076
ID ADS1498 standard; protein; 783 AA.
DE Pseudomonas aeruginosa quorum sensing controlled protein, SEQ ID 553.
PN W02004083385-A2.
PD 30-SEP-2004.
PA (IOWA) UNIV IOWA RES FOUND.
Query Match
Best Local Similarity 100.0%; Score 7; DB 8; Length 783;
RESULT 1077
ID ADI45247 standard; protein; 784 AA.
DE Rice isoprenoid biosynthesis-associated protein #89.
PN US2004010815-A1.
PD 15-JAN-2004.
PA (LANG-) LANGE B M.
PA (GHAS-) GHASSEMIAN M.
PA (BRIG-) BRIGGS S P.
PA (COOP-) COOPER B.
PA (GLAZ-) GLAZEBROOK J.
PA (GOFF-) GOFF S A.
PA (KATA-) KATAGIRI F.
PA (KREP-) KREPS J.
PA (MOUG-) MOUTHAMER T.
PA (PROV-) PROVART N.
PA (RICK-) RICKES D.
PA (ZHUT-) ZHU T.
Query Match
Best Local Similarity 100.0%; Score 7; DB 8; Length 784;
RESULT 1078
ID ABB58512 standard; protein; 787 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 2328.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match
Best Local Similarity 100.0%; Score 7; DB 4; Length 787;
RESULT 1079
ID AAG90377 standard; protein; 799 AA.
DE C. glutamicum protein fragment SEQ ID NO: 4131.
PN EP108790-A2.
PD 20-JUN-2001.
PA (KYOW-) KYOWA HAKKO KOGYO KK.
Query Match
Best Local Similarity 100.0%; Pred. No. 3e+03;
RESULT 1080
ID ADL65785 standard; protein; 799 AA.
DE C. glutamicum RXA-associated protein #71.
PN DE10154177-A1.
PD 08-MAY-2003.
PA (BADI-) BASF AG.
Query Match
Best Local Similarity 100.0%; Pred. No. 3e+03;
RESULT 1081
ID ABO69076 standard; protein; 805 AA.
DE Pseudomonas aeruginosa polypeptide #1251.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 100.0%; Pred. No. 3e+03;
RESULT 1082
ID AAB47019 standard; protein; 808 AA.
DE A. thaliana DGL.
PN CA2307960-A1.
PD 06-NOV-2000.
PA (UNMS) UNIV MICHIGAN STATE.
Query Match
Best Local Similarity 100.0%; Score 7; DB 4; Length 808;
RESULT 1083
ID ABB92279 standard; protein; 808 AA.
DE Herbicidially active polypeptide SEQ ID NO 1490.
PN W0200210210-A2.
PD 07-FEB-2002.
PA (PARB-) BAYER AG.
Query Match
Best Local Similarity 100.0%; Score 7; DB 5; Length 808;
RESULT 1084
ID ADB95044 standard; protein; 808 AA.
DE A. thaliana protein 21878 #SEQ ID 42.
PN W0200308440-A2.
PD 30-JAN-2003.
PA (SYGN-) SYNGENTA PARTICIPATIONS AG.
Query Match
Best Local Similarity 100.0%; Score 7; DB 7; Length 808;
RESULT 1085
ID ADJ63822 standard; protein; 808 AA.
DE Plant lipid metabolism protein PK239 SEQ ID NO:24.
PN W02004013304-A2.
PD 12-FEB-2004.
PA (BADI-) BASF PLANT SCI GMBH.
Query Match
Best Local Similarity 100.0%; Pred. No. 3e+03;
RESULT 1086
ID AAM07872 standard; protein; 859 AA.
DE Aluminum resistance gene ALR1.
PN W09634959-A1.
PD 07-NOV-1996.
PA (AUCC-) AUCCLAND UNISERVICES LTD.
Query Match
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
RESULT 1087
ID ADB08613 standard; protein; 892 AA.
DE Novel protein (useful for identifying genetic disorders) #768.
PN W02003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.

Query Match 1.0%; Score 7; DB 7; Length 892;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
RESULT 1088
ID ADE31112 standard; protein; 912 AA.
DE Human diagnostic and therapeutic polypeptide (DITHP), SEQ ID NO 244.
PN WO2003062376-A2.
PD 31-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 1.0%; Score 7; DB 7; Length 912;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
RESULT 1089
ID ABH65063 standard; protein; 921 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 21981.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 1.0%; Score 7; DB 4; Length 921;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
RESULT 1090
ID ABP62769 standard; protein; 984 AA.
DE Protein fragment #6 of S. roseosporus biosynthetic gene cluster.
PN WO200259322-A2.
PD 01-AUG-2002.
PA (MIAO/) MIAO V P W.
PA (BRIA/) BRIAN P.
PA (BALV/) BALVZ R H.
PA (SILV/) SILVA C J.
Query Match 1.0%; Score 7; DB 5; Length 984;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
RESULT 1091
ID AD721260 standard; protein; 984 AA.
DE Streptomyces roseosporus daptomycin biosynthesis gene cluster protein #6.
PN WO2003014297-A2.
PD 20-FEB-2003.
PA (CUBI-) CUBIST PHARM INC.
Query Match 1.0%; Score 7; DB 7; Length 984;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
RESULT 1092
ID ADM57327 standard; protein; 995 AA.
DE Recombinant protein production method related polypeptide SEQ ID NO: 8.
PN WO2004027067-A2.
PD 01-APR-2004.
PA (CYMO-) CYMIP AS.
Query Match 1.0%; Score 7; DB 8; Length 995;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
RESULT 1093
ID ABH93966 standard; protein; 1047 AA.
DE Hebticidally active polypeptide SEQ ID NO 3177.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match 1.0%; Score 7; DB 5; Length 1047;
Best Local Similarity 100.0%; Pred. No. 3.8e+03;
RESULT 1094
ID ABH83005 standard; protein; 1061 AA.
DE Human diagnostic and therapeutic protein SEQ ID NO:3254.
PN WO2004023373-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 1.0%; Score 7; DB 8; Length 1061;
Best Local Similarity 100.0%; Pred. No. 3.9e+03;
RESULT 1095
ID AAY00188 standard; protein; 1074 AA.
DE Enterococcus faecalis protein EF094.
PN WO9850554-A2.
PD 12-NOV-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.0%; Score 7; DB 2; Length 1074;
Best Local Similarity 100.0%; Pred. No. 3.9e+03;
RESULT 1096
ID AAY00206 standard; protein; 1074 AA.
DE Enterococcus faecalis protein EF102.
PN WO9850554-A2.

PD 12-NOV-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.0%; Score 7; DB 2; Length 1074;
Best Local Similarity 100.0%; Pred. No. 3.9e+03;
RESULT 1097
ID ABP43425 standard; protein; 1074 AA.
DE E faecalis EF102 protein.
PN US2002045737-A1.
PD 18-APR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.0%; Score 7; DB 5; Length 1074;
Best Local Similarity 100.0%; Pred. No. 3.9e+03;
RESULT 1098
ID ABP43407 standard; protein; 1074 AA.
DE E faecalis EF094 protein.
PN US2002045737-A1.
PD 18-APR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.0%; Score 7; DB 5; Length 1074;
Best Local Similarity 100.0%; Pred. No. 3.9e+03;
RESULT 1099
ID ABH88435 standard; protein; 1074 AA.
DE E faecalis novel protein #179.
PN US2003017495-A1.
PD 23-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.0%; Score 7; DB 6; Length 1074;
Best Local Similarity 100.0%; Pred. No. 3.9e+03;
RESULT 1100
ID ABH88453 standard; protein; 1074 AA.
DE E faecalis novel protein #197.
PN US2003017495-A1.
PD 23-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.0%; Score 7; DB 6; Length 1074;
Best Local Similarity 100.0%; Pred. No. 3.9e+03;
RESULT 1101
ID ABH13686 standard; protein; 1074 AA.
DE Enterococcus faecalis EF040 polypeptide #179.
PN US6448043-B1.
PD 10-SEP-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.0%; Score 7; DB 6; Length 1074;
Best Local Similarity 100.0%; Pred. No. 3.9e+03;
RESULT 1102
ID ABH13704 standard; protein; 1074 AA.
DE Enterococcus faecalis EF040 polypeptide #197.
PN US6448043-B1.
PD 10-SEP-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.0%; Score 7; DB 6; Length 1074;
Best Local Similarity 100.0%; Pred. No. 3.9e+03;
RESULT 1103
ID ADH87879 standard; protein; 1096 AA.
DE Enterococcus faecalis polypeptide #2359.
PN US6617156-B1.
PD 09-SEP-2003.
PA (DOUC/) DOUCETTE-STAMM L A.
PA (BUSM/) BUSH D.
Query Match 1.0%; Score 7; DB 7; Length 1096;
Best Local Similarity 100.0%; Pred. No. 4e+03;
RESULT 1104
ID AAE37912 standard; protein; 1104 AA.
DE Human CGPD-1 protein.
PN WO2003050253-A2.
PD 19-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 1.0%; Score 7; DB 7; Length 1104;
Best Local Similarity 100.0%; Pred. No. 4e+03;
RESULT 1105
ID AAY96613 standard; protein; 1140 AA.
DE Streptococcus pneumoniae UvrA-like protein.
PN GB2345288-A.

PD 05-JUL-2000.
PA (GLAX) GLAXO GROUP LTD.
Query Match 1.0%; Score 7; DB 3; Length 1140;
Best Local Similarity 100.0%; Pred. No. 4.2e+03;
RESULT 1106
ID ABR88899 standard; protein; 1158 AA.
DE Anopheles thioester-containing protein (TEP) 16 sequence.
PN EP1452184-A1.
PD 01-SEP-2004.
PA (EMBL-) EMBL.
Query Match 1.0%; Score 7; DB 8; Length 1158;
Best Local Similarity 100.0%; Pred. No. 4.2e+03;
RESULT 1107
ID ABR86758 standard; protein; 1240 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 27066.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 1.0%; Score 7; DB 4; Length 1240;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
RESULT 1108
ID ABR88898 standard; protein; 1340 AA.
DE Anopheles thioester-containing protein (TEP) 1 sequence.
PN EP1452184-A1.
PD 01-SEP-2004.
PA (EMBL-) EMBL.
Query Match 1.0%; Score 7; DB 8; Length 1340;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
RESULT 1109
ID AAV77195 standard; protein; 1346 AA.
DE S. venezuelae macroliide biosynthetic enzyme PkAIIV, SEQ ID NO:37.
PN W020000620-A2.
PD 06-JAN-2000.
PA (MINU) UNIV MINNESOTA.
Query Match 1.0%; Score 7; DB 3; Length 1346;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
RESULT 1110
ID AAV77203 standard; protein; 1346 AA.
DE S. venezuelae plk (macroliide biosynthesis) gene cluster protein #4.
PN W020000620-A2.
PD 06-JAN-2000.
PA (MINU) UNIV MINNESOTA.
Query Match 1.0%; Score 7; DB 3; Length 1346;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
RESULT 1111
ID AAB18640 standard; protein; 1346 AA.
DE Amino acid sequence of narbonolide synthase subunit 4 (PICAIIV).
PN US6117659-A.
PD 12-SEP-2000.
PA (KOSA-) KOSAN BIOSCIENCES INC.
Query Match 1.0%; Score 7; DB 3; Length 1346;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
RESULT 1112
ID AAV67204 standard; protein; 1346 AA.
DE Narbonolide synthase subunit 4 (PICAIIV) protein sequence.
PN W09961599-A2.
PD 02-DEC-1999.
PA (KOSA-) KOSAN BIOSCIENCES INC.
Query Match 1.0%; Score 7; DB 3; Length 1346;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
RESULT 1113
ID AAG71664 standard; protein; 1346 AA.
DE S. venezuelae narbonolide synthase subunit 4, PICAIIV.
PN W0200297062-A2.
PD 05-DEC-2002.
PA (KOSA-) KOSAN BIOSCIENCES INC.
Query Match 1.0%; Score 7; DB 6; Length 1346;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
RESULT 1114
ID AD09403 standard; protein; 1346 AA.
DE S. venezuelae narbonolide synthase subunit 4 (PICAIIV).
PN US6509455-B1.
PD 21-JAN-2003.

PA (KOSA-) KOSAN BIOSCIENCES INC.
Query Match 1.0%; Score 7; DB 6; Length 1346;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
RESULT 1115
ID ADH53447 standard; protein; 1346 AA.
DE Streptomyces venezuelae narbonolide synthase subunit 4 protein, PICAIIV.
PN US2005162262-A1.
PD 28-AUG-2003.
PA (ASHL) ASHLEY G.
PA (BETL) BETLACH M. C.
PA (BETL) BETLACH M.
PA (MCDA) MCDANIEL R.
PA (TANG) TANG L.
Query Match 1.0%; Score 7; DB 7; Length 1346;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
RESULT 1116
ID ADL91922 standard; protein; 1346 AA.
DE Streptomyces macroliide biosynthetic protein - PkIIV.
PN US2003194784-A1.
PD 16-OCT-2003.
PA (SHER) SHERMAN D. H.
PA (LIUH) LIU H.
PA (XUEY) XUE Y.
PA (ZHAO) ZHAO L.
Query Match 1.0%; Score 7; DB 8; Length 1346;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
RESULT 1117
ID ABR53267 standard; protein; 1522 AA.
DE Protein sequence #SEQ ID 1399.
PN EP1258494-A1.
PD 20-NOV-2002.
PA (CELL-) CELLZONE AG.
Query Match 1.0%; Score 7; DB 6; Length 1522;
Best Local Similarity 100.0%; Pred. No. 5.4e+03;
RESULT 1118
ID ADK63630 standard; protein; 1522 AA.
DE Disease treating protein complex-derived protein #838.
PN EP1338608-A2.
PD 27-AUG-2003.
PA (CELL-) CELLZONE AG.
Query Match 1.0%; Score 7; DB 7; Length 1522;
Best Local Similarity 100.0%; Pred. No. 5.4e+03;
RESULT 1119
ID ADM35845 standard; protein; 1522 AA.
DE Yeast Okazaki fragment endonuclease Dna2.
PN KR2002072712-A.
PD 18-SEP-2002.
PA (SEYO) SEO Y S.
Query Match 1.0%; Score 7; DB 7; Length 1522;
Best Local Similarity 100.0%; Pred. No. 5.4e+03;
RESULT 1120
ID ADS43628 standard; protein; 1522 AA.
DE Bacterial polypeptide #22058.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY) CAO Y.
PA (HINK) HINKLE G J.
PA (SLAT) SLATER S C.
PA (CHEN) CHEN X.
PA (GOLD) GOLDMAN B S.
Query Match 1.0%; Score 7; DB 8; Length 1522;
Best Local Similarity 100.0%; Pred. No. 5.4e+03;
RESULT 1121
ID ABR28343 standard; protein; 1631 AA.
DE Streptococcus polypeptide SEQ ID NO 5862.
PN W0200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 1.0%; Score 7; DB 5; Length 1631;
Best Local Similarity 100.0%; Pred. No. 5.8e+03;
RESULT 1122
ID ADG71666 standard; protein; 1666 AA.

DE Chlamydomonas reinhardtii PTB1 protein, SEQ ID NO:1.
PN JP2003265186-A.
PD 24-SEP-2003.
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
PA (UTVY) UNIV TOKYO.
Query Match 1.0%; Score 7; DB 7; Length 1666;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
RESULT 1123
ID ABB65038 standard; protein; 1662 AA.
DE Human diagnostic and therapeutic protease SEQ ID NO:5287.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 1.0%; Score 7; DB 8; Length 1662;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
RESULT 1124
ID ABB62819 standard; protein; 1663 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 15249.
PN WO20011042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 1.0%; Score 7; DB 4; Length 1663;
Best Local Similarity 100.0%; Pred. No. 6.8e+03;
RESULT 1125
ID ADB59362 standard; protein; 2910 AA.
DE Human cancer-associated (CA) protein sequence SEQ ID NO:18.
PN WO2004058288-A1.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 1.0%; Score 7; DB 8; Length 2910;
Best Local Similarity 100.0%; Pred. No. 9.8e+03;
RESULT 1126
ID ABB56630 standard; protein; 2911 AA.
DE Lung cancer-associated polypeptide #223.
PN WO200286443-A2.
PD 31-OCT-2002.
PD (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 1.0%; Score 7; DB 6; Length 2911;
Best Local Similarity 100.0%; Pred. No. 9.8e+03;
RESULT 1127
ID ABO07259 standard; protein; 2911 AA.
DE Human p53 modifying protein, SEQ ID 219.
PN WO200299122-A1.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 1.0%; Score 7; DB 6; Length 2911;
Best Local Similarity 100.0%; Pred. No. 9.8e+03;
RESULT 1128
ID ADB68615 standard; protein; 2911 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID421.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 1.0%; Score 7; DB 7; Length 2911;
Best Local Similarity 100.0%; Pred. No. 9.8e+03;
RESULT 1129
ID ADN38844 standard; protein; 2911 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:162.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 1.0%; Score 7; DB 7; Length 2911;
Best Local Similarity 100.0%; Pred. No. 9.8e+03;
RESULT 1130
ID ADQ18204 standard; protein; 2911 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 1021.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 1.0%; Score 7; DB 8; Length 2911;
Best Local Similarity 100.0%; Pred. No. 9.8e+03;
RESULT 1131
ID ABB60402 standard; protein; 2912 AA.
DE Novel human diagnostic protein #6393.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 1.0%; Score 7; DB 4; Length 2912;
Best Local Similarity 100.0%; Pred. No. 9.8e+03;
RESULT 1132
ID ABB20788 standard; protein; 3095 AA.
DE Rat C3b/C4b complement receptor like protein.
PN WO200210199-A2.
PD 07-FEB-2002.
PA (AMGE-) AMGEN INC.
Query Match 1.0%; Score 7; DB 5; Length 3095;
Best Local Similarity 100.0%; Pred. No. 1e+04;
RESULT 1133
ID AAB23749 standard; protein; 3972 AA.
DE S. avermitilis avermectin aglycon synthase protein SEQ ID NO:3.
PN WO200050605-A1.
PD 31-AUG-2000.
PA (KITA) KITASATO INST.
Query Match 1.0%; Score 7; DB 3; Length 3972;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
RESULT 1134
ID AAG65264 standard; protein; 3972 AA.
DE Streptomyces avermitilis protein SEQ ID NO: 4.
PN WO200162939-A1.
PD 30-AUG-2001.
PA (KYOW) KYOWA HAKKO KOGYO KK.
PA (KITA) KITASATO INST.
Query Match 1.0%; Score 7; DB 4; Length 3972;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
RESULT 1135
ID AAG65268 standard; protein; 3972 AA.
DE Streptomyces avermitilis protein derivative SEQ ID NO: 8.
PN WO200162939-A1.
PD 30-AUG-2001.
PA (KYOW) KYOWA HAKKO KOGYO KK.
PA (KITA) KITASATO INST.
Query Match 1.0%; Score 7; DB 4; Length 3972;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
RESULT 1136
ID ABB59051 standard; protein; 4547 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 3945.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 1.0%; Score 7; DB 4; Length 4547;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
RESULT 1137
ID ABB65685 standard; protein; 4899 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 24447.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 1.0%; Score 7; DB 4; Length 4899;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
RESULT 1138
ID ADU91934 standard; protein; 11877 AA.
DE Streptomyces venezuelae pik gene cluster protein.
PN US2003194784-A1.
PD 16-OCT-2003.
PA (SHER) SHERMAN D H.
PA (LIUH/) LIU H.
PA (XUEY/) XUE Y.
PA (ZHAO/) ZHAO L.
Query Match 1.0%; Score 7; DB 8; Length 11877;
Best Local Similarity 100.0%; Pred. No. 3.5e+04;
RESULT 1139
ID AAY77180 standard; protein; 12199 AA.
DE S. venezuelae pik gene cluster-encoded protein, SEQ ID NO:6.
PN WO200006020-A2.
PD 06-JAN-2000.

PA (MINU) UNIV MINNESOTA.
Query Match 0.8%; Score 6; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
RESULT 1140
ID AAR74921 standard; peptide: 8 AA.
DE Human 193P1E1B protein residues 173-180.
PN W0950908-A1.
PD 13-APR-1995.
PA (SUMU) SUMITOMO PHARM CO LTD.
Query Match 0.8%; Score 6; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
RESULT 1141
ID ADD99639 standard; peptide: 9 AA.
DE Human 193P1E1B protein peptide fragment 2631.
PN W02003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match 0.8%; Score 6; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
RESULT 1142
ID ADD97076 standard; peptide: 9 AA.
DE Human 193P1E1B protein peptide fragment 70.
PN W02003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match 0.8%; Score 6; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
RESULT 1143
ID ADD99119 standard; peptide: 9 AA.
DE Human 193P1E1B protein peptide fragment 2111.
PN W02003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match 0.8%; Score 6; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
RESULT 1144
ID ADD99105 standard; peptide: 9 AA.
DE Human 193P1E1B protein peptide fragment 2097.
PN W02003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match 0.8%; Score 6; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
RESULT 1145
ID ADD99567 standard; peptide: 9 AA.
DE Human 193P1E1B protein peptide fragment 2559.
PN W02003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match 0.8%; Score 6; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
RESULT 1146
ID ADD98532 standard; peptide: 9 AA.
DE Human 193P1E1B protein peptide fragment 1524.
PN W02003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match 0.8%; Score 6; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
RESULT 1147
ID ADD99106 standard; peptide: 9 AA.
DE Human 193P1E1B protein peptide fragment 2098.
PN W02003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match 0.8%; Score 6; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
RESULT 1148
ID ADD97325 standard; peptide: 9 AA.
DE Human 193P1E1B protein peptide fragment 319.
PN W02003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match 0.8%; Score 6; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
RESULT 1149
ID ADD99783 standard; peptide: 9 AA.
DE Human 193P1E1B protein peptide fragment 2775.
PN W02003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match 0.8%; Score 6; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
RESULT 1150
ID ADD99689 standard; peptide: 9 AA.
DE Human 193P1E1B protein peptide fragment 2681.
PN W02003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match 0.8%; Score 6; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
RESULT 1151
ID ADD98760 standard; peptide: 9 AA.
DE Human 193P1E1B protein peptide fragment 1752.
PN W02003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match 0.8%; Score 6; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
RESULT 1152
ID ADD99217 standard; peptide: 9 AA.
DE Human 193P1E1B protein peptide fragment 2209.
PN W02003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match 0.8%; Score 6; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
RESULT 1153
ID ADD97053 standard; peptide: 9 AA.
DE Human 193P1E1B protein peptide fragment 47.
PN W02003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match 0.8%; Score 6; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
RESULT 1154
ID ADD98456 standard; peptide: 9 AA.
DE Human 193P1E1B protein peptide fragment 1448.
PN W02003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match 0.8%; Score 6; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
RESULT 1155
ID ADD99266 standard; peptide: 9 AA.
DE Human 193P1E1B protein peptide fragment 2258.
PN W02003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match 0.8%; Score 6; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
RESULT 1156
ID ADD97623 standard; peptide: 9 AA.
DE Human 193P1E1B protein peptide fragment 617.
PN W02003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match 0.8%; Score 6; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
RESULT 1157
ID ADD97659 standard; peptide: 9 AA.
DE Human 193P1E1B protein peptide fragment 653.
PN W02003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match 0.8%; Score 6; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;

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Best Local Similarity 100.0%; Pred. No. 1.8e+06;
RESULT 1158
ID ADD99515 standard; peptide; 9 AA.
DE Human 193P1E1B protein peptide fragment 2507.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match 0.8%; Score 6; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
RESULT 1159
ID ADD99936 standard; peptide; 9 AA.
DE Human 193P1E1B protein peptide fragment 2928.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match 0.8%; Score 6; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
RESULT 1160
ID ADD97875 standard; peptide; 9 AA.
DE Human 193P1E1B protein peptide fragment 869.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match 0.8%; Score 6; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
RESULT 1161
ID ADD99235 standard; peptide; 9 AA.
DE Human 193P1E1B protein peptide fragment 2227.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match 0.8%; Score 6; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
RESULT 1162
ID ADD99455 standard; peptide; 9 AA.
DE Human 193P1E1B protein peptide fragment 2447.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match 0.8%; Score 6; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
RESULT 1163
ID ADD98169 standard; peptide; 9 AA.
DE Human 193P1E1B protein peptide fragment 1161.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match 0.8%; Score 6; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
RESULT 1164
ID ADD99017 standard; peptide; 9 AA.
DE Human 193P1E1B protein peptide fragment 2009.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match 0.8%; Score 6; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
RESULT 1165
ID ADO73283 standard; peptide; 9 AA.
DE Human 213P1F11 HLA motif bearing epitope #7382.
PN US2004019915-A1.
PD 29-JAN-2004.
PA (CHAL/) CHALITTA-EID P M.
PA (RAIT/) RAITANO A B.
PA (FARI/) FARIIS M.
PA (HUBE/) HUBERT R S.
PA (MORR/) MORRISON R K.
PA (GEWM/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match 0.8%; Score 6; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
RESULT 1166
ID ADO73127 standard; peptide; 9 AA.
DE Human 213P1F11 HLA motif bearing epitope #7226.
PN US2004019915-A1.
PD 29-JAN-2004.
PA (CHAL/) CHALITTA-EID P M.
PA (RAIT/) RAITANO A B.
PA (FARI/) FARIIS M.
PA (HUBE/) HUBERT R S.
PA (MORR/) MORRISON R K.
PA (GEWM/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match 0.8%; Score 6; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
RESULT 1167
ID ADP51254 standard; peptide; 9 AA.
DE Human 193P1E1B epitope #148.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALITTA-EID P M.
PA (FARI/) FARIIS M.
PA (HUBE/) HUBERT R S.
PA (GEWM/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match 0.8%; Score 6; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
RESULT 1168
ID ADP52033 standard; peptide; 9 AA.
DE Human 193P1E1B epitope #2227.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALITTA-EID P M.
PA (FARI/) FARIIS M.
PA (HUBE/) HUBERT R S.
PA (GEWM/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match 0.8%; Score 6; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
RESULT 1169
ID ADP52487 standard; peptide; 9 AA.
DE Human 193P1E1B epitope #2681.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALITTA-EID P M.
PA (FARI/) FARIIS M.
PA (HUBE/) HUBERT R S.
PA (GEWM/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match 0.8%; Score 6; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
RESULT 1170
ID ADP49876 standard; peptide; 9 AA.
DE Human 193P1E1B epitope #70.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALITTA-EID P M.
PA (FARI/) FARIIS M.
PA (HUBE/) HUBERT R S.
PA (GEWM/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match 0.8%; Score 6; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
RESULT 1171
ID ADP50967 standard; peptide; 9 AA.
DE Human 193P1E1B epitope #1161.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALITTA-EID P M.
PA (FARI/) FARIIS M.
PA (HUBE/) HUBERT R S.
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PA (GEWM/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e+06; Length 9;
RESULT 1172
ID ADP52437 standard; peptide; 9 AA.
DE Human 193P1E1B epitope #2631.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARIS M.
PA (HUBE/) HUBERT R S.
PA (GEWM/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e+06; Length 9;
RESULT 1173
ID ADP51917 standard; peptide; 9 AA.
DE Human 193P1E1B epitope #2111.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARIS M.
PA (HUBE/) HUBERT R S.
PA (GEWM/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e+06; Length 9;
RESULT 1174
ID ADP52734 standard; peptide; 9 AA.
DE Human 193P1E1B epitope #2928.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARIS M.
PA (HUBE/) HUBERT R S.
PA (GEWM/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e+06; Length 9;
RESULT 1175
ID ADP52064 standard; peptide; 9 AA.
DE Human 193P1E1B epitope #2258.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARIS M.
PA (HUBE/) HUBERT R S.
PA (GEWM/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e+06; Length 9;
RESULT 1176
ID ADP52313 standard; peptide; 9 AA.
DE Human 193P1E1B epitope #2507.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARIS M.
PA (HUBE/) HUBERT R S.
PA (GEWM/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e+06; Length 9;
RESULT 1177
ID ADP50125 standard; peptide; 9 AA.
DE Human 193P1E1B epitope #319.
PN US2004102407-A1.

PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARIS M.
PA (HUBE/) HUBERT R S.
PA (GEWM/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e+06; Length 9;
RESULT 1178
ID ADP51815 standard; peptide; 9 AA.
DE Human 193P1E1B epitope #2009.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARIS M.
PA (HUBE/) HUBERT R S.
PA (GEWM/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e+06; Length 9;
RESULT 1179
ID ADP51903 standard; peptide; 9 AA.
DE Human 193P1E1B epitope #2097.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARIS M.
PA (HUBE/) HUBERT R S.
PA (GEWM/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e+06; Length 9;
RESULT 1180
ID ADP51330 standard; peptide; 9 AA.
DE Human 193P1E1B epitope #1524.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARIS M.
PA (HUBE/) HUBERT R S.
PA (GEWM/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e+06; Length 9;
RESULT 1181
ID ADP52581 standard; peptide; 9 AA.
DE Human 193P1E1B epitope #2775.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARIS M.
PA (HUBE/) HUBERT R S.
PA (GEWM/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e+06; Length 9;
RESULT 1182
ID ADP52015 standard; peptide; 9 AA.
DE Human 193P1E1B epitope #2209.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARIS M.
PA (HUBE/) HUBERT R S.
PA (GEWM/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e+06; Length 9;
RESULT 1183
ID ADP50125 standard; peptide; 9 AA.
DE Human 193P1E1B epitope #319.
PN US2004102407-A1.

Best Local Similarity 100.0%; Pred. No. 1.8e+06;
RESULT 1183
ID ADP50423 standard; peptide; 9 AA.
DE Human 193P1E1B epitope #617.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARIS M.
PA (HUBE/) HUBERT R S.
PA (GEWM/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
RESULT 1184
ID ADP50675 standard; peptide; 9 AA.
DE Human 193P1E1B epitope #865.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARIS M.
PA (HUBE/) HUBERT R S.
PA (GEWM/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
RESULT 1185
ID ADP52365 standard; peptide; 9 AA.
DE Human 193P1E1B epitope #2559.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARIS M.
PA (HUBE/) HUBERT R S.
PA (GEWM/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
RESULT 1186
ID ADP51558 standard; peptide; 9 AA.
DE Human 193P1E1B epitope #1752.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARIS M.
PA (HUBE/) HUBERT R S.
PA (GEWM/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
RESULT 1187
ID ADP52253 standard; peptide; 9 AA.
DE Human 193P1E1B epitope #2447.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARIS M.
PA (HUBE/) HUBERT R S.
PA (GEWM/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
RESULT 1188
ID ADP49853 standard; peptide; 9 AA.
DE Human 193P1E1B epitope #47.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.

PA (FARI/) FARIS M.
PA (HUBE/) HUBERT R S.
PA (GEWM/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
RESULT 1189
ID ADP50459 standard; peptide; 9 AA.
DE Human 193P1E1B epitope #653.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARIS M.
PA (HUBE/) HUBERT R S.
PA (GEWM/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
RESULT 1190
ID ADP51904 standard; peptide; 9 AA.
DE Human 193P1E1B epitope #2098.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARIS M.
PA (HUBE/) HUBERT R S.
PA (GEWM/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
RESULT 1191
ID AAR59476 standard; peptide; 10 AA.
DE Neuropeptide for controlling muscle contraction.
PN JP06100590-A.
PD 12-APR-1994.
PA (SUNR) SUNTORY LTD.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1192
ID ADD97214 standard; peptide; 10 AA.
DE Human 193P1E1B protein peptide fragment 208.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1193
ID ADD98893 standard; peptide; 10 AA.
DE Human 193P1E1B protein peptide fragment 1885.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1194
ID ADE00146 standard; peptide; 10 AA.
DE Human 193P1E1B protein peptide fragment 3137.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1195
ID ADD97235 standard; peptide; 10 AA.
DE Human 193P1E1B protein peptide fragment 229.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1196

ID ADE00128 standard; peptide: 10 AA.
DE Human 193P1E1B protein peptide fragment 3119.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match 0.8%; Score 6; DB 7; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1197
ID ADE00321 standard; peptide: 10 AA.
DE Human 193P1E1B protein peptide fragment 3312.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match 0.8%; Score 6; DB 7; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1198
ID ADE08389 standard; peptide: 10 AA.
DE Human 193P1E1B protein peptide fragment 1381.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match 0.8%; Score 6; DB 7; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1199
ID ADE00477 standard; peptide: 10 AA.
DE Human 193P1E1B protein peptide fragment 3468.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match 0.8%; Score 6; DB 7; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1200
ID ADE0846 standard; peptide: 10 AA.
DE Human 193P1E1B protein peptide fragment 1038.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match 0.8%; Score 6; DB 7; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1201
ID ADE00260 standard; peptide: 10 AA.
DE Human 193P1E1B protein peptide fragment 3251.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match 0.8%; Score 6; DB 7; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1202
ID ADE097458 standard; peptide: 10 AA.
DE Human 193P1E1B protein peptide fragment 452.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match 0.8%; Score 6; DB 7; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1203
ID ADE097779 standard; peptide: 10 AA.
DE Human 193P1E1B protein peptide fragment 773.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match 0.8%; Score 6; DB 7; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1204
ID ADE097789 standard; peptide: 10 AA.
DE Human 193P1E1B protein peptide fragment 783.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match 0.8%; Score 6; DB 7; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1205
ID ADE00572 standard; peptide: 10 AA.

DE Human 193P1E1B protein peptide fragment 3563.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match 0.8%; Score 6; DB 7; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1206
ID ADE08579 standard; peptide: 10 AA.
DE Human 193P1E1B protein peptide fragment 1571.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match 0.8%; Score 6; DB 7; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1207
ID ADE08038 standard; peptide: 10 AA.
DE Human 193P1E1B protein peptide fragment 1030.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match 0.8%; Score 6; DB 7; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1208
ID ADE00277 standard; peptide: 10 AA.
DE Human 193P1E1B protein peptide fragment 3268.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match 0.8%; Score 6; DB 7; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1209
ID ADE00419 standard; peptide: 10 AA.
DE Human 193P1E1B protein peptide fragment 3410.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match 0.8%; Score 6; DB 7; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1210
ID ADE00145 standard; peptide: 10 AA.
DE Human 193P1E1B protein peptide fragment 3136.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match 0.8%; Score 6; DB 7; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1211
ID ADE097471 standard; peptide: 10 AA.
DE Human 193P1E1B protein peptide fragment 465.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match 0.8%; Score 6; DB 7; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1212
ID ADE098312 standard; peptide: 10 AA.
DE Human 193P1E1B protein peptide fragment 1304.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match 0.8%; Score 6; DB 7; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1213
ID ADE00322 standard; peptide: 10 AA.
DE Human 193P1E1B protein peptide fragment 3313.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match 0.8%; Score 6; DB 7; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1214
ID ADE097241 standard; peptide: 10 AA.
DE Human 193P1E1B protein peptide fragment 235.

PN W02003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match 0.8%; Score 6; DB 7; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1215
ID ADD97805 standard; peptide; 10 AA.
DE Human 193P1E1B protein peptide fragment 799.
PN W02003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match 0.8%; Score 6; DB 7; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1216
ID ADD97809 standard; peptide; 10 AA.
DE Human 193P1E1B protein peptide fragment 803.
PN W02003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match 0.8%; Score 6; DB 7; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1217
ID ADN14200 standard; peptide; 10 AA.
DE HIV B cell epitope #58.
PN US2003049253-A1.
PD 13-MAR-2003.
PA (LIFO/) LI P Q.
PA (CHUY/) CHU Y.
PA (OUUJ/) QIU J.
Query Match 0.8%; Score 6; DB 7; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1218
ID ADP53057 standard; peptide; 10 AA.
DE Human 193P1E1B epitope #3251.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALITA-EID P M.
PA (FARI/) FARIS M.
PA (HUBE/) HUBERT R S.
PA (GEWV/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match 0.8%; Score 6; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1219
ID ADP53216 standard; peptide; 10 AA.
DE Human 193P1E1B epitope #3410.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALITA-EID P M.
PA (FARI/) FARIS M.
PA (HUBE/) HUBERT R S.
PA (GEWV/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match 0.8%; Score 6; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1220
ID ADP52943 standard; peptide; 10 AA.
DE Human 193P1E1B epitope #3137.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALITA-EID P M.
PA (FARI/) FARIS M.
PA (HUBE/) HUBERT R S.
PA (GEWV/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match 0.8%; Score 6; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1221
ID ADP53074 standard; peptide; 10 AA.
DE Human 193P1E1B epitope #3268.

PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALITA-EID P M.
PA (FARI/) FARIS M.
PA (HUBE/) HUBERT R S.
PA (GEWV/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match 0.8%; Score 6; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1222
ID ADP53118 standard; peptide; 10 AA.
DE Human 193P1E1B epitope #3312.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALITA-EID P M.
PA (FARI/) FARIS M.
PA (HUBE/) HUBERT R S.
PA (GEWV/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match 0.8%; Score 6; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1223
ID ADP50605 standard; peptide; 10 AA.
DE Human 193P1E1B epitope #799.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALITA-EID P M.
PA (FARI/) FARIS M.
PA (HUBE/) HUBERT R S.
PA (GEWV/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match 0.8%; Score 6; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1224
ID ADP52942 standard; peptide; 10 AA.
DE Human 193P1E1B epitope #3136.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALITA-EID P M.
PA (FARI/) FARIS M.
PA (HUBE/) HUBERT R S.
PA (GEWV/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match 0.8%; Score 6; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1225
ID ADP50579 standard; peptide; 10 AA.
DE Human 193P1E1B epitope #773.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALITA-EID P M.
PA (FARI/) FARIS M.
PA (HUBE/) HUBERT R S.
PA (GEWV/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match 0.8%; Score 6; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1226
ID ADP52925 standard; peptide; 10 AA.
DE Human 193P1E1B epitope #3119.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALITA-EID P M.
PA (FARI/) FARIS M.
PA (HUBE/) HUBERT R S.
PA (GEWV/) GE W.
PA (JAKO/) JAKOBOVITS A.

Query Match 0.8%; Score 6; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1227
ID ADP50014 standard; peptide; 10 AA.
DE Human 193PIE1B epitope #208.
PD US2004102407-A1.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARI S M.
PA (HUBE/) HUBERT R S.
PA (GEMW/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match 0.8%; Score 6; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1228
ID ADP51691 standard; peptide; 10 AA.
DE Human 193PIE1B epitope #1865.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARI S M.
PA (HUBE/) HUBERT R S.
PA (GEMW/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match 0.8%; Score 6; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1229
ID ADP50035 standard; peptide; 10 AA.
DE Human 193PIE1B epitope #229.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARI S M.
PA (HUBE/) HUBERT R S.
PA (GEMW/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match 0.8%; Score 6; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1230
ID ADP53274 standard; peptide; 10 AA.
DE Human 193PIE1B epitope #3468.
PD US2004102407-A1.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARI S M.
PA (HUBE/) HUBERT R S.
PA (GEMW/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match 0.8%; Score 6; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1231
ID ADP50589 standard; peptide; 10 AA.
DE Human 193PIE1B epitope #783.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARI S M.
PA (HUBE/) HUBERT R S.
PA (GEMW/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match 0.8%; Score 6; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1232
ID ADP50609 standard; peptide; 10 AA.
DE Human 193PIE1B epitope #803.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.

PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARI S M.
PA (HUBE/) HUBERT R S.
PA (GEMW/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match 0.8%; Score 6; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1233
ID ADP53369 standard; peptide; 10 AA.
DE Human 193PIE1B epitope #3563.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARI S M.
PA (HUBE/) HUBERT R S.
PA (GEMW/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match 0.8%; Score 6; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1234
ID ADP50836 standard; peptide; 10 AA.
DE Human 193PIE1B epitope #1030.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARI S M.
PA (HUBE/) HUBERT R S.
PA (GEMW/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match 0.8%; Score 6; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1235
ID ADP51110 standard; peptide; 10 AA.
DE Human 193PIE1B epitope #1304.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARI S M.
PA (HUBE/) HUBERT R S.
PA (GEMW/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match 0.8%; Score 6; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1236
ID ADP50271 standard; peptide; 10 AA.
DE Human 193PIE1B epitope #465.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARI S M.
PA (HUBE/) HUBERT R S.
PA (GEMW/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match 0.8%; Score 6; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1237
ID ADP51377 standard; peptide; 10 AA.
DE Human 193PIE1B epitope #1571.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARI S M.
PA (HUBE/) HUBERT R S.
PA (GEMW/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match 0.8%; Score 6; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1238

ID ADP53119 standard; peptide; 10 AA.
DE Human 193P1E1B epitope #3313.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARI S M.
PA (HUBER/) HUBERT R S.
PA (GEMW/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match 0.8%; Score 6; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1239
ID ADP50041 standard; peptide; 10 AA.
DE Human 193P1E1B epitope #235.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARI S M.
PA (HUBER/) HUBERT R S.
PA (GEMW/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match 0.8%; Score 6; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1240
ID ADP50258 standard; peptide; 10 AA.
DE Human 193P1E1B epitope #452.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARI S M.
PA (HUBER/) HUBERT R S.
PA (GEMW/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match 0.8%; Score 6; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1241
ID ADP51187 standard; peptide; 10 AA.
DE Human 193P1E1B epitope #131.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARI S M.
PA (HUBER/) HUBERT R S.
PA (GEMW/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match 0.8%; Score 6; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1242
ID ADP50844 standard; peptide; 10 AA.
DE Human 193P1E1B epitope #1058.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARI S M.
PA (HUBER/) HUBERT R S.
PA (GEMW/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match 0.8%; Score 6; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 1243
ID AAR74926 standard; peptide; 11 AA.
DE Urea plasmidogen activator residues 173-182.
PN WO9509908-A1.
PD 13-APR-1995.
PA (SUMU) SUMITOMO PHARM CO LTD.
Query Match 0.8%; Score 6; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
RESULT 1244

ID AAR74924 standard; peptide; 11 AA.
DE Urea plasmidogen activator residues 173-183.
PN WO9509908-A1.
PD 13-APR-1995.
PA (SUMU) SUMITOMO PHARM CO LTD.
Query Match 0.8%; Score 6; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
RESULT 1245
ID AAB68774 standard; peptide; 11 AA.
DE Saccharopolyspora polyspora module 1 PKS peptide #1.
PN WO200104274-A2.
PD 18-JAN-2001.
PA (CHIL-) CHILDREN'S HOSPITAL OAKLAND RES INST.
Query Match 0.8%; Score 6; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
RESULT 1246
ID AAB68770 standard; peptide; 11 AA.
DE Rat FAS peptide #1.
PN WO200104274-A2.
PD 18-JAN-2001.
PA (CHIL-) CHILDREN'S HOSPITAL OAKLAND RES INST.
Query Match 0.8%; Score 6; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
RESULT 1247
ID AAB68775 standard; peptide; 11 AA.
DE Streptomyces venezuelae module 1 PKS peptide #1.
PN WO200104274-A2.
PD 18-JAN-2001.
PA (CHIL-) CHILDREN'S HOSPITAL OAKLAND RES INST.
Query Match 0.8%; Score 6; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
RESULT 1248
ID AAB68771 standard; peptide; 11 AA.
DE Human FAS peptide #1.
PN WO200104274-A2.
PD 18-JAN-2001.
PA (CHIL-) CHILDREN'S HOSPITAL OAKLAND RES INST.
Query Match 0.8%; Score 6; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
RESULT 1249
ID AAB68772 standard; peptide; 11 AA.
DE Caenorhabditis elegans FAS peptide #1.
PN WO200104274-A2.
PD 18-JAN-2001.
PA (CHIL-) CHILDREN'S HOSPITAL OAKLAND RES INST.
Query Match 0.8%; Score 6; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
RESULT 1250
ID AAF10873 standard; peptide; 11 AA.
DE Bovine uroplakin II protein fragment (1-11 amino acids).
PN US6290959-B1.
PD 18-SEP-2001.
PA (UNIV) UNIV NEW YORK STATE.
Query Match 0.8%; Score 6; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
RESULT 1251
ID AAR74922 standard; peptide; 12 AA.
DE Urea plasmidogen activator residues 173-183.
PN WO9509908-A1.
PD 13-APR-1995.
PA (SUMU) SUMITOMO PHARM CO LTD.
Query Match 0.8%; Score 6; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
RESULT 1252
ID AAW88589 standard; protein; 12 AA.
DE Secreted protein encoded by gene 56 clone HE20F09.
PN WO9854963-A2.
PD 10-DEC-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 0.8%; Score 6; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
RESULT 1253
ID ABB50356 standard; protein; 12 AA.

DE Human secreted protein encoded by gene 56 SEQ ID NO:304.
PN W0200162891-A2.
PD 30-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 0.8%; Score 6; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
RESULT 1254
ID ABR38980 standard; peptide; 12 AA.
DE Human copolymerease II alpha inhibitory protein fragment #SEQ ID 6.
PN W02003002737-A1.
PD 09-JUN-2003.
PA (RIKE-) RIKEN KK.
Query Match 0.8%; Score 6; DB 6; Length 12;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
RESULT 1255
ID ABO44613 standard; protein; 12 AA.
DE Novel human secreted protein #56.
PN US2003065160-A1.
PD 03-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 0.8%; Score 6; DB 6; Length 12;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
RESULT 1256
ID ABO26093 standard; protein; 12 AA.
DE Human protein from novel secreted protein gene 56.
PN US6525174-B1.
PD 25-FEB-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 0.8%; Score 6; DB 7; Length 12;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
RESULT 1257
ID AAB01945 standard; peptide; 13 AA.
DE Human Endothelase 2 repetitive peptide sequence.
PN W0200136604-A2.
PD 25-MAY-2001.
PA (CORV-) CORVAS INT INC.
Query Match 0.8%; Score 6; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
RESULT 1258
ID MAG98215 standard; peptide; 14 AA.
DE Human SNP associated peptide SEQ ID NO. 857.
PN W0200148245-A2.
PD 05-JUL-2001.
PA (CURA-) CURAGEN CORP.
Query Match 0.8%; Score 6; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
RESULT 1259
ID ABB56699 standard; peptide; 14 AA.
DE Human SNP related amino acid sequence SEQ ID NO:1464.
PN W0200138586-A2.
PD 31-MAY-2001.
PA (CURA-) CURAGEN CORP.
Query Match 0.8%; Score 6; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
RESULT 1260
ID ABG67423 standard; peptide; 14 AA.
DE Human ADP1 tryptic digest peptide #132.
PN W0200246767-A2.
PD 13-JUN-2002.
PA (OXFO-) OXFORD GLYSCSCIENCES UK LTD.
Query Match 0.8%; Score 6; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
RESULT 1261
ID AD23531 standard; peptide; 14 AA.
DE Alzheimer's disease-associated protein isoform tryptic peptide #140.
PN US2003064411-A1.
PD 03-APR-2003.
PA (HERA-) HERATH H M A C.
PA (PARE-) PAREKH R B.
PA (ROHL-) ROHLF C.
Query Match 0.8%; Score 6; DB 6; Length 14;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
RESULT 1262

ID ADM14199 standard; peptide; 14 AA.
DE HIV B cell epitope #57.
PN US2003049253-A1.
PD 13-MAR-2003.
PA (LIPO-) LI P Q.
PA (CHUY-) CHU Y.
PA (QIUU-) QIU J.
Query Match 0.8%; Score 6; DB 7; Length 14;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
RESULT 1263
ID ADO34385 standard; peptide; 14 AA.
DE Synthetic apolipoprotein-B mimicking peptide, SEQ ID No 162.
PN W02004043403-A2.
PD 27-MAY-2004.
PA (UABR-) UAB RES FOUND.
Query Match 0.8%; Score 6; DB 8; Length 14;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
RESULT 1264
ID ADO34421 standard; peptide; 14 AA.
DE Synthetic apolipoprotein-B mimicking peptide, SEQ ID No 198.
PN W02004043403-A2.
PD 27-MAY-2004.
PA (UABR-) UAB RES FOUND.
Query Match 0.8%; Score 6; DB 8; Length 14;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
RESULT 1265
ID AAG78745 standard; peptide; 15 AA.
DE Human ribose phosphate glycine amide synthetase 12 N-terminus.
PN W0200173065-A1.
PD 04-OCT-2001.
PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
Query Match 0.8%; Score 6; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
RESULT 1266
ID ADE00866 standard; peptide; 15 AA.
DE Human 193P1B1B protein peptide fragment 3857.
PN W02003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match 0.8%; Score 6; DB 7; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
RESULT 1267
ID ADE00911 standard; peptide; 15 AA.
DE Human 193P1B1B protein peptide fragment 3902.
PN W02003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match 0.8%; Score 6; DB 7; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
RESULT 1268
ID ADE01040 standard; peptide; 15 AA.
DE Human 193P1B1B protein peptide fragment 4031.
PN W02003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match 0.8%; Score 6; DB 7; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
RESULT 1269
ID ADE00912 standard; peptide; 15 AA.
DE Human 193P1B1B protein peptide fragment 3903.
PN W02003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match 0.8%; Score 6; DB 7; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
RESULT 1270
ID ADE00664 standard; peptide; 15 AA.
DE Human 193P1B1B protein peptide fragment 3655.
PN W02003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match 0.8%; Score 6; DB 7; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
RESULT 1271

RESULT 1271
ID ADE00810 standard; peptide; 15 AA.
DE Human 193PIE1B protein peptide fragment 3801.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match 0.8%; Score 6; DB 7; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
RESULT 1272
ID ADE00966 standard; peptide; 15 AA.
DE Human 193PIE1B protein peptide fragment 3957.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match 0.8%; Score 6; DB 7; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
RESULT 1273
ID ADE01108 standard; peptide; 15 AA.
DE Human 193PIE1B protein peptide fragment 4099.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match 0.8%; Score 6; DB 7; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
RESULT 1274
ID ADE01070 standard; peptide; 15 AA.
DE Human 193PIE1B protein peptide fragment 4061.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match 0.8%; Score 6; DB 7; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
RESULT 1275
ID ADE00825 standard; peptide; 15 AA.
DE Human 193PIE1B protein peptide fragment 3816.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match 0.8%; Score 6; DB 7; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
RESULT 1276
ID ADP53709 standard; peptide; 15 AA.
DE Human 193PIE1B epitope #3903.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALITTA-EID P M.
PA (FARI/) PARIS M.
PA (HUBE/) HUBERT R S.
PA (GEWM/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match 0.8%; Score 6; DB 8; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
RESULT 1277
ID ADP53622 standard; peptide; 15 AA.
DE Human 193PIE1B epitope #3816.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALITTA-EID P M.
PA (FARI/) PARIS M.
PA (HUBE/) HUBERT R S.
PA (GEWM/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match 0.8%; Score 6; DB 8; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
RESULT 1278
ID ADP53837 standard; peptide; 15 AA.
DE Human 193PIE1B epitope #4031.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALITTA-EID P M.
Query Match 0.8%; Score 6; DB 8; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;

PA (FARI/) PARIS M.
PA (HUBE/) HUBERT R S.
PA (GEWM/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match 0.8%; Score 6; DB 8; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
RESULT 1279
ID ADP53663 standard; peptide; 15 AA.
DE Human 193PIE1B epitope #3857.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALITTA-EID P M.
PA (FARI/) PARIS M.
PA (HUBE/) HUBERT R S.
PA (GEWM/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match 0.8%; Score 6; DB 8; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
RESULT 1280
ID ADP53763 standard; peptide; 15 AA.
DE Human 193PIE1B epitope #3957.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALITTA-EID P M.
PA (FARI/) PARIS M.
PA (HUBE/) HUBERT R S.
PA (GEWM/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match 0.8%; Score 6; DB 8; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
RESULT 1281
ID ADP53461 standard; peptide; 15 AA.
DE Human 193PIE1B epitope #3655.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALITTA-EID P M.
PA (FARI/) PARIS M.
PA (HUBE/) HUBERT R S.
PA (GEWM/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match 0.8%; Score 6; DB 8; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
RESULT 1282
ID ADP53905 standard; peptide; 15 AA.
DE Human 193PIE1B epitope #4099.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALITTA-EID P M.
PA (FARI/) PARIS M.
PA (HUBE/) HUBERT R S.
PA (GEWM/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match 0.8%; Score 6; DB 8; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
RESULT 1283
ID ADP53667 standard; peptide; 15 AA.
DE Human 193PIE1B epitope #4061.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALITTA-EID P M.
PA (FARI/) PARIS M.
PA (HUBE/) HUBERT R S.
PA (GEWM/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match 0.8%; Score 6; DB 8; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
RESULT 1284
ID ADP53607 standard; peptide; 15 AA.

DE Human 193P1E1B epitope #3801.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARI S M.
PA (HUBE/) HUBERT R S.
PA (GEMW/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match 0.8%; Score 6; DB 8; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
RESULT 1285
ID ADE53708 standard; peptide: 15 AA.
DE Human 193P1E1B epitope #3902.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARI S M.
PA (HUBE/) HUBERT R S.
PA (GEMW/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match 0.8%; Score 6; DB 8; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
RESULT 1286
ID AAR83658 standard; peptide: 17 AA.
DE Insect haemolymph antibacterial polypeptide #8.
PN WO9523513-A1.
PD 08-SEP-1995.
PA (SLOK) SLOAN KETTERING INST CANCER RES.
Query Match 0.8%; Score 6; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.6e+02;
RESULT 1287
ID AAR74918 standard; peptide: 18 AA.
DE Urea plasminogen activator residues 163-180.
PN WO9509908-A1.
PD 13-APR-1995.
PA (SUMU) SUMITOMO PHARM CO LTD.
Query Match 0.8%; Score 6; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 9e+02;
RESULT 1288
ID AAR9573 standard; peptide: 18 AA.
DE Wasp venom Bhrx-1 subunit (b).N-terminal peptide.
PN WO9616171-A1.
PD 30-MAY-1996.
PA (ZENE) ZENECA LTD.
PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
Query Match 0.8%; Score 6; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 9e+02;
RESULT 1289
ID ADI29454 standard; peptide: 19 AA.
DE ErbB ligand HB-EGF CCF/F motif peptide.
PN WO200405320-A2.
PD 15-JAN-2004.
PA (UMOR) UNIV MISSOURI.
Query Match 0.8%; Score 6; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
RESULT 1290
ID AAR83657 standard; peptide: 20 AA.
DE Insect haemolymph antibacterial polypeptide #7.
PN WO9523513-A1.
PD 08-SEP-1995.
PA (SLOK) SLOAN KETTERING INST CANCER RES.
Query Match 0.8%; Score 6; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.9e+02;
RESULT 1291
ID ABU08144 standard; peptide: 20 AA.
DE Human IL-1 RI signal peptide.
PN GB2375604-A.
PD 20-NOV-2002.
PA (WARN) WARNER LAMBERT CO.
Query Match 0.8%; Score 6; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.9e+02;

RESULT 1292
ID ADG17865 standard; peptide: 20 AA.
DE Binding affinity measurement-related peptide Segid67.
PN WO2003089662-A1.
PD 30-OCT-2003.
PA (REGC) UNIV CALIFORNIA.
Query Match 0.8%; Score 6; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.9e+02;
RESULT 1293
ID ADK52540 standard; peptide: 20 AA.
DE Fungal mycotoxin biosynthetic protein consensus sequence #2.
PN EP1329521-A1.
PD 23-JUL-2003.
PA (EVIA) EVIALIS T.
Query Match 0.8%; Score 6; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.9e+02;
RESULT 1294
ID ADN14077 standard; peptide: 20 AA.
DE HIV helper T cell epitope #44.
PN US2003049253-A1.
PD 13-MAR-2003.
PA (LIFO) LI F O.
PA (CHUY) CHU Y.
PA (QIUJ) QIU J.
Query Match 0.8%; Score 6; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.9e+02;
RESULT 1295
ID ADN14201 standard; peptide: 20 AA.
DE HIV B cell epitope #59.
PN US2003049253-A1.
PD 13-MAR-2003.
PA (LIFO) LI F O.
PA (CHUY) CHU Y.
PA (QIUJ) QIU J.
Query Match 0.8%; Score 6; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.9e+02;
RESULT 1296
ID AAB89179 standard; peptide: 21 AA.
DE HIV gp120 protein binding peptide #272.
PN WO200116182-A2.
PD 08-MAR-2001.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 0.8%; Score 6; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 1e+03;
RESULT 1297
ID AAB89181 standard; peptide: 21 AA.
DE HIV gp120 protein binding peptide #274.
PN WO200116182-A2.
PD 08-MAR-2001.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 0.8%; Score 6; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 1e+03;
RESULT 1298
ID AAB89180 standard; peptide: 21 AA.
DE HIV gp120 protein binding peptide #273.
PN WO200116182-A2.
PD 08-MAR-2001.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 0.8%; Score 6; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 1e+03;
RESULT 1299
ID AAU89796 standard; peptide: 21 AA.
DE Insulin/insulin-like growth factor receptor-binding peptide #1752.
PN WO200172771-A2.
PD 04-OCT-2001.
PA (DGIB-) DGI BIOTECHNOLOGIES LLC.
PA (NOVO) NOVO NORDISK AS.
Query Match 0.8%; Score 6; DB 5; Length 21;
Best Local Similarity 100.0%; Pred. No. 1e+03;
RESULT 1300
ID AAU89556 standard; peptide: 21 AA.
DE Insulin/insulin-like growth factor receptor-binding peptide #1512.
PN WO200172771-A2.

PD 04-OCT-2001.
PA (DGI-B-) DGI BIOTECHNOLOGIES LLC.
Query Match 0.8%; Score 6; DB 5; Length 21;
Best Local Similarity 100.0%; Pred. No. 1e+03;
RESULT 1301
ID AAM18205 standard; protein; 22 AA.
DE Peptide #4639 encoded by probe for measuring cervical gene expression.
PN WO200157278-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 1302
ID AAM47407 standard; peptide; 22 AA.
DE Peptide #57 for illustrating method of anticipating protein interaction.
PN WO200167299-A1.
PD 13-SEP-2001.
PA (DNUC) DAIICHI PHARM CO LTD.
PA (FUIT) FUJITSU LTD.
Query Match 0.8%; Score 6; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 1303
ID ABB31987 standard; peptide; 22 AA.
DE Peptide #4638 encoded by breast cell single exon nucleic acid probe.
PN WO200157271-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 1304
ID ABB22530 standard; protein; 22 AA.
DE Protein #4529 encoded by probe for measuring heart cell gene expression.
PN WO200157274-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 1305
ID AAM70365 standard; protein; 22 AA.
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 30671.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 1306
ID AAM57939 standard; protein; 22 AA.
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 30044.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 1307
ID ABB52060 standard; peptide; 22 AA.
DE Human liver peptide, SEQ ID NO 30708.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 1308
ID AAM05822 standard; protein; 22 AA.
DE Peptide #4504 encoded by probe for measuring breast gene expression.
PN WO200157270-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 1309
ID ABB28549 standard; protein; 22 AA.
DE Novel human diagnostic protein #28540.

PN WO200175067-A2.
PD 11-OCT-2001.
PA (HXSE-) HXSE INC.
Query Match 0.8%; Score 6; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 1310
ID ABB40009 standard; peptide; 22 AA.
DE Human peptide encoded by genome-derived single exon probe SEQ ID 29674.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 5; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 1311
ID AAO20901 standard; peptide; 22 AA.
DE Swine fever envelope protein E2 fragment #5.
PN WO200232453-A1.
PD 25-APR-2002.
PA (UYOI) UNIV QINGHUA.
PA (BEIJ-) BEIJING FEIKAI BIOTECH CO LTD.
Query Match 0.8%; Score 6; DB 5; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 1312
ID AAM19926 standard; protein; 23 AA.
DE Peptide #6360 encoded by probe for measuring cervical gene expression.
PN WO200157278-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 1313
ID ABB3934 standard; peptide; 23 AA.
DE Peptide #7440 encoded by human foetal liver single exon probe.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 1314
ID AAM33553 standard; protein; 23 AA.
DE Peptide #7590 encoded by probe for measuring placental gene expression.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 1315
ID ABB24479 standard; protein; 23 AA.
DE Protein #6478 encoded by probe for measuring heart cell gene expression.
PN WO200157274-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 1316
ID AAM73351 standard; protein; 23 AA.
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 33657.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 1317
ID AAM60679 standard; protein; 23 AA.
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 32784.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 1318
ID ABB55067 standard; peptide; 23 AA.
DE Human liver peptide, SEQ ID NO 33715.

PN W0200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 1319
ID A8G43304 standard; peptide; 23 AA.
DE Human peptide encoded by genome-derived single exon probe SEQ ID 32869.
PN W0200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 5; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 1320
ID AAP93093 standard; peptide; 25 AA.
DE CD4 anti-receptor peptide.
PN W08090782-A.
PD 19-OCT-1989.
PA (USDC) US SEC OF COMMERCE.
Query Match 0.8%; Score 6; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
RESULT 1321
ID AAR74927 standard; peptide; 25 AA.
DE Urea plasminogen activator residues 163-186.
PN W05090908-A1.
PD 13-APR-1995.
PA (SUMU) SUMITOMO PHARM CO LTD.
Query Match 0.8%; Score 6; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
RESULT 1322
ID AAV71483 standard; peptide; 25 AA.
DE Emt14chia chaffeensis p28 protein N-terminal signal peptide.
PN W0200032745-A2.
PD 08-JUN-2000.
PA (RERE-) RES DEV FOUND.
Query Match 0.8%; Score 6; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
RESULT 1323
ID AAU96113 standard; peptide; 25 AA.
DE S. pyogenes hyperimmune system reactive antigen SPO0287.4.
PN W02004078907-A2.
PD 16-SEP-2004.
PA (INTE-) INTERCELL AG.
Query Match 0.8%; Score 6; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
RESULT 1324
ID AOR84080 standard; peptide; 26 AA.
DE S. pyogenes hyperimmune system reactive antigen SPO0287.4.
PN W02004078907-A2.
PD 16-SEP-2004.
PA (INTE-) INTERCELL AG.
Query Match 0.8%; Score 6; DB 8; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
RESULT 1325
ID AAR11853 standard; peptide; 27 AA.
DE Bel natriuretic peptide.
PN JP03074400-A.
PD 28-MAR-1991.
PA (SMIB-) SMT BRYSTOL KK.
Query Match 0.8%; Score 6; DB 2; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
RESULT 1326
ID AAB91306 standard; peptide; 27 AA.
DE Atrial-natriuretic peptide (ANP) SEQ ID NO:482.
PN W0200069900-A2.
PD 23-NOV-2000.
PA (CONU-) CONUCHEM INC.
Query Match 0.8%; Score 6; DB 4; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
RESULT 1327
ID AAB91315 standard; peptide; 27 AA.
DE Atrial-natriuretic peptide (ANP) SEQ ID NO:491.

PN W0200069900-A2.
PD 23-NOV-2000.
PA (CONU-) CONUCHEM INC.
Query Match 0.8%; Score 6; DB 4; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
RESULT 1328
ID AAB91325 standard; peptide; 27 AA.
DE Atrial-natriuretic peptide (ANP) SEQ ID NO:501.
PN W0200069900-A2.
PD 23-NOV-2000.
PA (CONU-) CONUCHEM INC.
Query Match 0.8%; Score 6; DB 4; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
RESULT 1329
ID AAR26346 standard; peptide; 28 AA.
DE Spacer oligopeptide D28.
PN JP04190791-A.
PD 09-JUL-1992.
PA (SUMU) SUMITOMO SEIYAKU KK.
Query Match 0.8%; Score 6; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
RESULT 1330
ID AAR71663 standard; peptide; 29 AA.
DE Modified urinary plasminogen activator residues 159-188.
PN JP07039374-A.
PD 10-FEB-1995.
PA (SUMU) SUMITOMO SEIYAKU KK.
Query Match 0.8%; Score 6; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
RESULT 1331
ID AAR26347 standard; peptide; 30 AA.
DE Spacer oligopeptide D30.
PN JP04190791-A.
PD 09-JUL-1992.
PA (SUMU) SUMITOMO SEIYAKU KK.
Query Match 0.8%; Score 6; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
RESULT 1332
ID AAR42811 standard; peptide; 30 AA.
DE U-PA (159-188).
PN W09320194-A1.
PD 14-OCT-1993.
PA (SUMU) SUMITOMO PHARM CO LTD.
Query Match 0.8%; Score 6; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
RESULT 1333
ID AAR72872 standard; peptide; 30 AA.
DE Urokinase peptide fragment from amino acids 159-188.
PN JP07075580-A.
PD 20-MAR-1995.
PA (SUMU) SUMITOMO SEIYAKU KK.
Query Match 0.8%; Score 6; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
RESULT 1334
ID AAR93589 standard; peptide; 30 AA.
DE UK t-PA hybrid peptide CS19 residues 276-306.
PN W09508908-A1.
PD 13-APR-1995.
PA (SUMU) SUMITOMO PHARM CO LTD.
Query Match 0.8%; Score 6; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
RESULT 1335
ID AAR93591 standard; peptide; 30 AA.
DE UK t-PA hybrid peptide CS21 residues 276-306.
PN W09509908-A1.
PD 13-APR-1995.
PA (SUMU) SUMITOMO PHARM CO LTD.
Query Match 0.8%; Score 6; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
RESULT 1336
ID AAR76947 standard; peptide; 30 AA.
DE UK t-PA hybrid peptide CS16 residues 276-306.
PN W09509908-A1.

PD 13-APR-1995.
PA (SUMU) SUMITOMO PHARM CO LTD.
Query Match 0.8%; Score 6; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
RESULT 1337
ID AAR76946 standard; peptide; 30 AA.
DE UK t-PA hybrid peptide CS15 residues 276-306.
PN WO9509908-A1.
PD 13-APR-1995.
PA (SUMU) SUMITOMO PHARM CO LTD.
Query Match 0.8%; Score 6; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
RESULT 1338
ID AAR93592 standard; peptide; 30 AA.
DE UK t-PA hybrid peptide CS12 residues 276-306.
PN WO9509908-A1.
PD 13-APR-1995.
PA (SUMU) SUMITOMO PHARM CO LTD.
Query Match 0.8%; Score 6; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
RESULT 1339
ID AAR71666 standard; peptide; 30 AA.
DE Modified urinary plasminogen activator residues 159-188.
PN JP07039374-A.
PD 10-FEB-1995.
PA (SUMU) SUMITOMO SEIRYAKU KK.
Query Match 0.8%; Score 6; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
RESULT 1340
ID AAR72874 standard; peptide; 31 AA.
DE t-PA peptide fragment from amino acids 276-306.
PN JP07075580-A.
PD 20-MAR-1995.
PA (SUMU) SUMITOMO SEIRYAKU KK.
Query Match 0.8%; Score 6; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
RESULT 1341
ID AAR79104 standard; peptide; 31 AA.
DE Wild type tissue plasminogen activator residues 276-306.
PN JP07039374-A.
PD 10-FEB-1995.
PA (SUMU) SUMITOMO SEIRYAKU KK.
Query Match 0.8%; Score 6; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
RESULT 1342
ID AAM05988 standard; protein; 31 AA.
DE Peptide #4670 encoded by probe for measuring breast gene expression.
PN WO200157270-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
RESULT 1343
ID AAR24949 standard; peptide; 32 AA.
DE Urokinase fragment.
PN JP04144682-A.
PD 19-MAY-1992.
PA (SUMU) SUMITOMO SEIRYAKU KK.
Query Match 0.8%; Score 6; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
RESULT 1344
ID AAM16011 standard; protein; 33 AA.
DE Peptide #2445 encoded by probe for measuring cervical gene expression.
PN WO200157278-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
RESULT 1345
ID AAB35004 standard; peptide; 33 AA.
DE Peptide #2510 encoded by human foetal liver single exon probe.
PN WO200157277-A2.
PD 09-AUG-2001.

PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
RESULT 1346
ID AAM28512 standard; protein; 33 AA.
DE Peptide #2549 encoded by probe for measuring placental gene expression.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
RESULT 1347
ID ABB20416 standard; protein; 33 AA.
DE Protein #2415 encoded by probe for measuring heart cell gene expression.
PN WO200157274-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
RESULT 1348
ID AAM68189 standard; protein; 33 AA.
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 28495.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
RESULT 1349
ID AAM00415 standard; protein; 33 AA.
DE Human polypeptide SEQ ID NO 14307.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 0.8%; Score 6; DB 4; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
RESULT 1350
ID AAM55815 standard; protein; 33 AA.
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 27920.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
RESULT 1351
ID ABA49840 standard; peptide; 33 AA.
DE Human liver peptide, SEQ ID No 28489.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
RESULT 1352
ID AAM03745 standard; protein; 33 AA.
DE Peptide #2427 encoded by probe for measuring breast gene expression.
PN WO200157270-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
RESULT 1353
ID ABR72758 standard; peptide; 33 AA.
DE Anticancer peptide derived from human thrombin.
PN WO2003013569-A2.
PD 20-FEB-2003.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match 0.8%; Score 6; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
RESULT 1354
ID ABR72759 standard; peptide; 33 AA.
DE Anticancer peptide derived from human thrombin.
PN WO2003013569-A2.
PD 20-FEB-2003.
PA (TEXA) UNIV TEXAS SYSTEM.

Query Match 0.8%; Score 6; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
RESULT 1355
ID AAR74068 standard; peptide; 35 AA.
DE Superantigen peptide HIV Nef(31-65).
PN WO9511975-A2.
PD 04-MAY-1995.
PA (UYFL) UNIV FLORIDA.
Query Match 0.8%; Score 6; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
RESULT 1356
ID AAY39887 standard; peptide; 35 AA.
DE HIV Negative factor (Nef) protein residues 31-65.
PN US968514-A.
PD 19-OCT-1999.
PA (UYFL) UNIV FLORIDA.
Query Match 0.8%; Score 6; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
RESULT 1357
ID ABU61264 standard; peptide; 35 AA.
DE Human A domain from APOER2 #7.
PN WO200288171-A2.
PD 07-NOV-2002.
PA (MAXI-) MAXIGEN INC.
Query Match 0.8%; Score 6; DB 6; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
RESULT 1358
ID ADP21486 standard; peptide; 35 AA.
DE Human LDL receptor A domain peptide SeqID 62.
PN WO2004044011-A2.
PD 27-MAY-2004.
PA (AVID-) AVIDIA RES INST.
Query Match 0.8%; Score 6; DB 8; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
RESULT 1359
ID AA002449 standard; protein; 36 AA.
DE Human polypeptide SEQ ID NO 16341.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 0.8%; Score 6; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
RESULT 1360
ID AAR97691 standard; protein; 37 AA.
DE Rat P85 WW domain-1.
PN WO9617061-A1.
PD 06-JUN-1996.
PA (UYRQ) UNIV ROCKEFELLER.
PA (DELB-) DELBRUECK CENT MOLECULAR MEDICINE MAX.
Query Match 0.8%; Score 6; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
RESULT 1361
ID AAW21577 standard; protein; 37 AA.
DE Alzheimer's disease protein encoded by DNA from plasmid pGCS1243.
PN WO9721807-A1.
PD 19-JUN-1997.
PA (KYOW) KYOWA HAKKO KOCYO KK.
Query Match 0.8%; Score 6; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
RESULT 1362
ID AAY48444 standard; protein; 37 AA.
DE Human prostate cancer-associated protein 141.
PN DE1981194-A1.
PD 16-SEP-1999.
PA (META-) METAGEN GES GENOMFORSCHUNG MBH.
Query Match 0.8%; Score 6; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
RESULT 1363
ID AAB21981 standard; peptide; 37 AA.
DE F863/rat peptide containing a WW-domain #2.
PN WO2004048621-A2.
PD 24-AUG-2000.
PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.

Query Match 0.8%; Score 6; DB 3; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
RESULT 1364
ID AAR83566 standard; protein; 37 AA.
DE Colicin N 40-76 amino acid sequence SEQ ID NO:33.
PN WO2003057708-A2.
PD 17-JUL-2003.
PA (UYNE-) UNIV NEWCASTLE VENTURES LTD.
Query Match 0.8%; Score 6; DB 6; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
RESULT 1365
ID AAR74067 standard; peptide; 38 AA.
DE Superantigen peptide HIV Nef(1-38).
PN WO9511975-A2.
PD 04-MAY-1995.
PA (UYFL) UNIV FLORIDA.
Query Match 0.8%; Score 6; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
RESULT 1366
ID AAY39972 standard; peptide; 38 AA.
DE HIV Negative factor (Nef) protein residues 1-38.
PN US968514-A.
PD 19-OCT-1999.
PA (UYFL) UNIV FLORIDA.
Query Match 0.8%; Score 6; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
RESULT 1367
ID AAB70442 standard; peptide; 38 AA.
DE L. lactis signal peptide SP310 mutant amino acid sequence SEQ:55.
PN WO20011060-A2.
PD 15-FEB-2001.
PA (BIOT-) BIOTEKNOLOGISK INST.
Query Match 0.8%; Score 6; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
RESULT 1368
ID AB058270 standard; protein; 38 AA.
DE Human genome derived single exon protein #4504.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENNY) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Query Match 0.8%; Score 6; DB 8; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
RESULT 1369
ID AAR64211 standard; peptide; 39 AA.
DE Urinary plasminogen activator residues 150-188.
PN JP06327473-A.
PD 29-NOV-1994.
PA (SUMU) SUMITOMO SEIVAKU KK.
Query Match 0.8%; Score 6; DB 2; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
RESULT 1370
ID AA011683 standard; protein; 39 AA.
DE Human polypeptide SEQ ID NO 25575.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 0.8%; Score 6; DB 4; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
RESULT 1371
ID AAE32936 standard; peptide; 39 AA.
DE Human albumin-CD4 fusion protein junction peptide.
PN WO200279232-A2.
PD 10-OCT-2002.
PA (LEXI-) LEXIGEN PHARM CORP.
Query Match 0.8%; Score 6; DB 6; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
RESULT 1372
ID AAE32648 standard; peptide; 39 AA.
DE Albumin-CD4 fusion protein junction peptide.
PN WO200279415-A2.
PD 10-OCT-2002.

PA (LEXI-) LEXIGEN PHARM CORP.
 Query Match 0.8%; Score 6; DB 6; Length 39;
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;
 RESULT 1373
 ID ADF75022 standard; peptide; 39 AA.
 DE Human serum albumin-CD4 fusion protein junction sequence.
 PN US2003166877-A1.
 PD 04-SEP-2003.
 PA (LEXI-) LEXIGEN PHARM CORP.
 Query Match 0.8%; Score 6; DB 7; Length 39;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 RESULT 1374
 ID AAF71494 standard; protein; 40 AA.
 DE Antigenic peptide cross-reactive with HTLV-III env protein 3'ORF.
 PN WO8702988-A.
 PD 21-MAY-1987.
 PA (HARD-) HARVARD COLLEGE.
 Query Match 0.8%; Score 6; DB 1; Length 40;
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;
 RESULT 1375
 ID AAY48263 standard; protein; 40 AA.
 DE Human prostate cancer-associated protein 49.
 PN DE1981193-A1.
 PD 16-SEP-1999.
 PA (META-) METAGEN GES GENOMFORSCHUNG MBH.
 Query Match 0.8%; Score 6; DB 2; Length 40;
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;
 RESULT 1376
 ID AAB09340 standard; protein; 40 AA.
 DE Hepatitis GB virus protein sequence SEQ ID NO:467.
 PN US6051374-A.
 PD 18-APR-2000.
 PA (ABBO-) ABBOTT LAB.
 Query Match 0.8%; Score 6; DB 3; Length 40;
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;
 RESULT 1377
 ID AAE23150 standard; peptide; 40 AA.
 DE Influenza A virus subtype 16 haemagglutinin (HA) protein fragment #14.
 PN WO200224734-A2.
 PD 28-MAR-2002.
 PA (CHIR-) CHIRON SPA.
 Query Match 0.8%; Score 6; DB 5; Length 40;
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;
 RESULT 1378
 ID AAR07101 standard; protein; 41 AA.
 DE Melanocyte-stimulating hormone inhibitor #6.
 PN EP389950-A.
 PD 03-OCT-1990.
 PA (LLOY-) LLOYD CORP.
 Query Match 0.8%; Score 6; DB 2; Length 41;
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;
 RESULT 1379
 ID AAW24762 standard; peptide; 42 AA.
 DE Adhesin Pctr44 N-terminal peptide.
 PN WO9716542-A1.
 PD 09-MAY-1997.
 PA (UYME-) UNIV MELBOURNE.
 Query Match 0.8%; Score 6; DB 2; Length 42;
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;
 RESULT 1380
 ID AAC02438 standard; protein; 42 AA.
 DE Human polypeptide SEQ ID NO 16330.
 PN WO200164835-A2.
 PD 07-SEP-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 0.8%; Score 6; DB 4; Length 42;
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;
 RESULT 1381
 ID ABO60596 standard; protein; 42 AA.
 DE Human genome derived single exon protein #6830.
 PN US2003194704-A1.
 PD 16-OCT-2003.

PA (PENN/) PENN S G.
 PA (RANK/) RANK D R.
 PA (HANZ/) HANZEL D K.
 Query Match 0.8%; Score 6; DB 8; Length 42;
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;
 RESULT 1382
 ID AAR58896 standard; protein; 43 AA.
 DE Human-223 cadherin-related molecule.
 PN WO9414960-A2.
 PD 07-JUL-1994.
 PA (DOHE-) DOHENY EYE INST.
 Query Match 0.8%; Score 6; DB 2; Length 43;
 Best Local Similarity 100.0%; Pred. No. 2e+03;
 RESULT 1383
 ID AAR87135 standard; peptide; 43 AA.
 DE Protocadherin clone HUMAN-223.
 PN WO9600289-A1.
 PD 04-JAN-1996.
 PA (DOHE-) DOHENY EYE INST.
 Query Match 0.8%; Score 6; DB 2; Length 43;
 Best Local Similarity 100.0%; Pred. No. 2e+03;
 RESULT 1384
 ID AAY21020 standard; protein; 43 AA.
 DE Human glial fibrillary acidic protein GFAP mutant fragment 29.
 PN WO9845322-A2.
 PD 15-OCT-1998.
 PA (ROYA-) ROYAL NETHERLANDS ACAD ARTS & SCI.
 PA (UYRO-) UNIV ROTTERDAM ERASMUS.
 PA (UYUT-) RIJKSUNIV UTRECHT.
 Query Match 0.8%; Score 6; DB 2; Length 43;
 Best Local Similarity 100.0%; Pred. No. 2e+03;
 RESULT 1385
 ID AAY32350 standard; peptide; 43 AA.
 DE Human C1qR EGF-2 peptide.
 PN WO9955839-A1.
 PD 04-NOV-1999.
 PA (REGC-) UNIV CALIFORNIA.
 Query Match 0.8%; Score 6; DB 3; Length 43;
 Best Local Similarity 100.0%; Pred. No. 2e+03;
 RESULT 1386
 ID ABG77431 standard; protein; 43 AA.
 DE Selected interacting domain (SID) polypeptide #242.
 PN WO200259255-A2.
 PD 01-AUG-2002.
 PA (HYBR-) HYBRIGENICS.
 Query Match 0.8%; Score 6; DB 5; Length 43;
 Best Local Similarity 100.0%; Pred. No. 2e+03;
 RESULT 1387
 ID AAE30226 standard; peptide; 43 AA.
 DE Human LP288 YWTD Island 2 repeat peptide #1.
 PN WO200274906-A2.
 PD 26-SEP-2002.
 PA (ELIL-) LILLY & CO ELI.
 Query Match 0.8%; Score 6; DB 6; Length 43;
 Best Local Similarity 100.0%; Pred. No. 2e+03;
 RESULT 1388
 ID ADR51552 standard; protein; 43 AA.
 DE DR-binding receptor region of HB-EGF from humans.
 PN WO2004069870-A2.
 PD 19-AUG-2004.
 PA (UYLE-) RIJKSUNIV LEIDEN.
 Query Match 0.8%; Score 6; DB 8; Length 43;
 Best Local Similarity 100.0%; Pred. No. 2e+03;
 RESULT 1389
 ID ADR51550 standard; protein; 43 AA.
 DE DR-binding receptor region of HB-EGF from pigs.
 PN WO2004069870-A2.
 PD 19-AUG-2004.
 PA (UYLE-) RIJKSUNIV LEIDEN.
 Query Match 0.8%; Score 6; DB 8; Length 43;
 Best Local Similarity 100.0%; Pred. No. 2e+03;
 RESULT 1390
 ID AAC01303 standard; protein; 44 AA.

DE Human polypeptide SEQ ID NO 15195.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 0.8%; Score 6; DB 4; Length 44;
Best Local Similarity 100.0%; Pred. No. 2e+03;
RESULT 1391
ID ABR51549 standard; protein; 44 AA.
DE DT-binding receptor region of HB-EGF from rabbit.
PN WO2004069870-A2.
PD 19-AUG-2004.
PA (UYLE-) RIJKSUNIV LEIDEN.
Query Match 0.8%; Score 6; DB 8; Length 44;
Best Local Similarity 100.0%; Pred. No. 2e+03;
RESULT 1392
ID ABR51551 standard; protein; 44 AA.
DE DT-binding receptor region of HB-EGF from monkeys.
PN WO2004069870-A2.
PD 19-AUG-2004.
PA (UYLE-) RIJKSUNIV LEIDEN.
Query Match 0.8%; Score 6; DB 8; Length 44;
Best Local Similarity 100.0%; Pred. No. 2e+03;
RESULT 1393
ID AAR64212 standard; peptide; 45 AA.
DE Urinary plasminogen activator residues 159-203.
PN JF06327473-A.
PD 29-NOV-1994.
PA (SUMU) SUMITOMO SEIRYAKU KK.
Query Match 0.8%; Score 6; DB 2; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
RESULT 1394
ID AAY08546 standard; protein; 45 AA.
DE C-terminal alpha-CTD protein fragment FTSH_HELPY.
PN W06925723-A2.
PD 27-MAY-1999.
PA (YISS) YISSUM RES & DEV CO.
Query Match 0.8%; Score 6; DB 2; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
RESULT 1395
ID AAG2119 standard; protein; 45 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 23559.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 0.8%; Score 6; DB 3; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
RESULT 1396
ID AAM1431 standard; protein; 45 AA.
DE Peptide #665 encoded by probe for measuring cervical gene expression.
PN WO200157278-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
RESULT 1397
ID ABB33178 standard; peptide; 45 AA.
DE Peptide #684 encoded by human foetal liver single exon probe.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
RESULT 1398
ID AAM26641 standard; protein; 45 AA.
DE Peptide #678 encoded by probe for measuring placental gene expression.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
RESULT 1399
ID ABB28006 standard; peptide; 45 AA.
DE Human peptide #657 encoded by breast cell single exon nucleic acid probe.
PN WO200157271-A2.

PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
RESULT 1400
ID ABB16643 standard; protein; 45 AA.
DE Protein #642 encoded by probe for measuring heart cell gene expression.
PN WO200157274-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
RESULT 1401
ID AAM66362 standard; protein; 45 AA.
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 26668.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
RESULT 1402
ID AAM53974 standard; protein; 45 AA.
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 26079.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
RESULT 1403
ID AAG48028 standard; peptide; 45 AA.
DE Human liver peptide, SEQ ID NO 26676.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
RESULT 1404
ID AAM01963 standard; protein; 45 AA.
DE Peptide #645 encoded by probe for measuring human breast gene expression.
PN WO200157270-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
RESULT 1405
ID AAG36010 standard; peptide; 45 AA.
DE Human peptide encoded by genome-derived single exon probe SEQ ID 25675.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 5; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
RESULT 1406
ID ADN05538 standard; protein; 45 AA.
DE Antipeptidic protein sequence #935.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GERTH) GENEVECH INC.
Query Match 0.8%; Score 6; DB 8; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
RESULT 1407
ID ABB03327 standard; protein; 46 AA.
DE Human musculoskeletal system related polypeptide SEQ ID NO 1274.
PN WO200155367-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 0.8%; Score 6; DB 4; Length 46;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
RESULT 1408
ID AAO01399 standard; protein; 46 AA.
DE Human polypeptide SEQ ID NO 15291.
PN WO200164835-A2.
PD 07-SEP-2001.

PA (HYSE-) HYSEQ INC.
Query Match 0.8%; Score 6; DB 4; Length 46;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
RESULT 1409
ID AAC08005 standard; protein; 46 AA.
DE Human polypeptide SEQ ID NO 21897.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 0.8%; Score 6; DB 4; Length 46;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
RESULT 1410
ID ADH32592 standard; protein; 46 AA.
DE Yeast smORF387-encoded polypeptide, SEQ ID NO:1050.
PN WO200268693-A2.
PD 06-SEP-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 0.8%; Score 6; DB 5; Length 46;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
RESULT 1411
ID ABU12621 standard; protein; 46 AA.
DE Novel human musculoskeletal system antigen #241.
PN US2002147140-A1.
PD 10-OCT-2002.
PA (ROSE/) ROSEN C A.
PA (ROBE/) ROSEN S M.
PA (BARA/) BARASH S C.
Query Match 0.8%; Score 6; DB 6; Length 46;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
RESULT 1412
ID ADJ28647 standard; protein; 46 AA.
DE Human musculoskeletal system-associated protein - SEQ ID 1274.
PN US200400948-A1.
PD 15-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 0.8%; Score 6; DB 8; Length 46;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
RESULT 1413
ID AD607325 standard; protein; 46 AA.
DE *Staphylococcus epidermis* polypeptide seqid 6620.
PN US2004147734-A1.
PD 29-JUL-2004.
PA (DOUC/) DOUCETTE-STAMM L.
PA (BOSH/) BUSH D.
Query Match 0.8%; Score 6; DB 8; Length 46;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
RESULT 1414
ID AAW28321 standard; protein; 47 AA.
DE *Staphylococcus aureus* protein of unknown function.
PN WO9730070-A1.
PD 21-AUG-1997.
PA (SMK) SMITHKLINE BEECHAM CORP.
Query Match 0.8%; Score 6; DB 2; Length 47;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
RESULT 1415
ID AAG18782 standard; protein; 47 AA.
DE Zee maye protein fragment SEQ ID NO: 20328.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 0.8%; Score 6; DB 3; Length 47;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
RESULT 1416
ID AAM47202 standard; peptide; 47 AA.
DE Modular enzyme system related ACP-domain N-terminal peptide AVEA1_3.
PN WO200181564-A2.
PD 01-NOV-2001.
PA (ACTI-) ACTINODRUG PHARM GMBH.
Query Match 0.8%; Score 6; DB 5; Length 47;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
RESULT 1417
ID ADP96929 standard; protein; 47 AA.
DE Human 193P1E1B protein variant 1 fragment #2.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match 0.8%; Score 6; DB 7; Length 47;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
RESULT 1418
ID ADP49728 standard; peptide; 47 AA.
DE Human 193P1E1Bv.1.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARIS M.
PA (HUBE/) HUBERT R S.
PA (GEWM/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match 0.8%; Score 6; DB 8; Length 47;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
RESULT 1419
ID AAB33113 standard; protein; 48 AA.
DE *Pinus radiata* transcription factor protein sequence #240.
PN WO200053724-A2.
PD 14-SEP-2000.
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
Query Match 0.8%; Score 6; DB 3; Length 48;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
RESULT 1420
ID ABP43712 standard; protein; 48 AA.
DE PRO566 protein.
PN WO200231111-A2.
PD 18-APR-2002.
PA (HYSE-) HYSEQ INC.
Query Match 0.8%; Score 6; DB 5; Length 48;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
RESULT 1421
ID AAE36818 standard; protein; 48 AA.
DE Human HB-EGF domain.
PN WO2003014159-A1.
PD 20-FEB-2003.
PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
PA (BIOM-) BIOMOLECULAR RES INST LTD.
PA (HALI-) HALI INST MEDICAL RES WALTER & ELIZA.
PA (LUDW-) LUDWIG INST CANCER RES.
Query Match 0.8%; Score 6; DB 6; Length 48;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
RESULT 1422
ID ADN48881 standard; peptide; 48 AA.
DE Heparin-binding epidermal-growth factor (HB-EGF) peptide.
PN US6727077-B1.
PD 27-APR-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (GEOU-) UNIV GEORGETOWN MEDICAL CENT.
Query Match 0.8%; Score 6; DB 8; Length 48;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
RESULT 1423
ID ABB38598 standard; peptide; 49 AA.
DE Peptide #6104 encoded by human foetal liver single exon probe.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 49;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
RESULT 1424
ID AAM32054 standard; protein; 49 AA.
DE Peptide #6091 encoded by probe for measuring placental gene expression.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 49;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
RESULT 1425
ID AAM71762 standard; protein; 49 AA.
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 32068.
PN WO2003050255-A2.

PN W0200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
RESULT 1426
ID AAM59226 standard; protein; 49 AA.
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 31331.
PN W0200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
RESULT 1427
ID ABG51447 standard; peptide; 49 AA.
DE Human liver peptide, SEQ ID No 32095.
PN W0200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
RESULT 1428
ID ABG41576 standard; peptide; 49 AA.
DE Human peptide encoded by genome-derived single exon probe SEQ ID 31241.
PN W0200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
RESULT 1429
ID ADK14940 standard; protein; 49 AA.
DE Urinary specific protein #46.
PN W02003057839-A2.
PD 17-JUL-2003.
PA (DIAD-) DIADEXUS INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
RESULT 1430
ID AAG04489 standard; protein; 50 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 535.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
RESULT 1431
ID AAG37508 standard; protein; 50 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 46130.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
RESULT 1432
ID AAB22229 standard; protein; 50 AA.
DE Protein #4228 encoded by probe for measuring heart cell gene expression.
PN W0200157274-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
RESULT 1433
ID AAM70055 standard; protein; 50 AA.
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 30361.
PN W0200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
RESULT 1434
ID AAM40213 standard; protein; 50 AA.
DE Propionibacterium acnes immunogenic protein #1109.
PN W0200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.

Query Match
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
RESULT 1435
ID AAM57648 standard; protein; 50 AA.
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 29753.
PN W0200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
RESULT 1436
ID ABG51748 standard; peptide; 50 AA.
DE Human liver peptide, SEQ ID No 30396.
PN W0200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
RESULT 1437
ID AAM05532 standard; protein; 50 AA.
DE Peptide #4214 encoded by probe for measuring breast gene expression.
PN W0200157270-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
RESULT 1438
ID ABG39686 standard; peptide; 50 AA.
DE Human peptide encoded by genome-derived single exon probe SEQ ID 29351.
PN W0200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
RESULT 1439
ID AEM36732 standard; protein; 50 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #1408.
PN W0200303515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
RESULT 1440
ID AAE36799 standard; protein; 50 AA.
DE Human HB-EGF protein EGF-like domain.
PN W02003014159-A1.
PD 20-FEB-2003.
PA (CSIR-) COMMONWEALTH SCI & IND RES ORG.
PA (BIOM-) BIOMOLECULAR RES INST LTD.
PA (HALT-) HALT INST MEDICAL RES WALTER & ELIZA.
PA (LUDW-) LUDWIG INST CANCER RES.
Query Match
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
RESULT 1441
ID AAM67925 standard; protein; 51 AA.
DE Fragment of human secreted protein encoded by gene 3.
PN W09842738-A1.
PD 01-OCT-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
RESULT 1442
ID AAG04488 standard; protein; 51 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 534.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
RESULT 1443
ID AAG37507 standard; protein; 51 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 46129.
PN EP1033405-A2.
PD 06-SEP-2000.

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Query Match 0.8%; Score 6; DB 3; Length 51;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
RESULT 1444
ID AA053334 standard; protein; 51 AA.
DE Propionibacterium acnes immunogenic protein #14230.
PN W0200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 0.8%; Score 6; DB 4; Length 51;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
RESULT 1445
ID ABP11027 standard; protein; 51 AA.
DE Human OREX protein sequence SEQ ID NO:22036.
PN W0200192523-A2.
PD 06-DEC-2001.
PA (CURA-) CURAGEN CORP.
Query Match 0.8%; Score 6; DB 5; Length 51;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
RESULT 1446
ID ABW49853 standard; protein; 51 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #14529.
PN W02003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 0.8%; Score 6; DB 6; Length 51;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
RESULT 1447
ID AAW21562 standard; protein; 52 AA.
DE LENO rat cholecystokinin-A receptor fragment, encoded by exon 1.
PN JP09065900-A.
PD 11-MAR-1997.
PA (SHO-) SHIONOGI & CO LTD.
Query Match 0.8%; Score 6; DB 2; Length 52;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
RESULT 1448
ID AAR4514 standard; protein; 53 AA.
DE Plasmid pCDM8-D09 - D44 fragment D09.
PN W09324624-A1.
PD 09-DEC-1993.
PA (SUMU-) SUMITOMO PHARM CO LTD.
Query Match 0.8%; Score 6; DB 2; Length 53;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
RESULT 1449
ID AAW91699 standard; protein; 53 AA.
DE Human immune/haematopoietic antigen SEQ ID NO:19292.
PN W0200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 0.8%; Score 6; DB 4; Length 53;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
RESULT 1450
ID AAM00082 standard; protein; 53 AA.
DE Sucrose transporter sequence #150.
PN W0200144476-A2.
PD 21-JUN-2001.
PA (BADI-) BASF PLANT SCI GMBH.
Query Match 0.8%; Score 6; DB 4; Length 53;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
RESULT 1451
ID AAR64213 standard; peptide; 54 AA.
DE Urinary plasminogen activator residues 150-203.
PN JP06327473-A.
PD 29-NOV-1994.
PA (SUMU-) SUMITOMO SEIYAKU KK.
Query Match 0.8%; Score 6; DB 2; Length 54;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
RESULT 1452
ID AAW46238 standard; protein; 54 AA.
DE Propionibacterium acnes immunogenic protein #7134.
PN W0200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 0.8%; Score 6; DB 4; Length 54;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
RESULT 1453
ID AAW39328 standard; protein; 54 AA.
DE Propionibacterium acnes immunogenic protein #224.
PN W0200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 0.8%; Score 6; DB 4; Length 54;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
RESULT 1454
ID ABU02285 standard; protein; 54 AA.
DE S. pneumoniae type 4 strain protein from coding region #1863.
PN W0200277021-A2.
PD 03-OCT-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 0.8%; Score 6; DB 6; Length 54;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
RESULT 1455
ID ABW42757 standard; protein; 54 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #7433.
PN W02003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 0.8%; Score 6; DB 6; Length 54;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
RESULT 1456
ID ABW35847 standard; protein; 54 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #523.
PN W02003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 0.8%; Score 6; DB 6; Length 54;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
RESULT 1457
ID AAR45145 standard; protein; 55 AA.
DE Plasmid pCDM8-D09 - D44 fragment D11.
PN W09324624-A1.
PD 09-DEC-1993.
PA (SUMU-) SUMITOMO PHARM CO LTD.
Query Match 0.8%; Score 6; DB 2; Length 55;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
RESULT 1458
ID AAR45146 standard; protein; 56 AA.
DE Plasmid pCDM8-D09 - D44 fragment D(1+11).
PN W09324624-A1.
PD 09-DEC-1993.
PA (SUMU-) SUMITOMO PHARM CO LTD.
Query Match 0.8%; Score 6; DB 2; Length 56;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
RESULT 1459
ID AAR64210 standard; peptide; 56 AA.
DE Tissue plasminogen activator residues 266-321.
PN JP06327473-A.
PD 29-NOV-1994.
PA (SUMU-) SUMITOMO SEIYAKU KK.
Query Match 0.8%; Score 6; DB 2; Length 56;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
RESULT 1460
ID AAG21118 standard; protein; 56 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 23558.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 0.8%; Score 6; DB 3; Length 56;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
RESULT 1461
ID AAG55284 standard; protein; 56 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 70861.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 0.8%; Score 6; DB 3; Length 56;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
RESULT 1462
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ID AAM14482 standard; protein, 56 AA.
DE Peptide #916 encoded by probe for measuring cervical gene expression.
PN WO200157278-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 56;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
RESULT 1463
ID ABB31430 standard; peptide, 56 AA.
DE Peptide #936 encoded by human foetal liver single exon probe.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 56;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
RESULT 1464
ID AAM26895 standard; protein, 56 AA.
DE Peptide #932 encoded by probe for measuring placental gene expression.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 56;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
RESULT 1465
ID ABB28255 standard; peptide, 56 AA.
DE Human peptide #906 encoded by breast cell single exon nucleic acid probe.
PN WO200157271-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 56;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
RESULT 1466
ID ABB18869 standard; protein, 56 AA.
DE Protein #888 encoded by probe for measuring heart cell gene expression.
PN WO200157274-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 56;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
RESULT 1467
ID AAM66609 standard; protein, 56 AA.
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 26915.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 56;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
RESULT 1468
ID AAM54215 standard; protein, 56 AA.
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 26320.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 56;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
RESULT 1469
ID ABB48277 standard; peptide, 56 AA.
DE Human liver peptide, SEQ ID NO 26925.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 56;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
RESULT 1470
ID AAM02209 standard; protein, 56 AA.
DE Peptide #891 encoded by probe for measuring human breast gene expression.
PN WO200157270-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 56;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
RESULT 1471
ID ABB05146 standard; protein, 56 AA.

DE Human OREF protein sequence SEQ ID NO:10274.
PN WO200192523-A2.
PD 06-DEC-2001.
PA. (CURA-) CURAGEN CORP.
Query Match 0.8%; Score 6; DB 5; Length 56;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
RESULT 1472
ID ABB09848 standard; protein, 56 AA.
DE Human OREF protein sequence SEQ ID NO:19678.
PN WO200192523-A2.
PD 06-DEC-2001.
PA (CURA-) CURAGEN CORP.
Query Match 0.8%; Score 6; DB 5; Length 56;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
RESULT 1473
ID ABB36261 standard; peptide, 56 AA.
DE Human peptide encoded by genome-derived single exon probe SEQ ID 25926.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 5; Length 56;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
RESULT 1474
ID ABB05586 standard; protein, 56 AA.
DE M. tuberculosis and M. leprae marker protein #237.
PN WO200274903-A2.
PD 26-SEP-2002.
PA (INSP) INST PASTEUR.
Query Match 0.8%; Score 6; DB 5; Length 56;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
RESULT 1475
ID ABB47344 standard; protein, 56 AA.
DE Thermococcus kodakaraensis KOD1 protein sequence SeqID1222.
PN WO2004022736-A1.
PD 18-MAR-2004.
PA (INSC-) JAPAN SCI & TECHNOLOGY CORP.
Query Match 0.8%; Score 6; DB 8; Length 56;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
RESULT 1476
ID AAG10655 standard; protein, 57 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 9063.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 0.8%; Score 6; DB 3; Length 57;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
RESULT 1477
ID AAR45147 standard; protein, 58 AA.
DE Plasmid pCDM8-D09 - D44 fragment D(14).
PN WO9324624-A1.
PD 09-DEC-1993.
PA (SUMU) SUMITOMO PHARM CO LTD.
Query Match 0.8%; Score 6; DB 2; Length 58;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
RESULT 1478
ID AAO1116 standard; protein, 58 AA.
DE Human polypeptide SEQ ID NO 25008.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 0.8%; Score 6; DB 4; Length 58;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
RESULT 1479
ID AAO02406 standard; protein, 58 AA.
DE Human polypeptide SEQ ID NO 16298.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 0.8%; Score 6; DB 4; Length 58;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
RESULT 1480
ID AAB41904 standard; protein, 59 AA.
DE Human OREF ORF1668 polypeptide sequence SEQ ID NO:3336.
PN WO200058473-A2.

PD 05-OCT-2000.
PA (CORA-) CORAGEN CORP.
Query Match 0.8%; Score 6; DB 3; Length 59;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
RESULT 1481
ID AAB90620 standard; protein; 59 AA.
DE Human secreted protein, SEQ ID NO: 163.
PN WO200121658-A1.
PD 29-MAR-2001.
PA (HUMA-) HUMAN GENOME SCT INC.
Query Match 0.8%; Score 6; DB 4; Length 59;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
RESULT 1482
ID AAG99892 standard; peptide; 59 AA.
DE ERA binding domain polypeptide SEQ ID NO 334.
PN WO200153458-A2.
PD 26-JUL-2001.
PA (SMIX) SMITHKLINE BEECHAM CORP.
PA (SMIX) SMITHKLINE BEECHAM PLC.
Query Match 0.8%; Score 6; DB 4; Length 59;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
RESULT 1483
ID AAM96307 standard; protein; 59 AA.
DE Human reproductive system related antigen SEQ ID NO: 4965.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCT INC.
Query Match 0.8%; Score 6; DB 4; Length 59;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
RESULT 1484
ID AAO11933 standard; protein; 59 AA.
DE Human polypeptide SEQ ID NO 25825.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 0.8%; Score 6; DB 4; Length 59;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
RESULT 1485
ID AAU64191 standard; protein; 59 AA.
DE Propionibacterium acnes immunogenic protein #25087.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 0.8%; Score 6; DB 4; Length 59;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
RESULT 1486
ID AAU53121 standard; protein; 59 AA.
DE Propionibacterium acnes immunogenic protein #4017.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 0.8%; Score 6; DB 4; Length 59;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
RESULT 1487
ID AAU55216 standard; protein; 59 AA.
DE Propionibacterium acnes immunogenic protein #26112.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 0.8%; Score 6; DB 4; Length 59;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
RESULT 1488
ID AABM1735 standard; protein; 59 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #26411.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 0.8%; Score 6; DB 4; Length 59;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
RESULT 1489
ID AABM39640 standard; protein; 59 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #4316.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 0.8%; Score 6; DB 6; Length 59;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
RESULT 1490
ID AABM60710 standard; protein; 59 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #25386.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 0.8%; Score 6; DB 6; Length 59;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
RESULT 1491
ID ABB70853 standard; protein; 60 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 39351.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 0.8%; Score 6; DB 4; Length 60;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
RESULT 1492
ID ABB41719 standard; peptide; 60 AA.
DE Peptide #9225 encoded by human foetal liver single exon probe.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 60;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
RESULT 1493
ID AAM35515 standard; protein; 60 AA.
DE Peptide #9552 encoded by probe for measuring placental gene expression.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 60;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
RESULT 1494
ID AAM75403 standard; protein; 60 AA.
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 35709.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 60;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
RESULT 1495
ID AAU52361 standard; protein; 60 AA.
DE Propionibacterium acnes immunogenic protein #13257.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 0.8%; Score 6; DB 4; Length 60;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
RESULT 1496
ID AAU63335 standard; protein; 60 AA.
DE Propionibacterium acnes immunogenic protein #24231.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 0.8%; Score 6; DB 4; Length 60;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
RESULT 1497
ID AAU61570 standard; protein; 60 AA.
DE Propionibacterium acnes immunogenic protein #22466.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 0.8%; Score 6; DB 4; Length 60;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
RESULT 1498
ID AAM62593 standard; protein; 60 AA.
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 34698.
PN WO200157275-A2.
PD 09-AUG-2001.

PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; length 60;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
RESULT 1499
ID ABG57158 standard; peptide; 60 AA
DE Human liver peptide; SEQ ID NO 35806.
PN W0200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; length 60;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
RESULT 1500
ID ABG44990 standard; peptide; 60 AA.
DE Human peptide encoded by genome-derived single exon probe SEQ ID 34655.
PN W0200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 5; length 60;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;

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OM protein - protein search, using sw model

Run on: July 12, 2005, 17:19:03 ; Search time 44 Seconds
(without alignments)
1574.456 Million cell updates/sec

Title: US-10-063-546-38
Perfect score: 720
Sequence: 1 MELGWTQLGLRFLQLLLS.....LSTAFKVLPRKDWIRNMK 720

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1500 summaries

Database :

PIR 79: *
1: p1r1: *
2: p1r2: *
3: p1r3: *
4: p1r4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	178	24.7	181	2 T08805	hypothetical prote
2	232	1.2	232	2 T08372	hypothetical prote
3	9	1.2	276	2 T29125	ketoacyl reductase
4	9	1.2	730	1 BWHU1	procollagen C-endo
5	9	1.2	823	1 A58788	procollagen C-endo
6	9	1.2	986	1 B58788	procollagen C-endo
7	9	1.2	991	2 I49540	procollagen C-endo
8	9	1.2	1464	2 S58984	development protei
9	9	1.2	2531	2 T31070	notch homolog - se
10	9	1.1	114	2 S00996	ig kappa chain pre
11	11	1.1	158	2 G70323	conserved hypochet
12	8	1.1	235	2 D42696	thrombin (EC 3.4.2
13	8	1.1	235	2 H42696	thrombin (EC 3.4.2
14	8	1.1	235	2 C42696	thrombin (EC 3.4.2
15	8	1.1	240	2 AB0338	probable membrane
16	8	1.1	302	2 T25020	hypothetical prote
17	8	1.1	395	2 A82283	vibriobactin-speci
18	8	1.1	407	1 KPB07	coagulation factor
19	8	1.1	486	2 T38174	probable GCSL/GUO3
20	8	1.1	737	2 AG2156	hypothetical prote
21	8	1.1	1019	2 A38738	coagulation factor
22	8	1.1	1070	2 T31069	collid-BMP-1 like
23	7	1.0	59	2 B89983	hypothetical prote
24	7	1.0	75	2 A86487	unknown protein [1
25	7	1.0	91	2 B96528	protein F27315.6 [
26	7	1.0	114	2 D72600	hypothetical prote
27	7	1.0	143	2 A85072	hypothetical prote
28	7	1.0	167	2 S05364	hypothetical prote
29	7	1.0	168	2 D86534	CT066 hypothetical

30	7	1.0	168	2 D72089	CT066 hypothetical
31	7	1.0	171	2 E81580	conserved hypochet
32	7	1.0	173	2 T45501	hypothetical prote
33	7	1.0	178	2 F86271	protein Fl6A14.6 [
34	7	1.0	191	2 G75299	cellulium resistan
35	7	1.0	193	2 G64241	hypothetical prote
36	7	1.0	196	2 JC4257	beta A4-crystallin
37	7	1.0	201	1 S16262	auxin-binding prot
38	7	1.0	209	2 S27494	nods protein - Bra
39	7	1.0	211	2 AC0268	probable exported
40	7	1.0	212	2 AB0652	probable outer mem
41	7	1.0	212	2 S07797	acid protein precu
42	7	1.0	212	2 C85706	probable outer mem
43	7	1.0	212	2 D90848	probable outer mem
44	7	1.0	213	2 B86828	hypothetical prote
45	7	1.0	215	2 T50589	probable Tetr-fam1
46	7	1.0	227	2 D69296	conserved hypochet
47	7	1.0	231	2 A86592	low calcium respon
48	7	1.0	231	2 H72031	type III secretion
49	7	1.0	232	2 C83139	outer membrane pro
50	7	1.0	235	2 E42696	thrombin (EC 3.4.2
51	7	1.0	236	2 F84273	hypothetical prote
52	7	1.0	239	2 G42696	thrombin (EC 3.4.2
53	7	1.0	239	2 B82123	chemotaxis protein
54	7	1.0	243	2 A56338	venom proteinase (
55	7	1.0	247	2 G86011	glycerophosphodies
56	7	1.0	247	2 G91165	glycerophosphodies
57	7	1.0	250	2 A10206	probable chaperone
58	7	1.0	255	2 S07553	hypothetical prote
59	7	1.0	259	2 A12835	N-acetylaminomoyl-L
60	7	1.0	259	2 D97613	hypothetical prote
61	7	1.0	260	2 A36402	corticocortropin / 11
62	7	1.0	263	2 S05433	corticocortropin / 11
63	7	1.0	265	2 E70520	hypothetical prote
64	7	1.0	270	2 S04380	opacity protein P.
65	7	1.0	271	2 T50620	hypothetical prote
66	7	1.0	307	2 B82343	D-isomer specific
67	7	1.0	312	2 S67052	hypothetical prote
68	7	1.0	315	2 A87249	conserved hypochet
69	7	1.0	333	2 A84055	transcription regu
70	7	1.0	336	2 G87202	probable membrane
71	7	1.0	337	2 D72690	hypothetical prote
72	7	1.0	339	2 AG2041	queuine tRNA-ribos
73	7	1.0	349	2 C72630	probable threonine
74	7	1.0	350	2 T25172	hypothetical prote
75	7	1.0	351	2 S67649	MSS2 protein - Yea
76	7	1.0	355	2 T13831	NADH2 dehydrogenas
77	7	1.0	355	2 T13830	NADH2 dehydrogenas
78	7	1.0	355	2 T14016	NADH2 dehydrogenas
79	7	1.0	355	2 T14009	NADH2 dehydrogenas
80	7	1.0	355	2 T14012	NADH2 dehydrogenas
81	7	1.0	355	2 T14011	NADH2 dehydrogenas
82	7	1.0	355	2 T11737	NADH2 dehydrogenas
83	7	1.0	355	2 T11737	NADH2 dehydrogenas
84	7	1.0	355	2 T11737	NADH2 dehydrogenas
85	7	1.0	355	2 T11737	NADH2 dehydrogenas
86	7	1.0	355	2 T11737	NADH2 dehydrogenas
87	7	1.0	355	2 T11737	NADH2 dehydrogenas
88	7	1.0	355	2 T11737	NADH2 dehydrogenas
89	7	1.0	355	2 T11737	NADH2 dehydrogenas
90	7	1.0	355	2 T11737	NADH2 dehydrogenas
91	7	1.0	355	2 T11737	NADH2 dehydrogenas
92	7	1.0	355	2 T11737	NADH2 dehydrogenas
93	7	1.0	355	2 T11737	NADH2 dehydrogenas
94	7	1.0	355	2 T11737	NADH2 dehydrogenas
95	7	1.0	355	2 T11737	NADH2 dehydrogenas
96	7	1.0	355	2 T11737	NADH2 dehydrogenas
97	7	1.0	355	2 T11737	NADH2 dehydrogenas
98	7	1.0	355	2 T11737	NADH2 dehydrogenas
99	7	1.0	355	2 T11737	NADH2 dehydrogenas
100	7	1.0	355	2 T11737	NADH2 dehydrogenas
101	7	1.0	355	2 T11737	NADH2 dehydrogenas
102	7	1.0	355	2 T11737	NADH2 dehydrogenas

103	7	1.0	355	2	T11602	NADH2 dehydrogenas	176	6	0.8	27	2	A33431	artrial natriuretic
104	7	1.0	355	2	T11601	NADH2 dehydrogenas	177	6	0.8	35	2	D82224	hypothetical prote
105	7	1.0	355	2	T12109	NADH2 dehydrogenas	178	6	0.8	40	2	D82433	hypothetical prote
106	7	1.0	355	2	T12107	NADH2 dehydrogenas	179	6	0.8	48	2	G81543	hypothetical prote
107	7	1.0	355	2	T12119	NADH2 dehydrogenas	180	6	0.8	53	2	G82813	hypothetical prote
108	7	1.0	355	2	A48358	ORF355 - Bradyrhiz	181	6	0.8	54	2	A95210	conserved hypotet
109	7	1.0	355	2	A28700	mandelate racemase	182	6	0.8	54	2	H81814	probable small sec
110	7	1.0	372	2	A83260	hypothetical prote	183	6	0.8	55	1	FECUCU	ferredoxin 244Fe-4
111	7	1.0	375	2	A81227	conserved hypotet	184	6	0.8	55	2	T07197	hypothetical prote
112	7	1.0	375	2	F81999	probable integral	185	6	0.8	56	2	E87173	conserved hypotet
113	7	1.0	387	1	S75050	IMP dehydrogenase	186	6	0.8	57	2	S66318	protein kinase AK5
114	7	1.0	387	2	AC1813	IMP dehydrogenase	187	6	0.8	57	2	S66316	hypothetical prote
115	7	1.0	398	2	B83438	probable transport	188	6	0.8	59	2	A83209	hypothetical prote
116	7	1.0	437	2	F69383	coenzyme F390 synt	189	6	0.8	62	2	G59147	comotoxin Im5.1 pr
117	7	1.0	437	2	J50237	hypothetical 48K p	190	6	0.8	64	2	T08457	probable outer env
118	7	1.0	439	2	T49189	kinesin heavy chai	191	6	0.8	64	2	H75204	ferredoxin PAB3048
119	7	1.0	459	2	T08594	probable sulfate a	192	6	0.8	66	2	D98068	degenerate transpo
120	7	1.0	461	2	D70561	hypothetical prote	193	6	0.8	67	2	AC1954	hypothetical prote
121	7	1.0	472	2	T27755	hypothetical prote	194	6	0.8	68	2	T00189	hypothetical prote
122	7	1.0	479	2	H90042	hypothetical prote	195	6	0.8	68	2	A93993	hypothetical prote
123	7	1.0	489	2	S69027	ammonium transport	196	6	0.8	69	2	A82949	hypothetical prote
124	7	1.0	492	2	T23349	hypothetical prote	197	6	0.8	70	1	R5EC31	ribosomal protein
125	7	1.0	492	2	S46225	ammonium transport	198	6	0.8	70	2	G91236	50S ribosomal subu
126	7	1.0	493	2	A33809	cartilage matrix p	199	6	0.8	70	2	G86083	hypothetical prote
127	7	1.0	494	1	A23079	lymphocyte surface	200	6	0.8	70	2	G82588	hypothetical prote
128	7	1.0	497	2	S43609	roA protein - Str	201	6	0.8	71	2	I60082	CD4 receptor - Hum
129	7	1.0	497	2	H70168	hypothetical prote	202	6	0.8	71	2	H86751	prophage p12 prote
130	7	1.0	505	2	C90569	hypothetical prote	203	6	0.8	73	2	H83204	conserved hypotet
131	7	1.0	529	2	T18595	hypothetical prote	204	6	0.8	73	2	F97136	hypothetical prote
132	7	1.0	532	2	A72694	hypothetical prote	205	6	0.8	75	2	J01429	hypothetical 8.1K
133	7	1.0	544	2	S06602	modulo antigen - f	206	6	0.8	75	2	D82592	hypothetical prote
134	7	1.0	553	2	D95071	metallo-beta-lacta	207	6	0.8	77	2	T06954	hypothetical prote
135	7	1.0	553	2	B97939	conserved hypotet	208	6	0.8	77	2	AC2101	lipoprotein (Impor
136	7	1.0	556	2	S02154	NADH2 dehydrogenas	209	6	0.8	78	2	A42506	F-ORF-B protein -
137	7	1.0	561	2	C75543	6-aminohexanoate-c	210	6	0.8	79	2	D69309	conserved hypotet
138	7	1.0	580	2	D84772	probable sugar tra	211	6	0.8	80	2	E97949	hypothetical prote
139	7	1.0	581	2	T38864	probable regulator	212	6	0.8	84	2	S27152	heparin-binding ep
140	7	1.0	582	2	F71431	hypothetical prote	213	6	0.8	85	2	G64217	ribosomal protein
141	7	1.0	583	2	T25690	hypothetical prote	214	6	0.8	85	2	T12211	auxin-induced prot
142	7	1.0	585	2	T18736	hypothetical prote	215	6	0.8	86	2	T02494	hypothetical prote
143	7	1.0	617	2	S10511	hypothetical prote	216	6	0.8	86	2	E90660	damage-inducible p
144	7	1.0	617	2	D90487	thrombin (EC 3.4.2	217	6	0.8	86	2	C85511	DNA-damage-inducib
145	7	1.0	618	2	A35827	maltose ABC transp	218	6	0.8	86	2	C64747	hypothetical prote
146	7	1.0	622	1	TBRU	thrombin (EC 3.4.2	219	6	0.8	87	2	T10462	hypothetical prote
147	7	1.0	625	1	TBBO	thrombin (EC 3.4.2	220	6	0.8	87	2	T50008	hypothetical prote
148	7	1.0	658	2	T04831	probable serine/th	221	6	0.8	88	2	B82860	hypothetical prote
149	7	1.0	678	2	D87607	hypothetical prote	222	6	0.8	88	2	C97251	probable membrane
150	7	1.0	684	2	H96646	hypothetical prote	223	6	0.8	88	2	AB1901	hypothetical prote
151	7	1.0	684	2	T02149	hypothetical prote	224	6	0.8	91	2	C81922	hypothetical prote
152	7	1.0	707	2	JC2218	procollagen C-endo	225	6	0.8	91	2	AE0710	probable exported
153	7	1.0	708	2	T43109	cyclolysin B transp	226	6	0.8	92	2	F36905	conserved hypotet
154	7	1.0	746	2	C95110	competence protein	227	6	0.8	94	2	T44722	probable transcrip
155	7	1.0	783	2	B83232	conserved hypotet	228	6	0.8	95	2	C83517	hypothetical prote
156	7	1.0	790	2	G02678	cadherin-14 huma	229	6	0.8	98	2	B82483	hypothetical prote
157	7	1.0	791	2	H96839	hypothetical prote	230	6	0.8	98	2	T44883	hypothetical prote
158	7	1.0	826	2	T06036	hypothetical prote	231	6	0.8	98	2	S03386	antigen (clone 22)
159	7	1.0	833	2	S50225	potassium transpor	232	6	0.8	99	2	S44658	ZK353.2 protein -
160	7	1.0	841	2	T38703	hypothetical prote	233	6	0.8	100	2	C71012	hypothetical prote
161	7	1.0	856	2	T16543	hypothetical prote	234	6	0.8	102	2	D84024	transposase - Bact
162	7	1.0	859	2	S66827	aluminium resistan	235	6	0.8	104	2	F45681	orf 61.2 - phage T
163	7	1.0	903	2	E88221	protein T01H3.2 (1	236	6	0.8	104	2	C69068	divalent cation to
164	7	1.0	980	2	T24336	hypothetical prote	237	6	0.8	105	2	D90392	conserved hypotet
165	7	1.0	995	2	A88483	protein COSD1.1 (238	6	0.8	106	2	G71517	probable L21 ribos
166	7	1.0	1048	2	T31653	hypothetical prote	239	6	0.8	107	2	G84532	similar to gibbere
167	7	1.0	1100	2	JC8033	leukocyte formin p	240	6	0.8	108	2	A28657	hypothetical prote
168	7	1.0	1240	2	T04833	hypothetical prote	241	6	0.8	108	2	B53291	tetracenomycin-bio
169	7	1.0	1346	2	T17412	polyketide synthas	242	6	0.8	109	2	T43985	hypothetical prote
170	7	1.0	1522	2	S48904	probable purine nu	243	6	0.8	109	2	T44129	hypothetical prote
171	7	1.0	1742	2	T49451	kinesin-like prote	244	6	0.8	113	2	T45195	hypothetical prote
172	7	1.0	1822	2	T50207	probable protein t	245	6	0.8	113	2	T26771	hypothetical prote
173	7	1.0	2605	2	T18552	safamycin Mx1 syn	246	6	0.8	114	2	H72705	hypothetical prote
174	7	1.0	2907	2	A57278	fibrillin-2 precur	247	6	0.8	115	2	D96530	probable ribosomal
175	7	1.0	2918	2	A54105	fibrillin-2 precur	248	6	0.8	116	2	D96530	probable ribosomal

249	6	0.8	117	2	151573	gene wnt-2 protein
250	6	0.8	117	2	H90021	50S ribosomal prot
251	6	0.8	117	2	C72511	hypothetical prote
252	6	0.8	118	2	H71564	hypothetical prote
253	6	0.8	118	2	T14660	hypothetical prote
254	6	0.8	118	2	JC5793	elongin B - fruit
255	6	0.8	119	2	F70941	hypothetical prote
256	6	0.8	122	2	H64217	ribosomal protein
257	6	0.8	122	2	S62831	ribosomal protein
258	6	0.8	123	2	E71163	hypothetical prote
259	6	0.8	123	2	S72389	hypothetical prote
260	6	0.8	123	2	S75382	hypothetical prote
261	6	0.8	124	1	KNI171	nonstructural prot
262	6	0.8	124	2	A81163	conserved hypotnet
263	6	0.8	124	2	F81942	probable regulator
264	6	0.8	126	2	T47297	hypothetical prote
265	6	0.8	127	2	T14956	hypothetical prote
266	6	0.8	127	2	F69377	moxydenum-pterin-
267	6	0.8	127	2	T05261	cold-regulated pro
268	6	0.8	129	2	T06188	probable DNA-direc
269	6	0.8	129	2	S52792	Ig kappa chain V r
270	6	0.8	129	2	C69488	LSU ribosomal prot
271	6	0.8	129	2	E75602	hypothetical prote
272	6	0.8	130	2	S57896	polyketide synthas
273	6	0.8	130	2	T35906	probable quinone b
274	6	0.8	130	2	B83992	hypothetical prote
275	6	0.8	131	2	T49455	hypothetical prote
276	6	0.8	131	2	T29078	hypothetical prote
277	6	0.8	132	2	T50416	40S ribosomal prot
278	6	0.8	132	2	H87626	hypothetical prote
279	6	0.8	133	2	E71062	hypothetical prote
280	6	0.8	133	2	F81748	conserved hypotnet
281	6	0.8	133	2	H81191	hypothetical prote
282	6	0.8	134	2	E71945	hypothetical prote
283	6	0.8	134	2	E64561	conserved hypotnet
284	6	0.8	134	2	B72651	hypothetical prote
285	6	0.8	136	2	E69376	hypothetical prote
286	6	0.8	136	2	E80394	ferric uptake regu
287	6	0.8	137	2	A83852	hypothetical prote
288	6	0.8	138	2	D83824	transcription regu
289	6	0.8	138	2	T29558	hypothetical prote
290	6	0.8	139	2	G90414	conserved hypotnet
291	6	0.8	140	2	E81659	conserved hypotnet
292	6	0.8	141	2	T33271	hypothetical prote
293	6	0.8	141	2	S55247	hemoglobin alpha-A
294	6	0.8	141	2	T39720	ORF10 - Agrobacter
295	6	0.8	141	2	G72661	hypothetical prote
296	6	0.8	143	2	S50549	hypothetical prote
297	6	0.8	143	2	B72627	hypothetical prote
298	6	0.8	144	2	T49457	hypothetical prote
299	6	0.8	145	2	C64447	hypothetical prote
300	6	0.8	145	2	E84251	hypothetical prote
301	6	0.8	146	2	H64340	hypothetical prote
302	6	0.8	147	2	S01655	alpha-amylose/tryp
303	6	0.8	147	2	T35980	probable pepide t
304	6	0.8	149	2	T35846	probable integrat
305	6	0.8	149	2	T49200	hypothetical prote
306	6	0.8	150	2	AC1720	transcription regu
307	6	0.8	151	2	C71503	probable rRNA meth
308	6	0.8	151	2	B87624	transcription regu
309	6	0.8	151	2	A97008	transcription regu
310	6	0.8	152	2	D98270	hypothetical prote
311	6	0.8	153	2	T06564	hypothetical prote
312	6	0.8	153	2	C98238	alpha-amylose/tryp
313	6	0.8	153	2	AH3047	conserved hypotnet
314	6	0.8	153	2	AB1907	hypothetical prote
315	6	0.8	154	2	E83634	hypothetical prote
316	6	0.8	155	2	B90143	hypothetical prote
317	6	0.8	155	2	A82884	conserved hypotnet
318	6	0.8	156	2	G69233	N-terminal acetylt
319	6	0.8	157	2	T28321	ORF MSV160 hypothe
320	6	0.8	158	2	D82499	hypothetical prote
321	6	0.8	159	2	B70635	hypothetical prote
322	6	0.8	159	2	A72709	hypothetical prote
323	6	0.8	159	2	D86743	hypothetical prote
324	6	0.8	159	2	D86286	Similar to gb - Ar
325	6	0.8	160	2	H55545	ARA-III adhesin -
326	6	0.8	160	2	T35987	probable ribosome-
327	6	0.8	160	2	AC0835	Sera (tmRNA)-bindi
328	6	0.8	160	2	AE0135	Sera-binding prote
329	6	0.8	160	2	T48148	hypothetical prote
330	6	0.8	161	2	T31531	hypothetical prote
331	6	0.8	161	2	E90372	conserved hypotnet
332	6	0.8	162	2	H75071	transcription regu
333	6	0.8	162	2	C97657	pepx protein [mpo
334	6	0.8	162	2	AC2881	DNA-binding protei
335	6	0.8	162	2	H70803	probable transcrip
336	6	0.8	162	2	AB1950	hypothetical prote
337	6	0.8	162	2	H71093	hypothetical prote
338	6	0.8	163	2	B97290	3-isopropylmalate
339	6	0.8	164	2	A45512	cold-regulated pro
340	6	0.8	164	2	UC4675	transcription fact
341	6	0.8	165	2	AB0851	hypothetical prote
342	6	0.8	165	2	S70217	sipe protein - Sal
343	6	0.8	165	2	A57357	sica protein - Sal
344	6	0.8	165	2	H86948	probable transcrip
345	6	0.8	166	2	I39546	hypothetical prote
346	6	0.8	167	2	E71391	NADH2 dehydrogenas
347	6	0.8	167	2	AD0601	DNA protection dur
348	6	0.8	167	2	B90740	global regulator p
349	6	0.8	167	2	A46401	DNA-binding protei
350	6	0.8	167	2	D85580	global regulator,
351	6	0.8	167	2	AG0306	probable DNA-bind
352	6	0.8	167	2	E11411	hypothetical prote
353	6	0.8	168	2	A69708	signal peptidase I
354	6	0.8	169	2	B48489	nitrate reductase
355	6	0.8	170	2	A88638	protein P58F.3 [i
356	6	0.8	171	2	S76982	hypothetical prote
357	6	0.8	171	2	T41924	hypothetical prote
358	6	0.8	172	2	AG3532	D-lactate dehydrat
359	6	0.8	172	2	G82151	peptidoglycan-asso
360	6	0.8	172	2	G69087	conserved hypotnet
361	6	0.8	172	2	AE2283	hypothetical prote
362	6	0.8	172	2	D71136	hypothetical prote
363	6	0.8	173	2	H70113	ribosomal protein
364	6	0.8	174	2	E69038	heat shock protein
365	6	0.8	175	2	T07877	self-pruning prote
366	6	0.8	175	2	AC3014	MuTr/mudix family
367	6	0.8	175	2	G86458	unknown protein,
368	6	0.8	176	2	A34680	DNA-binding protei
369	6	0.8	176	2	AE0866	conserved hypotnet
370	6	0.8	177	2	S45878	hypothetical prote
371	6	0.8	177	2	E95222	conserved hypotnet
372	6	0.8	177	2	D75309	protein-tyrosine p
373	6	0.8	177	2	E98086	conserved hypotnet
374	6	0.8	178	2	A93637	probable NADH2 deh
375	6	0.8	178	2	B42845	3-hydroxybutyrate
376	6	0.8	178	2	H84789	hypothetical prote
377	6	0.8	178	2	A86836	hypothetical prote
378	6	0.8	178	2	S26481	calcium-binding pr
379	6	0.8	179	2	G75452	ribonuclease H - D
380	6	0.8	179	2	G90003	ATP synthase delta
381	6	0.8	180	2	PC1305	genome polypotein
382	6	0.8	180	2	PC1304	genome polypotein
383	6	0.8	180	2	PC1303	genome polypotein
384	6	0.8	180	2	T23339	hypothetical prote
385	6	0.8	182	2	T33915	meiotic recombinat
386	6	0.8	182	2	A72361	hypothetical prote
387	6	0.8	183	2	E69432	hypothetical prote
388	6	0.8	183	2	T07677	plastid-specific pr
389	6	0.8	184	2	T09609	uropodlaklin II - hum
390	6	0.8	184	2	A54135	uropodlaklin II precu
391	6	0.8	184	2	UC7839	uropodlaklin II prote
392	6	0.8	184	2	E87506	hypothetical prote
393	6	0.8	185	2	F70479	flavodoxin - Aquif
394	6	0.8	185	2	B81732	general stress pro

395	6	0.8	185	2	E71469	probable general s
396	6	0.8	185	2	A49713	uroplakin II precu
397	6	0.8	186	1	R5B98E	ribosomal protein
398	6	0.8	186	2	T41601	hypothetical prote
399	6	0.8	187	2	G75022	hypothetical prote
400	6	0.8	187	2	B83084	probable transcrip
401	6	0.8	188	2	S70680	bpiu protein - Bor
402	6	0.8	189	1	XMECFD	3-octaprenyl-4-hyd
403	6	0.8	189	2	AB0801	probable decarboxy
404	6	0.8	189	2	C91028	3-octaprenyl-4-hyd
405	6	0.8	189	2	D85872	3-octaprenyl-4-hyd
406	6	0.8	189	2	D71658	3-octaprenyl-4-hyd
407	6	0.8	189	2	T51064	hypothetical prote
408	6	0.8	189	2	AB0361	probable iron-sulp
409	6	0.8	190	2	AB0338	probable 3-octapre
410	6	0.8	191	2	A97800	hypothetical prote
411	6	0.8	191	2	C64574	hypothetical prote
412	6	0.8	192	2	A45836	MHC class II histo
413	6	0.8	192	2	H72099	phenylacrylate dec
414	6	0.8	192	2	H86523	phenylacrylate dec
415	6	0.8	192	2	E75021	probable transcrip
416	6	0.8	193	2	T30325	hypothetical prote
417	6	0.8	194	1	H5H10	histone H1-0 - hum
418	6	0.8	194	2	C82041	general secretion
419	6	0.8	196	2	D86190	decarboxylase (imp
420	6	0.8	196	2	A63096	phenylacrylic acid
421	6	0.8	196	2	AC3629	3-octaprenyl-4-hyd
422	6	0.8	197	1	R5WUL9	probable decarboxy
423	6	0.8	197	2	E95411	probable lipoprote
424	6	0.8	197	2	B70761	hypothetical prote
425	6	0.8	197	2	D87309	hypothetical prote
426	6	0.8	197	2	H75188	hypothetical prote
427	6	0.8	198	2	E81391	probable transcrip
428	6	0.8	198	2	AC1890	hypothetical prote
429	6	0.8	199	2	A46681	glutathione transf
430	6	0.8	199	2	G75575	hypothetical prote
431	6	0.8	200	2	B95349	probable decarboxy
432	6	0.8	201	2	C36885	bo-type ubiquitinol
433	6	0.8	201	2	AD2419	SOS function regul
434	6	0.8	201	2	C69271	hypothetical prote
435	6	0.8	202	2	H81731	CDP-diacylglycerol
436	6	0.8	202	2	C71469	probable glycerol-
437	6	0.8	202	2	T37025	probable sigma fac
438	6	0.8	202	2	AD2197	hypothetical prote
439	6	0.8	202	2	D72573	hypothetical prote
440	6	0.8	203	2	S74809	lexa protein - Sym
441	6	0.8	203	2	AH0223	probable glycosida
442	6	0.8	204	2	C38129	bo-type ubiquitinol
443	6	0.8	204	2	S03246	nef protein (clone
444	6	0.8	204	2	G71172	hypothetical prote
445	6	0.8	205	1	XMBSTI	regulatory protein
446	6	0.8	205	1	ASLJH3	nef protein - huma
447	6	0.8	205	2	D85764	probable oxidoredu
448	6	0.8	205	2	G64914	dimethylsulfoxide
449	6	0.8	205	2	G90915	probable oxidoredu
450	6	0.8	205	2	T01744	ribosomal protein
451	6	0.8	205	2	S43467	nef protein - huma
452	6	0.8	205	2	D69036	conserved hypotnet
453	6	0.8	205	2	C83325	maf protein VC0418
454	6	0.8	205	2	UC7975	HIV accessory prot
455	6	0.8	206	1	ASLJ12	nef protein - huma
456	6	0.8	206	1	ASLJFV	nef protein - huma
457	6	0.8	206	1	ASLJVL	nef protein - huma
458	6	0.8	206	2	A86609	glycerol-3-P phosp
459	6	0.8	206	2	B72016	CDP-diacylglycerol
460	6	0.8	206	2	S03245	nef protein (clone
461	6	0.8	206	2	S33986	nef protein - huma
462	6	0.8	206	2	S03244	nef protein (clone
463	6	0.8	206	2	A39268	heparin-binding pr
464	6	0.8	208	1	A38432	heparin-binding EG
465	6	0.8	208	1	A41914	diphtheria toxin re
466	6	0.8	208	2	E41636	GTP-binding protei
467	6	0.8	208	2	E64357	ribosomal protein
468	6	0.8	208	2	D87565	conserved hypotnet
469	6	0.8	209	2	A99460	conserved hypotnet
470	6	0.8	209	2	C87521	hypothetical prote
471	6	0.8	209	2	T07779	dehydrin homolog C
472	6	0.8	210	2	G95858	probable 3-octapre
473	6	0.8	210	2	D84238	hypothetical prote
474	6	0.8	210	2	H75361	leu/phe-tRNA-prote
475	6	0.8	211	1	ZKEP74	transcription regu
476	6	0.8	211	2	T47580	ribosomal protein
477	6	0.8	211	2	S45464	hypothetical prote
478	6	0.8	212	1	Q0LJZR	nef protein - huma
479	6	0.8	212	1	S37973	DNA-directed RNA p
480	6	0.8	214	2	D46601	glutathione transf
481	6	0.8	214	2	E46601	glutathione transf
482	6	0.8	214	2	T14920	hypothetical prote
483	6	0.8	215	2	C46681	glutathione transf
484	6	0.8	215	2	AD0455	thiamine-phosphate
485	6	0.8	215	2	T45985	hypothetical prote
486	6	0.8	215	2	T16383	hypothetical prote
487	6	0.8	216	1	C64081	L-fuculose-phospha
488	6	0.8	216	2	D86564	yege family (impor
489	6	0.8	216	2	G72060	yege family - Chla
490	6	0.8	216	2	G72509	hypothetical prote
491	6	0.8	217	2	D82407	outer membrane pro
492	6	0.8	218	2	F85571	probable carboxyla
493	6	0.8	218	2	H90720	probable carboxyla
494	6	0.8	218	2	F64806	YpgJ protein - Bsc
495	6	0.8	218	2	B64595	endonuclease III -
496	6	0.8	218	2	C71918	endonuclease III -
497	6	0.8	218	2	A70601	hypothetical prote
498	6	0.8	218	2	T50440	hypothetical prote
499	6	0.8	218	2	AG3301	glycerone kinase (
500	6	0.8	218	2	H87666	conserved hypotnet
501	6	0.8	218	2	E75389	hypothetical prote
502	6	0.8	218	2	G69374	hypothetical prote
503	6	0.8	218	2	A13612	hypothetical cytos
504	6	0.8	220	2	S20581	14-3-3 protein hom
505	6	0.8	220	2	T26991	hypothetical prote
506	6	0.8	221	2	B70890	hypothetical prote
507	6	0.8	221	2	A11232	oligopeptide ABC t
508	6	0.8	222	2	AC1495	ribulose-5-phospha
509	6	0.8	222	2	T35145	glutamate transpor
510	6	0.8	222	2	AH0991	cell division ATP-
511	6	0.8	222	2	AB1408	hypothetical prote
512	6	0.8	223	2	AG1166	Ribulose-5-Phospha
513	6	0.8	223	2	C81397	phosphoribosylform
514	6	0.8	223	2	T34828	potassium uptake p
515	6	0.8	223	2	D75040	hypothetical prote
516	6	0.8	223	2	T31703	hypothetical prote
517	6	0.8	224	1	R5SP11	ribosomal protein
518	6	0.8	224	2	C86571	L4 ribosomal prote
519	6	0.8	224	2	H72055	ribosomal protein
520	6	0.8	224	2	C81417	probable transcrip
521	6	0.8	224	2	T71101	hypothetical prote
522	6	0.8	225	2	B97580	hypothetical prote
523	6	0.8	225	2	AH2800	conserved hypotnet
524	6	0.8	225	2	T29632	hypothetical prote
525	6	0.8	226	2	A35968	tox regulon trans
526	6	0.8	227	2	T22144	hypothetical prote
527	6	0.8	227	2	A87351	flagellar hook ass
528	6	0.8	227	2	T41133	hypothetical prote
529	6	0.8	228	2	AB0438	conserved hypotnet
530	6	0.8	228	2	B82087	probable smp prote
531	6	0.8	229	2	S70599	cycochrome-c oxida
532	6	0.8	229	2	S14207	cycochrome-c oxida
533	6	0.8	229	2	C90912	probable antilemi
534	6	0.8	229	2	P90972	antilemmator (im
535	6	0.8	229	2	C85820	antilemmator (im
536	6	0.8	229	2	T48348	lysine decarboxyla
537	6	0.8	230	1	KN1V16	nonstructural prot
538	6	0.8	230	1	KN1V45	nonstructural prot
539	6	0.8	230	1	KN1V46	nonstructural prot
540	6	0.8	230	1	KN1V47	nonstructural prot

541	6	0.8	230	1	MNIVA8	nonstructural prot	614	6	0.8	257	2	T00064	MERS protein - mou
542	6	0.8	230	2	A45575	nonstructural prot	615	6	0.8	257	2	T00780	myb-related protei
543	6	0.8	230	2	G70504	probable cmk prote	616	6	0.8	257	2	T33392	hypothetical prote
544	6	0.8	231	2	S57271	14-3-3 protein lft	617	6	0.8	258	2	T07389	14-3-3 protein lft
545	6	0.8	231	2	D49934	phosphoglycolate p	618	6	0.8	258	2	T04131	14-3-3 protein, is
546	6	0.8	231	2	B69858	hypothetical prote	619	6	0.8	258	2	AF0016	probable biotin bi
547	6	0.8	231	2	AI3283	transcription regu	620	6	0.8	258	2	AH2615	hypothetical prote
548	6	0.8	232	2	AG2555	hypothetical prote	621	6	0.8	258	2	G86764	hypothetical prote
549	6	0.8	233	2	I55654	MHC class II prote	622	6	0.8	258	2	T31647	hypothetical prote
550	6	0.8	233	2	C82360	cell division ATP-	623	6	0.8	259	1	A47237	14-3-3 protein hom
551	6	0.8	233	2	A72786	hypothetical transp	624	6	0.8	259	2	B69113	cell division inh
552	6	0.8	233	2	H75359	hypothetical prote	625	6	0.8	259	2	G97397	ubiquitinone/menqu
553	6	0.8	234	2	S61309	nitrate reductase	626	6	0.8	259	2	D81083	conserved hypochet
554	6	0.8	234	2	T07686	transcription fact	627	6	0.8	259	2	D81659	conserved hypochet
555	6	0.8	234	2	F95952	probable membrane-	628	6	0.8	260	1	S30927	14-3-3 protein hom
556	6	0.8	234	2	C97001	ABC transporter, A	629	6	0.8	260	2	T07388	14-3-3 protein lft
557	6	0.8	235	2	B98108	response regulator	630	6	0.8	260	2	T02051	14-3-3 protein hom
558	6	0.8	235	2	E95243	response regulator	631	6	0.8	260	2	S20580	14-3-3 protein hom
559	6	0.8	235	2	C75030	hypothetical prote	632	6	0.8	260	2	D69299	hypothetical prote
560	6	0.8	236	2	AH3230	hypothetical prote	633	6	0.8	260	2	T51079	related to chitina
561	6	0.8	236	2	E42600	probable octopine	634	6	0.8	261	1	S18911	14-3-3 protein hom
562	6	0.8	236	2	T10417	p25 protein - Orgy	635	6	0.8	261	2	S52110	sepiapterin reduct
563	6	0.8	236	2	T02432	ethylene-responsive	636	6	0.8	261	2	A71192	probable glucose 1
564	6	0.8	237	2	E97712	transcription acti	637	6	0.8	261	2	S52899	14-3-3 protein hom
565	6	0.8	237	2	C70157	hypothetical prote	638	6	0.8	261	2	H83442	probable enoyl-CoA
566	6	0.8	238	2	I71907	MHC H2-IE-beta cel	639	6	0.8	261	2	H70100	conserved hypochet
567	6	0.8	238	2	T14629	hypothetical prote	640	6	0.8	261	2	D64166	hypothetical prote
568	6	0.8	239	2	A72623	hypothetical prote	641	6	0.8	262	2	H71390	cytochrome-c oxida
569	6	0.8	239	2	D81351	hypothetical prote	642	6	0.8	262	2	T04406	14-3-3b protein -
570	6	0.8	240	2	T24239	hypothetical prote	643	6	0.8	262	2	S57276	14-3-3 protein hom
571	6	0.8	241	2	I48657	I-E(I-beta) protei	644	6	0.8	262	2	T47002	hypothetical prote
572	6	0.8	241	2	T23823	hypothetical prote	645	6	0.8	262	2	AH0238	probable phosphate
573	6	0.8	241	2	H81536	hypothetical prote	646	6	0.8	262	2	T22148	hypothetical prote
574	6	0.8	242	2	B82815	conserved hypochet	647	6	0.8	263	2	F87043	BCF subfamily alim
575	6	0.8	243	2	TX0162	lectin I - furze	648	6	0.8	263	2	T26031	hypothetical prote
576	6	0.8	244	2	C95901	probable short cha	649	6	0.8	263	2	T18930	hypothetical prote
577	6	0.8	244	2	S76160	hypothetical prote	650	6	0.8	264	1	HLMSB1	H-2 class II histo
578	6	0.8	245	2	S28827	chlorophyll a/b-bi	651	6	0.8	264	1	HLMSB	H-2 class II histo
579	6	0.8	246	1	S56439	ammonium transp	652	6	0.8	264	1	C64368	cell division inh
580	6	0.8	246	2	T51631	probable transcrip	653	6	0.8	264	2	A30529	H-2 class II histo
581	6	0.8	246	2	AF1054	cybQ protein (limp	654	6	0.8	264	2	I56055	MHC E-beta-E - mou
582	6	0.8	246	2	H86118	ammonium transp	655	6	0.8	264	2	A81668	conserved hypochet
583	6	0.8	246	2	H91277	ammonium transp	656	6	0.8	264	2	E71509	hypothetical prote
584	6	0.8	247	2	JT0555	MHC class II histo	657	6	0.8	264	2	T13116	protein gp30 - pha
585	6	0.8	247	2	S23474	rod-core linker po	658	6	0.8	264	2	D71037	hypothetical prote
586	6	0.8	247	2	H90419	hypothetical prote	659	6	0.8	265	2	T30346	NADH2 dehydrogen
587	6	0.8	248	2	S53727	14-3-3 protein hom	660	6	0.8	265	2	T12599	NADH2 dehydrogen
588	6	0.8	249	2	F87153	probable pseudouri	661	6	0.8	265	2	T12601	NADH2 dehydrogen
589	6	0.8	249	2	H72200	conserved hypochet	662	6	0.8	265	2	T12601	hypothetical prote
590	6	0.8	250	2	T06338	probable vacuolar	663	6	0.8	266	2	D83210	hypothetical prote
591	6	0.8	250	2	S58362	nucleolar protein	664	6	0.8	266	2	T40318	hypothetical prote
592	6	0.8	250	2	S61626	hypothetical prote	665	6	0.8	266	2	AB3571	nickel transport A
593	6	0.8	250	2	T46912	hypothetical prote	666	6	0.8	267	2	H85090	14-3-3-like protei
594	6	0.8	250	2	H95161	conserved hypochet	667	6	0.8	267	2	C86472	probable 14-3-3 pr
595	6	0.8	250	2	G98027	conserved hypochet	668	6	0.8	267	2	S40006	trypsin (EC 3.4.21
596	6	0.8	250	2	E84708	probable signal pe	669	6	0.8	267	2	A98129	hypothetical prote
597	6	0.8	251	2	S47970	14-3-3 protein hom	670	6	0.8	267	2	AE3158	hypothetical prote
598	6	0.8	252	2	F84728	probable CCR4-asso	671	6	0.8	267	2	H90368	hypothetical prote
599	6	0.8	253	1	DLDO1A	discoicidin I chain	672	6	0.8	267	2	G84862	probable clathrin
600	6	0.8	253	1	DLDO1C	discoicidin I chain	673	6	0.8	268	2	H87708	exodeoxyribonuclea
601	6	0.8	253	2	AE0809	conserved hypochet	674	6	0.8	268	2	AG4123	tryptophan syntha
602	6	0.8	253	2	E64025	hypothetical prote	675	6	0.8	268	2	S11324	transcription fact
603	6	0.8	254	2	T07387	14-3-3 protein lft	676	6	0.8	268	2	T04965	hypothetical prote
604	6	0.8	254	2	S55375	14-3-3 protein p	677	6	0.8	268	2	T40606	hypothetical prote
605	6	0.8	254	2	T07103	14-3-3 protein hom	678	6	0.8	269	2	T36639	probable substrate
606	6	0.8	255	2	T04127	14-3-3 protein, is	679	6	0.8	269	2	AG3538	ubiquitinone/menau
607	6	0.8	255	2	T02050	GPI4-c protein hom	680	6	0.8	269	2	AE0466	probable haloacid
608	6	0.8	256	2	T04153	trypsin (EC 3.4.21	681	6	0.8	270	2	AB1308	conserved hypochet
609	6	0.8	256	2	T10109	amidease yeadh (limpo	682	6	0.8	270	2	AB1580	conserved hypochet
610	6	0.8	256	2	T44452	probable pseudouri	683	6	0.8	270	2	F69362	conserved hypochet
611	6	0.8	256	2	D70565	probable membrane	684	6	0.8	271	2	A85552	probable carboxyla
612	6	0.8	256	2	A10267	probable membrane	685	6	0.8	271	2	F90701	probable carboxyla
613	6	0.8	256	2	G71121	hypothetical prote	686	6	0.8	271	2	G64783	probable carboxyla

687	6	0.8	272	2	B75293	687	6	0.8	295	2	F83412	probable transcrip
688	6	0.8	272	2	AG2819	760	6	0.8	295	2	T32202	hypothetical prote
689	6	0.8	272	2	G97597	761	6	0.8	295	2	AD3225	ABC transporter, m
690	6	0.8	273	2	D81878	762	6	0.8	297	2	T46590	probable regulator
691	6	0.8	273	2	D81140	763	6	0.8	297	2	S55063	conserved hypotnet
692	6	0.8	273	2	T49994	764	6	0.8	297	2	H90154	hypothetical prote
693	6	0.8	273	2	F82999	765	6	0.8	297	2	D83357	probable transcrip
694	6	0.8	273	2	AG6280	766	6	0.8	297	2	T27525	hypothetical prote
695	6	0.8	273	2	A13630	767	6	0.8	298	2	AH0947	probable sugar kin
696	6	0.8	273	2	AC3573	768	6	0.8	298	2	C55223	minor tail protein
697	6	0.8	273	2	G83403	769	6	0.8	298	2	A28260	chromosomal protei
698	6	0.8	274	2	C05924	770	6	0.8	299	2	AE0269	conserved hypotnet
699	6	0.8	274	2	G86977	771	6	0.8	299	2	A87530	phosphorylase fami
700	6	0.8	274	2	H83707	772	6	0.8	299	2	S30861	hypothetical prote
701	6	0.8	274	2	D96840	773	6	0.8	300	1	S40827	probable sugar kin
702	6	0.8	274	2	H70247	774	6	0.8	300	1	F91229	probable kinase yi
703	6	0.8	275	2	S40007	775	6	0.8	300	2	E86076	probable kinase yi
704	6	0.8	275	2	S40005	776	6	0.8	301	2	AD0660	probable transcrip
705	6	0.8	275	2	E70693	777	6	0.8	301	2	E86486	protein F2809.4 [l
706	6	0.8	275	2	G83522	778	6	0.8	302	2	S69188	probable flavonol
707	6	0.8	276	2	JE0218	779	6	0.8	302	2	AF3306	dipeptide transpor
708	6	0.8	276	2	E84373	780	6	0.8	302	2	E84421	probable phosphati
709	6	0.8	278	2	AE0210	781	6	0.8	302	2	B70888	hypothetical prote
710	6	0.8	278	2	AD0146	782	6	0.8	302	2	PC4287	protein kinase (EC
711	6	0.8	279	1	S74824	783	6	0.8	302	2	D83082	probable permease
712	6	0.8	279	2	C70458	784	6	0.8	303	2	S77278	lipote acid synth
713	6	0.8	279	2	B70328	785	6	0.8	303	2	T36509	probable molybdopt
714	6	0.8	280	2	T36066	786	6	0.8	303	2	B72218	hypothetical prote
715	6	0.8	280	2	B84498	787	6	0.8	304	2	F83987	heat-shock protein
716	6	0.8	280	2	H72504	788	6	0.8	304	2	D72316	ribosomal large su
717	6	0.8	281	2	T43945	789	6	0.8	304	2	A96642	hypothetical prote
718	6	0.8	281	2	T05522	790	6	0.8	304	2	S75441	hypothetical prote
719	6	0.8	281	2	JE0418	791	6	0.8	305	2	T23022	hypothetical prote
720	6	0.8	282	2	AB1728	792	6	0.8	305	2	T20585	hypothetical prote
721	6	0.8	282	2	AC1054	793	6	0.8	306	2	A48552	transfer protein t
722	6	0.8	282	2	D81075	794	6	0.8	306	2	B83723	hypothetical prote
723	6	0.8	284	2	S75817	795	6	0.8	307	2	H70214	antigen, P35 homol
724	6	0.8	284	2	T24479	796	6	0.8	307	2	S55596	hypothetical prote
725	6	0.8	284	2	F81431	797	6	0.8	308	2	I40166	aspartate carbamoy
726	6	0.8	285	2	B83588	798	6	0.8	308	2	S77938	EBNA-LP protein -
727	6	0.8	285	2	F70194	799	6	0.8	308	2	T05297	hypothetical prote
728	6	0.8	285	2	AH0200	800	6	0.8	308	2	E90670	probable transcrip
729	6	0.8	286	2	E97720	801	6	0.8	309	2	E84550	hypothetical prote
730	6	0.8	286	2	A71722	802	6	0.8	310	2	AE3398	N-acetyl-gamma-glu
731	6	0.8	286	2	B83343	803	6	0.8	311	2	G90407	homoserine kinase
732	6	0.8	286	2	E91277	804	6	0.8	312	2	F82889	holliday junction
733	6	0.8	286	2	E86118	805	6	0.8	312	2	T45834	hypothetical prote
734	6	0.8	286	2	S86436	806	6	0.8	312	2	A12282	hypothetical prote
735	6	0.8	287	2	E75202	807	6	0.8	313	2	C69286	hypothetical prote
736	6	0.8	287	2	S03787	808	6	0.8	314	2	E96759	probable tumor-rel
737	6	0.8	287	2	AF0970	809	6	0.8	314	2	D97318	ABC-type MDR trans
738	6	0.8	287	2	F65165	810	6	0.8	316	2	E70664	hypothetical prote
739	6	0.8	287	2	H86040	811	6	0.8	316	2	B97086	hypothetical prote
740	6	0.8	287	2	G91193	812	6	0.8	316	2	B87185	3',5'-cyclic-nucle
741	6	0.8	287	2	E69778	813	6	0.8	317	1	E87185	hypothetical prote
742	6	0.8	288	2	G64102	814	6	0.8	317	2	E82672	ATP sulfurylase, s
743	6	0.8	288	2	T23721	815	6	0.8	317	2	S72871	hypothetical prote
744	6	0.8	288	2	D47468	816	6	0.8	318	1	F70536	3',5'-cyclic-nucle
745	6	0.8	290	2	E70141	817	6	0.8	318	2	C71168	hypothetical prote
746	6	0.8	290	2	T24747	818	6	0.8	319	2	AC2536	hypothetical prote
747	6	0.8	290	2	D71546	819	6	0.8	320	2	T10281	hypothetical prote
748	6	0.8	290	2	F81700	820	6	0.8	321	2	F97122	exopolysphatase
749	6	0.8	291	2	S05508	821	6	0.8	321	2	T27463	hypothetical prote
750	6	0.8	291	2	A97387	822	6	0.8	321	2	G72347	hypothetical prote
751	6	0.8	291	2	AB2605	823	6	0.8	321	2	F81030	ABC transporter, p
752	6	0.8	292	2	S54533	824	6	0.8	321	2	F81976	probable ferric en
753	6	0.8	292	2	T34529	825	6	0.8	321	2	A69088	conserved hypotnet
754	6	0.8	292	2	T52257	826	6	0.8	322	2	G72421	iron (III) ABC tran
755	6	0.8	292	2	H70513	827	6	0.8	322	2	E64238	hypothetical prote
756	6	0.8	293	1	D69300	828	6	0.8	322	2	E70306	conserved hypotnet
757	6	0.8	293	2	T41928	829	6	0.8	322	2	AF2725	transcription regu
758	6	0.8	293	2	T31618	830	6	0.8	322	2	B97507	probable transcrip
759	6	0.8	293	2	B75570	831	6	0.8	323	2	T2492	hypothetical prote
						832	6	0.8	323	2	T47447	sulfoctransferase-1

833	6	0.8	323	2	E83454	flagellar motor sw	506	6	0.8	344	2	C75203	hypothetical prote
834	6	0.8	324	2	T07832	probable steroid s	507	6	0.8	345	2	T17065	NADH2 dehydrogenas
835	6	0.8	324	2	F86788	transcription regu	508	6	0.8	345	2	JC1174	antidase (EC 3.5.1.
836	6	0.8	325	1	A45470	hydroxymethylglu	509	6	0.8	345	2	S73729	MC307 homolog H08
837	6	0.8	325	2	T1610	probable cinnamyl-	510	6	0.8	345	2	A98251	hypothetical prote
838	6	0.8	325	2	T07833	probable steroid s	511	6	0.8	345	2	AB3035	conserved hypochet
839	6	0.8	325	2	T57009	3-hydroxy-3-methyl	512	6	0.8	346	2	UC7523	catabolite control
840	6	0.8	325	2	G90040	uroporphyrin-III C	513	6	0.8	346	2	C96739	hypothetical prote
841	6	0.8	325	2	T23426	hypothetical prote	514	6	0.8	346	2	D42087	al-phenomone recep
842	6	0.8	326	2	T03928	probable peroxidase	515	6	0.8	346	2	S64693	pheromone receptor
843	6	0.8	326	2	F86407	probable sulfoxtran	516	6	0.8	346	2	T46914	hypothetical prote
844	6	0.8	326	2	A84452	probable steroid s	517	6	0.8	347	2	T22655	hypothetical prote
845	6	0.8	326	2	A41732	heterogeneous ribo	518	6	0.8	348	2	D84798	probable mitochond
846	6	0.8	326	2	S49537	hypothetical prote	519	6	0.8	348	2	D84922	probable sugar tra
847	6	0.8	327	2	AB1822	pyruvate dehydroge	520	6	0.8	348	2	T31681	bacs protein - Bac
848	6	0.8	327	2	T19529	hypothetical prote	521	6	0.8	348	2	F96997	uncharacterized co
849	6	0.8	328	2	T27911	hypothetical prote	522	6	0.8	350	2	T25366	hypothetical prote
850	6	0.8	328	2	T50104	hypothetical prote	523	6	0.8	351	2	G96923	NADH-dependent fla
851	6	0.8	328	2	B95307	hypothetical prote	524	6	0.8	351	2	T01845	hypothetical prote
852	6	0.8	328	2	B95404	probable ABC trans	525	6	0.8	352	2	A39042	fatty-acid synthas
853	6	0.8	329	2	T47448	sulfoxtranferase-1	526	6	0.8	352	2	E83519	quinolinate synthe
854	6	0.8	329	2	C97264	UDP-galactose 4-ep	527	6	0.8	353	2	S74379	probable ATPase -
855	6	0.8	329	2	AD1170	lipote-protein li	528	6	0.8	353	2	F84252	phycocyanin alpha
856	6	0.8	329	2	AP1527	lipote-protein li	529	6	0.8	353	2	H71223	probable dolichol-
857	6	0.8	329	2	T09897	hypothetical prote	530	6	0.8	354	2	C81986	probable O-sialogl
858	6	0.8	329	2	H85520	probable LysR-like	531	6	0.8	354	2	C81040	O-sialoglycoprotei
859	6	0.8	330	2	H88115	protein F53C3.1 li	532	6	0.8	355	2	C86592	antipeptidase P l
860	6	0.8	330	2	F72428	oligopeptide ABC t	533	6	0.8	355	2	B72032	proline dipeptidas
861	6	0.8	330	2	A85074	ABC transporter, A	534	6	0.8	356	2	T36951	probable zinc-cont
862	6	0.8	330	2	B97941	hypothetical prote	535	6	0.8	356	2	H84934	UDP-N-acetylmutama
863	6	0.8	331	2	F70212	hypothetical prote	536	6	0.8	356	2	H72214	hypothetical prote
864	6	0.8	331	2	B87359	riboflavin biosynt	537	6	0.8	356	2	AC1888	hypothetical prote
865	6	0.8	331	2	E82170	peptide ABC transp	538	6	0.8	357	2	E64233	membrane transport
866	6	0.8	332	2	T47703	Ca-dependent solut	539	6	0.8	358	2	T45934	hypothetical prote
867	6	0.8	332	2	A1355	low-affinity inorg	540	6	0.8	358	2	JQ0596	nucleosid prote
868	6	0.8	332	2	AB1726	low-affinity inorg	541	6	0.8	359	2	T36443	probable penicilli
869	6	0.8	333	1	H64400	hypothetical prote	542	6	0.8	359	2	T29647	hypothetical prote
870	6	0.8	333	2	A84523	probable steroid s	543	6	0.8	360	2	D83255	3-isopropylmalate
871	6	0.8	333	2	A41881	collagenase Pric (544	6	0.8	361	1	SYEBKR	choisimate synthas
872	6	0.8	334	2	T19637	hypothetical prote	545	6	0.8	361	1	SYECCR	choisimate synthas
873	6	0.8	334	2	B87545	hypothetical prote	546	6	0.8	361	2	AF0804	choisimate synthas
874	6	0.8	334	2	AB3414	probable transcrip	547	6	0.8	361	2	E91030	choisimate synthas
875	6	0.8	335	2	G70369	sialoglycoproteina	548	6	0.8	361	2	F85874	choisimate synthas
876	6	0.8	335	2	F96999	hydrogenase format	549	6	0.8	361	2	F82115	choisimate synthas
877	6	0.8	335	2	H81677	conserved hypochet	550	6	0.8	361	2	JC6314	major porin protei
878	6	0.8	335	2	H91191	hypothetical prote	551	6	0.8	361	2	A43510	basic membrane pro
879	6	0.8	335	2	A86039	probable LPS biosy	552	6	0.8	362	2	D72734	probable histidine
880	6	0.8	335	2	AB2193	hypothetical prote	553	6	0.8	362	2	G84526	hypothetical prote
881	6	0.8	335	2	T33457	hypothetical prote	554	6	0.8	364	2	AB2993	glycosyltransferas
882	6	0.8	335	2	E71215	hypothetical prote	555	6	0.8	364	2	H70776	hypothetical prote
883	6	0.8	335	2	E61299	lipopolysaccharide	556	6	0.8	365	1	A44974	ferredoxin-NADP re
884	6	0.8	336	2	CE1073	ADP-heptose-LPS he	557	6	0.8	365	2	T23220	hypothetical prote
885	6	0.8	336	2	B81869	lipopolysaccharide	558	6	0.8	366	1	JN0146	hypothetical prote
886	6	0.8	336	2	A97305	hypothetical prote	559	6	0.8	366	2	A64950	membrane-bound pen
887	6	0.8	337	2	AH0972	lipopolysaccharide	560	6	0.8	366	2	C85800	probable cytochrom
888	6	0.8	339	2	AD0009	glycerol-3-phospha	561	6	0.8	366	2	G90951	probable cytochrom
889	6	0.8	339	2	T46731	hypothetical prote	562	6	0.8	366	2	JE0105	testicular serine
890	6	0.8	339	2	E85962	probable taurine u	563	6	0.8	366	2	F87508	GTP-binding protei
891	6	0.8	339	2	E82211	conserved hypochet	564	6	0.8	367	2	S68680	stress-activated p
892	6	0.8	339	2	G82113	lipoprotein-34 NLP	565	6	0.8	367	2	JE0104	testicular serine
893	6	0.8	339	2	F97121	probable membrane-	566	6	0.8	367	2	H81088	membrane-bound lyc
894	6	0.8	340	2	T35394	probable glycerol	567	6	0.8	368	2	G85587	hypothetical prote
895	6	0.8	340	2	T14774	hypothetical prote	568	6	0.8	368	2	F90737	hypothetical prote
896	6	0.8	341	2	T33221	hypothetical prote	569	6	0.8	368	2	H64815	Yjhr protein - Bac
897	6	0.8	341	2	AB1394	galactosyltransfer	570	6	0.8	369	1	RDSPXX	ferredoxin-NADP re
898	6	0.8	341	2	AB1769	galactosyltransfer	571	6	0.8	369	2	F81674	conserved hypochet
899	6	0.8	342	2	H86893	elongation factor	572	6	0.8	369	2	S37314	cycH protein - Bra
900	6	0.8	342	2	A10043	conserved hypochet	573	6	0.8	369	2	H82404	hypothetical prote
901	6	0.8	342	2	AP1398	ATP binding protei	574	6	0.8	370	2	F95363	probable serine-py
902	6	0.8	342	2	AC1774	ATP binding protei	575	6	0.8	370	2	C96979	similar to spore g
903	6	0.8	342	2	C86811	hypothetical prote	576	6	0.8	370	2	AF1432	recf protein limpo
904	6	0.8	343	2	G72218	conserved hypochet	577	6	0.8	370	2	H72748	probable glycerol
905	6	0.8	344	1	S49978	aspartate-semialde	578	6	0.8	370	2	T33382	hypothetical prote

979	6	0.8	371	2	C70237	hypothetical prote
980	6	0.8	371	2	T18558	probable mitochond
981	6	0.8	372	1	A55510	chorismate synthas
982	6	0.8	372	1	D69442	conserved hypotnet
983	6	0.8	372	2	S18953	fix23-1 protein -
984	6	0.8	372	2	T09612	secreted glycoprot
985	6	0.8	373	2	A82398	maltose/maltodextr
986	6	0.8	373	2	G90398	hypothetical prote
987	6	0.8	373	2	E72216	alanine-tRNA ligas
988	6	0.8	374	2	D90338	hypothetical prote
989	6	0.8	374	2	G89846	hypothetical prote
990	6	0.8	375	2	S17253	alcohol dehydrogen
991	6	0.8	375	2	D82585	imidazoleglycerolp
992	6	0.8	375	2	A83802	NAD biosynthesis n
993	6	0.8	375	2	C90746	probable enzyme [i
994	6	0.8	375	2	G85596	probable enzyme yb
995	6	0.8	375	2	C64824	probable RNA methy
996	6	0.8	376	1	F64705	conserved hypotnet
997	6	0.8	376	2	F71815	hypothetical prote
998	6	0.8	376	2	AD1915	hypothetical prote
999	6	0.8	377	2	G85975	hypothetical prote
1000	6	0.8	379	2	T32778	hypothetical prote
1001	6	0.8	379	2	T21417	hypothetical prote
1002	6	0.8	380	2	A55259	kappa oploid recep
1003	6	0.8	380	2	T43016	DNA mismatch repai
1004	6	0.8	380	2	G86656	ABC transporter pe
1005	6	0.8	380	2	A12185	hypothetical prote
1006	6	0.8	381	2	A43769	fodrin alpha chain
1007	6	0.8	381	2	S65212	hypothetical prote
1008	6	0.8	381	2	T34692	probable transmemb
1009	6	0.8	382	2	E88249	mmp protein VC1037
1010	6	0.8	382	2	G86791	hypothetical prote
1011	6	0.8	382	2	T38092	hypothetical prote
1012	6	0.8	382	2	A13175	conserved hypotnet
1013	6	0.8	383	1	A25978	alcohol dehydrogen
1014	6	0.8	383	2	S32975	gene BCR2 protein
1015	6	0.8	383	2	B83205	hypothetical prote
1016	6	0.8	383	2	T23041	hypothetical prote
1017	6	0.8	383	2	A71139	hypothetical prote
1018	6	0.8	384	2	G91130	N-acetylglactosam
1019	6	0.8	385	2	T52483	hypothetical prote
1020	6	0.8	385	2	T47535	hypothetical prote
1021	6	0.8	385	2	T51127	Gesp synthase [lmp
1022	6	0.8	385	2	A82651	hypothetical prote
1023	6	0.8	385	2	D97433	polyamine transpor
1024	6	0.8	386	1	S22315	smbNP-associated p
1025	6	0.8	386	2	H71511	probable 2-compone
1026	6	0.8	386	2	T09598	cyclin 4, D-type -
1027	6	0.8	387	2	H71708	pol (A) POLYMERASE
1028	6	0.8	387	2	T38876	probable ribosomal
1029	6	0.8	387	2	F82815	voltage-gated pota
1030	6	0.8	387	2	C86640	multidrug efflux t
1031	6	0.8	387	2	S00867	colicin N - Bacher
1032	6	0.8	387	2	T47013	hypothetical prote
1033	6	0.8	387	2	E83679	multidrug-efflux t
1034	6	0.8	387	2	E97028	probable amidohydr
1035	6	0.8	387	2	AD0237	probable membrane
1036	6	0.8	387	2	A86322	F6a14.9 protein -
1037	6	0.8	388	2	H83714	alanine racemase B
1038	6	0.8	388	2	A82663	mmp protein [lmpor
1039	6	0.8	389	2	B86017	probable 3-oxoacyl
1040	6	0.8	389	2	B91171	probable 3-oxoacyl
1041	6	0.8	389	2	C83202	algnate biosynthe
1042	6	0.8	390	2	F97445	mmp protein homolo
1043	6	0.8	390	2	A83384	N-acetylumramoyl-L
1044	6	0.8	391	2	F83269	fatty-acid oxidat
1045	6	0.8	391	2	B70625	protein T20D3.3 [i
1046	6	0.8	391	2	B70625	probable PPE prote
1047	6	0.8	392	2	F83610	probable fatty aci
1048	6	0.8	392	2	AB1505	hietidyl-tRNA synt
1049	6	0.8	392	2	S72984	hypothetical prote
1050	6	0.8	392	2	T34095	zinc finger protei
1051	6	0.8	393	2	AB0035	cystathionine beta
1052	6	0.8	393	2	AB1146	hietidyl-tRNA synt
1053	6	0.8	393	2	F91195	probable integrase
1054	6	0.8	393	2	G86042	probable integrase
1055	6	0.8	393	2	A55859	regulatory protei
1056	6	0.8	393	2	D96577	hypothetical prote
1057	6	0.8	393	2	E97309	probable amidohydr
1058	6	0.8	394	2	US0600	t-plasminogen acti
1059	6	0.8	394	2	T44463	integrase int [lmp
1060	6	0.8	394	2	S26431	intermediate filam
1061	6	0.8	394	2	S39739	efflux protein hom
1062	6	0.8	395	1	Q0ECCR	hypothetical 45.2K
1063	6	0.8	395	1	F69148	hypothetical prote
1064	6	0.8	395	2	T00574	probable protein k
1065	6	0.8	395	2	A40270	cyclin E - human
1066	6	0.8	395	2	A91129	hypothetical prote
1067	6	0.8	395	2	H85973	hypothetical prote
1068	6	0.8	395	2	AB3543	succinyl-diaminopi
1069	6	0.8	395	2	A95660	hypothetical prote
1070	6	0.8	395	2	B83313	probable type II s
1071	6	0.8	396	2	AB2309	hypothetical prote
1072	6	0.8	397	2	A82108	flagellar hook- ass
1073	6	0.8	397	2	AE1142	penicillin-binding
1074	6	0.8	398	2	C81729	mcr/TnaB//Tyro perm
1075	6	0.8	398	2	D83506	conserved hypotnet
1076	6	0.8	398	2	AH1500	penicillin-binding
1077	6	0.8	399	2	F82657	beta-ketoacyl-[ACP
1078	6	0.8	399	2	A31137	hemocyanin - giant
1079	6	0.8	399	2	F89893	hypothetical prote
1080	6	0.8	400	1	JC1428	ketol-acid reducto
1081	6	0.8	400	2	G64104	pantothenate metab
1082	6	0.8	400	2	F86887	hypothetical prote
1083	6	0.8	400	2	T04460	protein kinase AME
1084	6	0.8	402	2	T25031	hypothetical prote
1085	6	0.8	402	2	AD1417	drug-efflux transp
1086	6	0.8	402	2	AF1792	lectin Cl - sea ur
1087	6	0.8	402	2	S71137	endosperm specific
1088	6	0.8	402	2	T04348	hypothetical prote
1089	6	0.8	403	2	C83881	homeotic protein 1
1090	6	0.8	403	1	S23802	probable high-affi
1091	6	0.8	403	1	S01828	cytokeratin 19 - m
1092	6	0.8	403	2	T45580	hypothetical prote
1093	6	0.8	403	2	T27948	hypothetical prote
1094	6	0.8	403	2	UC5171	D-galactose-bindin
1095	6	0.8	404	2	T40532	ketol-acid reducto
1096	6	0.8	404	2	G01507	LIM domain transcr
1097	6	0.8	404	2	A55444	integral membrane
1098	6	0.8	404	2	B46189	orf within vasococ
1099	6	0.8	404	2	T00089	ABC transporter rg
1100	6	0.8	405	1	AH2995	conserved hypotnet
1101	6	0.8	405	2	AB0793	probable MR-MLR-fa
1102	6	0.8	405	2	AB0793	homeotic protein 1
1103	6	0.8	406	1	I58187	homeotic protein 1
1104	6	0.8	406	1	I48186	homeotic protein 1
1105	6	0.8	406	1	I48637	homeotic protein 1
1106	6	0.8	406	1	I50375	homeotic protein 1
1107	6	0.8	406	1	G70639	hypothetical prote
1108	6	0.8	406	2	B89942	conserved hypotnet
1109	6	0.8	407	2	AC2721	MFS permease [lmpo
1110	6	0.8	407	2	G97502	probable mfs trans
1111	6	0.8	408	2	B95214	hypothetical prote
1112	6	0.8	408	2	H98250	hypothetical prote
1113	6	0.8	409	2	UC1378	arylalialphospha
1114	6	0.8	409	2	C95042	hypothetical prote
1115	6	0.8	410	2	T34717	probable transmemb
1116	6	0.8	410	2	S68515	probable arginine
1117	6	0.8	410	2	D84785	hypothetical prote
1118	6	0.8	410	2	S38238	hypothetical prote
1119	6	0.8	411	2	H95048	3-oxoacyl-(acyl)-ca
1120	6	0.8	411	2	PC2061	genome polypotein
1121	6	0.8	411	2	AE3485	florfenicol resist
1122	6	0.8	411	2	S40064	3-deoxy-manno-octu
1123	6	0.8	412	2	H70915	probable pgk prote
1124	6	0.8	412	2	H75484	hypothetical prote

1125	6	0.8	413	2	T43170	probable triacylgly	1198	6	0.8	431	2	T00698	methionyl aminopep
1126	6	0.8	413	2	S61305	cydH protein - Par	1199	6	0.8	431	2	JS0599	t-plasminogen acti
1127	6	0.8	413	2	A82726	conserved hypotnet	1200	6	0.8	431	2	F86179	hypothetical prote
1128	6	0.8	413	2	T26915	hypothetical prote	1201	6	0.8	432	1	RMCQ74	T-cell surface gly
1129	6	0.8	414	2	H70667	probable oxidoredu	1202	6	0.8	432	1	RMCQ74	T-cell surface gly
1130	6	0.8	414	2	F97919	3-oxoacyl-l-acyl-ca	1203	6	0.8	432	2	E71442	probable asparagin
1131	6	0.8	414	2	E90572	hypothetical prote	1204	6	0.8	432	2	E89954	conserved hypotnet
1132	6	0.8	414	2	E87316	periplasmic phosph	1205	6	0.8	433	1	JN0560	u-plasminogen acti
1133	6	0.8	414	2	E87292	pentapeptide repes	1206	6	0.8	433	1	UKBAY	u-plasminogen acti
1134	6	0.8	414	2	A29835	SalI protein - Bsc	1207	6	0.8	433	2	D75480	UDP-N-acetylmuramo
1135	6	0.8	414	2	AT0277	probable phage-rel	1208	6	0.8	434	2	A86305	FelI. 5 protein - A
1136	6	0.8	415	2	TE8144	corticotropin-rele	1209	6	0.8	435	2	H82501	nicotinate phospho
1137	6	0.8	415	2	D81909	probable integral	1210	6	0.8	435	2	T47737	hypothetical prote
1138	6	0.8	415	2	D81107	conserved hypotnet	1211	6	0.8	435	2	AB1786	cellobiose phospho
1139	6	0.8	415	2	T49072	hypothetical prote	1212	6	0.8	435	2	E83362	probable 2-ketogluc
1140	6	0.8	416	1	S06763	calreticulin precu	1213	6	0.8	436	2	G97701	polynucleotide ade
1141	6	0.8	416	1	ACCH3N	nicotinic acetylch	1214	6	0.8	436	2	JC5599	cholecystokinin-A
1142	6	0.8	416	1	D71277	cytosine-cRNA liga	1215	6	0.8	436	2	S74385	hypothetical prote
1143	6	0.8	417	2	D98078	conserved hypotnet	1216	6	0.8	436	2	S48399	hypothetical prote
1144	6	0.8	417	2	G98200	sarcosine oxidase	1217	6	0.8	436	2	F86486	protein F2809.3 [I
1145	6	0.8	417	2	AB3086	sarcosine oxidase	1218	6	0.8	436	2	G97186	diverged glycosylc
1146	6	0.8	417	2	AB3056	sarcosine oxidase	1219	6	0.8	437	2	S34959	NADH2 dehydrogenas
1147	6	0.8	417	2	T05207	hypothetical prote	1220	6	0.8	437	2	A55682	keratin 13, type I
1148	6	0.8	417	2	A97063	NAD(FAD)-dependent	1221	6	0.8	438	1	S11225	transcription fact
1149	6	0.8	418	2	H97437	cyclopropane-fatty	1222	6	0.8	438	2	JC1179	transcription fact
1150	6	0.8	418	2	AC2656	cyclopropane-fatty	1223	6	0.8	438	2	AF3215	ABC transporter, m
1151	6	0.8	418	2	E96765	hypothetical prote	1224	6	0.8	438	2	AH2285	hypothetical prote
1152	6	0.8	418	2	H83126	probable secretion	1225	6	0.8	439	1	TVC2WC	transforming prote
1153	6	0.8	419	2	C84813	probable protein X	1226	6	0.8	439	1	TVMS	transforming prote
1154	6	0.8	419	2	D86785	diaminopimelate de	1227	6	0.8	439	1	T25494	probable cytochrom
1155	6	0.8	419	2	JC4123	pregnancy-specific	1228	6	0.8	440	1	A35875	transcription fact
1156	6	0.8	419	2	S75647	glutamate N-acetyl	1229	6	0.8	440	1	Q08Y7Y	TYA protein - yeas
1157	6	0.8	419	2	B89788	hypothetical prote	1230	6	0.8	440	2	S43113	phosphopyruvate hy
1158	6	0.8	419	2	P83673	PTS system, galact	1231	6	0.8	440	2	I48291	transcription fact
1159	6	0.8	420	2	B98288	hypothetical prote	1232	6	0.8	440	2	I50213	protein-tyrosine-p
1160	6	0.8	420	2	B95100	conserved hypotnet	1233	6	0.8	440	2	S57044	TYA protein - yeas
1161	6	0.8	420	2	D97968	conserved hypotnet	1234	6	0.8	440	2	A22671	TYA protein - yeas
1162	6	0.8	421	2	B84702	hypothetical prote	1235	6	0.8	440	2	S57046	TYA protein - yeas
1163	6	0.8	422	2	H82236	iron-containing al	1236	6	0.8	440	2	S69837	TYA protein - yeas
1164	6	0.8	422	2	P89805	xanthine permease	1237	6	0.8	440	2	S45866	TYA protein - yeas
1165	6	0.8	423	2	A13309	cRNA adenyliltrans	1238	6	0.8	440	2	S69964	TYA protein - yeas
1166	6	0.8	423	2	A99230	sarcosine oxidase	1239	6	0.8	440	2	S50947	TYA protein - yeas
1167	6	0.8	423	2	AH1407	PTS system galacti	1240	6	0.8	440	2	S51894	TYA protein - yeas
1168	6	0.8	423	2	AH1763	PTS system galacti	1241	6	0.8	440	2	S69840	TYA protein - yeas
1169	6	0.8	423	2	T31342	ragd protein - Bra	1242	6	0.8	440	2	S69985	TYA protein - yeas
1170	6	0.8	424	2	C64362	aconitate hydratase	1243	6	0.8	440	2	S69971	TYA protein - yeas
1171	6	0.8	424	2	T35535	probable secreted	1244	6	0.8	440	2	S69976	TYA protein - yeas
1172	6	0.8	424	2	AD2017	cell wall-binding	1245	6	0.8	440	2	S53588	TYA protein - yeas
1173	6	0.8	426	2	A81933	probable malate de	1246	6	0.8	440	2	S70228	TYA protein - yeas
1174	6	0.8	426	2	C81173	malate oxidoreduct	1247	6	0.8	440	2	S53553	TYA protein - yeas
1175	6	0.8	426	2	T52285	ubiquinol-threonine-8	1248	6	0.8	440	2	S51249	TYA protein YDB557
1176	6	0.8	426	2	E70058	ubiquinol-cytochro	1249	6	0.8	440	2	S61577	TYA protein - yeas
1177	6	0.8	427	2	S55905	phosphotransferase	1250	6	0.8	440	2	S40909	TYA protein - yeas
1178	6	0.8	427	2	G69067	N-ethylmaleimide ch	1251	6	0.8	440	2	D69596	branched-chain aml
1179	6	0.8	427	2	T29376	hypothetical prote	1252	6	0.8	440	2	D64186	conserved hypotnet
1180	6	0.8	427	2	A86493	polymorphic outer	1253	6	0.8	440	2	C97620	probable proteinas
1181	6	0.8	428	1	TYHUEK	transforming prote	1254	6	0.8	441	1	A53988	transcription fact
1182	6	0.8	428	2	D70969	probable oxidoredu	1255	6	0.8	441	1	TVCHTE	transcription fact
1183	6	0.8	428	2	D70343	glycine hydroxymet	1256	6	0.8	441	1	C38575	glucuronate 2-dehydr
1184	6	0.8	428	2	JN0692	cholecystokinin cy	1257	6	0.8	441	2	E84264	isochoformate synt
1185	6	0.8	428	2	P85485	flavoprotein, elec	1258	6	0.8	441	2	UKPG	u-plasminogen acti
1186	6	0.8	428	2	P90634	flavoprotein [impo	1259	6	0.8	442	1	G84465	probable cytochrom
1187	6	0.8	428	2	C64725	fixC protein - Bsc	1260	6	0.8	442	2	G59102	hypothetical prote
1188	6	0.8	428	2	B75133	cytochrome-c3 hydr	1261	6	0.8	443	2	F30010	NADH2 dehydrogenas
1189	6	0.8	428	2	T06290	hypothetical prote	1262	6	0.8	443	2	I39538	alpha-amylase - Ae
1190	6	0.8	428	2	G56273	protein-histidine	1263	6	0.8	443	2	A42685	cholecystokinin re
1191	6	0.8	429	2	E70979	carbon dioxide-fix	1264	6	0.8	444	2	H71243	probable helicase
1192	6	0.8	429	2	JC4965	ellI protein - mou	1265	6	0.8	444	2	T26762	hypothetical prote
1193	6	0.8	429	2	C84194	hypothetical prote	1266	6	0.8	445	2	E75075	hybrid cluster 14F
1194	6	0.8	429	2	A70949	hypothetical prote	1267	6	0.8	446	2	F86815	hypothetical prote
1195	6	0.8	430	2	F87472	FMN oxidoreductase	1268	6	0.8	446	2	T07907	hydroxyproline-ric
1196	6	0.8	431	1	UKHU	u-plasminogen acti	1269	6	0.8	446	2	A75209	DNA repair protein
1197	6	0.8	431	2	P84077	homoserine dehydro	1270	6	0.8	446	2		

1271	6	0.8	447	2	C66233	1344	6	0.8	471	2	E83173	hypothetical prote
1272	6	0.8	448	2	A81919	1345	6	0.8	471	2	A84741	probable myrosinase
1273	6	0.8	449	2	AC1019	1346	6	0.8	472	2	T47436	protein kinase-lik
1274	6	0.8	449	2	T23126	1347	6	0.8	472	2	E98020	hypothetical prote
1275	6	0.8	450	2	C67463	1348	6	0.8	472	2	T51559	probable flavonol
1276	6	0.8	450	2	T08701	1349	6	0.8	473	2	E86955	conserved hypothet
1277	6	0.8	451	2	A85836	1350	6	0.8	473	2	G70975	hypothetical prote
1278	6	0.8	451	2	C64976	1351	6	0.8	474	2	S30227	transposase - C1os
1279	6	0.8	451	2	G90990	1352	6	0.8	474	2	H82564	3-isopropylmalate
1280	6	0.8	451	2	T36217	1353	6	0.8	474	2	T20694	hypothetical prote
1281	6	0.8	452	2	I49595	1354	6	0.8	475	2	A70318	aldohyde dehydroge
1282	6	0.8	452	2	C69214	1355	6	0.8	476	2	T47606	UMP synthase - Ara
1283	6	0.8	454	1	C69214	1356	6	0.8	476	2	S46440	bifunctional UMP s
1284	6	0.8	455	2	B90619	1357	6	0.8	477	1	A34369	t-plaaminogen acti
1285	6	0.8	455	2	S50725	1358	6	0.8	477	2	JS0597	t-plaaminogen acti
1286	6	0.8	456	1	KRMH5	1359	6	0.8	477	2	JS0598	hypothetical prote
1287	6	0.8	456	2	T40386	1360	6	0.8	477	2	T46304	hypothetical prote
1288	6	0.8	456	2	H85022	1361	6	0.8	478	2	E90495	aldohyde dehydroge
1289	6	0.8	456	2	T05612	1362	6	0.8	478	2	S36183	translation elonga
1290	6	0.8	456	2	S47924	1363	6	0.8	478	2	UQ2240	translational elonga
1291	6	0.8	457	2	AC1056	1364	6	0.8	478	2	S52602	TYA protein - yeas
1292	6	0.8	457	2	B86121	1365	6	0.8	478	2	T25899	hypothetical prote
1293	6	0.8	457	2	B91280	1366	6	0.8	479	2	T51919	related to aldehyd
1294	6	0.8	457	2	S56459	1367	6	0.8	479	2	D72354	lipopolyaccharide
1295	6	0.8	457	2	AH0898	1368	6	0.8	479	2	S48705	serine/threonine p
1296	6	0.8	457	2	E83643	1369	6	0.8	480	2	T04849	protein kinase hom
1297	6	0.8	457	2	B82268	1370	6	0.8	480	2	B35843	lipopolyaccharide
1298	6	0.8	458	1	RHMUT4	1371	6	0.8	482	2	E97012	probable non-proce
1299	6	0.8	458	2	B90621	1372	6	0.8	483	2	A85723	altronate oxidore
1300	6	0.8	458	2	B90625	1373	6	0.8	483	2	D64906	legaturoonate reduc
1301	6	0.8	458	2	B90615	1374	6	0.8	483	2	H90894	altronate oxidore
1302	6	0.8	458	2	B90617	1375	6	0.8	484	1	TVMVFT	gag-myc polypotei
1303	6	0.8	458	2	T11176	1376	6	0.8	484	2	D89781	hypothetical prote
1304	6	0.8	458	2	T11528	1377	6	0.8	484	2	T33492	hypothetical prote
1305	6	0.8	458	2	B99613	1378	6	0.8	485	1	TVCHET	transcription fact
1306	6	0.8	458	2	B90627	1379	6	0.8	485	2	AD0041	thamulokinase (EC
1307	6	0.8	458	2	B90623	1380	6	0.8	485	2	B69795	glutamy1-cRNA (Gln)
1308	6	0.8	458	2	B97324	1381	6	0.8	485	2	A70706	probable phos prot
1309	6	0.8	459	2	S10196	1382	6	0.8	486	2	T32431	probable cytochrom
1310	6	0.8	459	2	T11411	1383	6	0.8	486	2	T51582	glutamy1-cRNA (Gln
1311	6	0.8	459	2	T11189	1384	6	0.8	487	2	H69477	coenzyme F420-quin
1312	6	0.8	459	2	T11256	1385	6	0.8	487	2	E98326	hypothetical prote
1313	6	0.8	459	2	T11084	1386	6	0.8	488	1	TVFVFS	transcription fact
1314	6	0.8	459	2	AEO679	1387	6	0.8	488	2	F95875	hypothetical prote
1315	6	0.8	459	2	G90080	1388	6	0.8	489	2	UC4787	snaw protein - Cal
1316	6	0.8	459	2	G81187	1389	6	0.8	490	2	D70008	nicotinate phospho
1317	6	0.8	459	2	T81914	1390	6	0.8	490	2	G70108	hypothetical prote
1318	6	0.8	459	2	T24742	1391	6	0.8	491	2	A70658	UDP-N-acetylmutra
1319	6	0.8	459	2	D86256	1392	6	0.8	491	2	D97311	amino acid transpo
1320	6	0.8	460	2	T24248	1393	6	0.8	492	2	AG1838	hypothetical prote
1321	6	0.8	461	2	A43782	1394	6	0.8	492	2	G71112	catalase (EC 1.11.
1322	6	0.8	461	2	C86935	1395	6	0.8	492	2	S41288	genome polypotein
1323	6	0.8	461	2	D81418	1396	6	0.8	492	2	C68316	protein T10022.7 l
1324	6	0.8	461	2	T00621	1397	6	0.8	493	2	T51453	serine/threonine s
1325	6	0.8	462	2	T28699	1398	6	0.8	493	2	A85441	cytochrome P450-1i
1326	6	0.8	463	2	S72992	1399	6	0.8	495	2	S60589	acetylcholine rece
1327	6	0.8	463	2	T39621	1400	6	0.8	495	2	G82371	FXG-related prote
1328	6	0.8	464	2	AC2774	1401	6	0.8	496	2	T11376	cytochrome-c oxida
1329	6	0.8	464	2	E97554	1402	6	0.8	496	2	H70668	probable polyketid
1330	6	0.8	464	2	AF0761	1403	6	0.8	496	2	G87546	acid-CoA ligase, p
1331	6	0.8	464	2	C83328	1404	6	0.8	496	2	TI7908	proline/lysine-ric
1332	6	0.8	465	2	S03325	1405	6	0.8	497	2	B81728	serine proteinase,
1333	6	0.8	465	2	T40697	1406	6	0.8	497	2	B27785	acetyl-CoA acetyl
1334	6	0.8	466	2	C64690	1407	6	0.8	498	1	S52570	phosphoprotein pho
1335	6	0.8	467	2	E64974	1408	6	0.8	498	2	B95893	probable succinate
1336	6	0.8	468	2	A12956	1409	6	0.8	498	2	A41359	potassium channel
1337	6	0.8	469	2	AE1220	1410	6	0.8	499	1	B29042	nitrogenase (EC 1.
1338	6	0.8	469	2	AH1573	1411	6	0.8	499	1	A55346	phosphoprotein pho
1339	6	0.8	470	2	B90481	1412	6	0.8	499	2	A24572	nicotinic acetylch
1340	6	0.8	470	2	D85111	1413	6	0.8	499	2	B34332	glutelin 2 precurs
1341	6	0.8	470	2	T31049	1414	6	0.8	499	2	S06350	glutelin type 1 pr
1342	6	0.8	470	2	T45272	1415	6	0.8	499	2	A27033	glutelin precursor
1343	6	0.8	471	2	S35019	1416	6	0.8	499	2	H87460	hypothetical prote

1417	6	0.8	499	2	T47879	hypothetical prote
1418	6	0.8	499	2	S22571	integrase-like pro
1419	6	0.8	500	1	A44001	gag polyprotein -
1420	6	0.8	501	2	C82414	aminopeptidase VCA
1421	6	0.8	502	2	T35743	ribosomal protein
1422	6	0.8	502	2	A37040	nicotinic acetylch
1423	6	0.8	502	2	T19876	lipoprotein lipa -
1424	6	0.8	503	2	T46852	anthranilate synth
1425	6	0.8	503	2	A53956	nicotinic acetylch
1426	6	0.8	503	2	A54868	nuclear respirator
1427	6	0.8	504	2	AB2843	hydrolyase limpo
1428	6	0.8	504	2	C66428	hypothetical prote
1429	6	0.8	505	1	FWYCA	H+-transporting tw
1430	6	0.8	506	2	G31090	H+-transporting tw
1431	6	0.8	506	2	AE1807	ATP synthase chain
1432	6	0.8	506	2	D82081	UDP-N-acetylmuram
1433	6	0.8	506	2	T41623	probable protein k
1434	6	0.8	507	1	A39072	steroid 17alpha-mo
1435	6	0.8	507	2	T51658	terminal deoxynuci
1436	6	0.8	507	2	T07012	acetyl-CoA carboxy
1437	6	0.8	507	2	C96988	probable membrane
1438	6	0.8	508	1	UPBSHS	lactidine ammonia-
1439	6	0.8	509	2	E70764	probable cobI prot
1440	6	0.8	509	2	E80504	hypothetical prote
1441	6	0.8	509	2	S45631	DNA primase chain
1442	6	0.8	509	2	A13300	sugar transport AT
1443	6	0.8	510	2	T29642	hypothetical prote
1444	6	0.8	511	2	A54676	antitoxin - human
1445	6	0.8	512	2	S04672	H+-transporting tw
1446	6	0.8	512	2	A05196	hypothetical prote
1447	6	0.8	512	2	B69146	glutathione-regula
1448	6	0.8	512	2	B69024	conserved hypotet
1449	6	0.8	513	2	F83162	nitrate reductase
1450	6	0.8	513	2	A81850	probable integrase
1451	6	0.8	513	2	C81092	oxalate/formate an
1452	6	0.8	513	2	H69735	endo-L,4-beta-xyla
1453	6	0.8	514	2	A10671	respiratory nitrat
1454	6	0.8	514	2	C70446	hypothetical prote
1455	6	0.8	515	2	T43152	hypothetical prote
1456	6	0.8	515	2	B81318	probable two-domai
1457	6	0.8	516	2	T48238	hypothetical prote
1458	6	0.8	517	2	F86921	probable acyl CoA
1459	6	0.8	517	2	D90073	hypothetical prote
1460	6	0.8	517	2	T27927	hypothetical prote
1461	6	0.8	518	2	D64244	H+-transporting tw
1462	6	0.8	518	2	C70887	probable Propionyl
1463	6	0.8	520	2	H95884	probable regulator
1464	6	0.8	522	2	S51557	cytochrome P450, 3
1465	6	0.8	523	2	B95922	hypothetical nucle
1466	6	0.8	523	2	A53196	orphan hormone nuc
1467	6	0.8	523	2	S68517	nuclear hormone re
1468	6	0.8	525	2	A70735	probable guaH prot
1469	6	0.8	525	2	G71317	hypothetical prote
1470	6	0.8	525	2	T34178	hypothetical prote
1471	6	0.8	526	1	T45058	phosphoprotein pho
1472	6	0.8	526	2	A81135	phosphoribosylam
1473	6	0.8	527	2	A42032	epidermal growth f
1474	6	0.8	528	2	C85527	regulator for prp
1475	6	0.8	528	2	H90676	regulator for prp
1476	6	0.8	529	2	C86958	probable GMP synth
1477	6	0.8	529	2	A95423	probable ABC trans
1478	6	0.8	529	2	T27922	hypothetical prote
1479	6	0.8	530	2	H81885	purH bifunctional
1480	6	0.8	530	2	T12031	hypothetical prote
1481	6	0.8	530	2	U79683	peptidoglycan reco
1482	6	0.8	530	2	T28212	hypothetical prote
1483	6	0.8	530	2	C82442	probable peptide A
1484	6	0.8	531	2	AD0666	conserved hypotet
1485	6	0.8	531	2	T05644	hypothetical prote
1486	6	0.8	531	2	T52462	hypothetical prote
1487	6	0.8	531	2	T28222	hypothetical prote
1488	6	0.8	533	2	B26446	vire2 protein - Ag
1489	6	0.8	533	2	S73755	adhesin P1 precurs

1490	6	0.8	534	2	D71698	cytochrome-c oxida
1491	6	0.8	535	2	C96618	probable squalene
1492	6	0.8	536	2	T38210	scd2 protein - fis
1493	6	0.8	536	2	AG1482	hypothetical prote
1494	6	0.8	536	2	AB3038	conserved hypotet
1495	6	0.8	538	2	G83653	oligopeptide ABC t
1496	6	0.8	538	2	T40992	hypothetical prote
1497	6	0.8	539	2	G95405	hypothetical prote
1498	6	0.8	540	1	OXECMD	L-aspartate oxidas
1499	6	0.8	540	2	H91058	guinolinate synthe
1500	6	0.8	540	2	AB0830	L-aspartate oxidas

ALIGNMENTS

RESULT 1
 T08805
 hypothetical protein DKFZp586H2123.1 - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
 C/Accession: T08805
 R:Amstrong, W.; Witkner, U.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
 submitted to the Protein Sequence Database, May 1999
 A/Reference number: Z16472
 A/Accession: T08805
 A/Molecule type: mRNA
 A/Residues: 1-181 <ANS>
 A/Cross-references: UNIPROT:Q9Y432; EMBL:AL050214
 A/Experimental source: adult uterus; clone DKFZp586H2123
 C/Genetics:
 A/Note: DKFZp586H2123.1

Query Match 24.7%; Score 178; DB 2; Length 181;
 Best Local Similarity 100.0%; Pred. No. 2,4e-182; Indels 0; Gaps 0;

Qy	543	ISATILHPNDPILMDADIALILKLDKARISTRVQPICLAASRDLSFQESHITTVAGWN	602
Db	4	ISATILHPNDPILMDADIALILKLDKARISTRVQPICLAASRDLSFQESHITTVAGWN	63
Qy	603	VLADVRSFGKNDTLRSQVSVVDSLLCEQHEDHGIPVSVTTDMFCASWEPTAPSDICT	662
Db	64	VLADVRSFGKNDTLRSQVSVVDSLLCEQHEDHGIPVSVTTDMFCASWEPTAPSDICT	123
Qy	663	AETGCIAAVSFPGASPEPRWHLMGLVSWSYDTCRSRLSTATFKKVLPPFDMIERNNK	720
Db	124	AETGCIAAVSFPGASPEPRWHLMGLVSWSYDTCRSRLSTATFKKVLPPFDMIERNNK	181

RESULT 2

E70372
 hypothetical protein ag_836 - Aquifex aeolicus
 C/Species: Aquifex aeolicus
 C/Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
 C/Accession: E70372
 R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ove
 V.
 Nature 392, 353-358, 1998
 A/Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
 A/Reference number: A70300; MUID:98196666; PMID:9537320
 A/Accession: E70372
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown
 A/Molecule type: DNA
 A/Residues: 1-232 <AGP>
 A/Cross-references: UNIPROT:O67008; GB:AE000709; MID:G2983373; PID:AC06970.1; PID:G2983
 A/Experimental source: strain VFS
 C/Genetics:
 A/Gene: ag_836

Query Match 1.2%; Score 9; DB 2; Length 232;
 Best Local Similarity 100.0%; Pred. No. 0.45; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0;

OY 88 FENCKSCRN 96
 |||||
 DB 23 FENCKSCRN 31

RESULT 3

T29125
 ketocycl1 reductase homolog - Streptomyces coelicolor
 C:Species: Streptomyces coelicolor
 C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T29125
 R:Parkhill, J.; Barrell, B.G.; Raeburn, M.A.
 submitted to the EMBL Data Library, August 1998
 A:Reference number: 217215
 A:Accession: T29125
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-276 <PAR>
 A:Cross-references: UNIPROT:O86553; EMBL:AL031350; PIDN:CAA20507.1
 C:Genetics:
 A:Note: SCIF2.16c
 C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 1.2%; Score 9; DB 2; Length 276;
 Best Local Similarity 100.0%; Pred. No. 0.53;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 670 AVSFGRRAS 678
 |||||
 DB 225 AVSFGRRAS 233

RESULT 4

BHMH1
 procollagen C-endopeptidase (EC 3.4.24.19) precursor, splice form BMP1 - human
 N:Alternate names: bone morphogenic protein 1 (BMP1)
 C:Species: Homo sapiens (man)
 C:Date: 16-Sep-1992 #sequence_revision 03-Aug-1995 #text_change 18-Jun-1999
 C:Accession: A37278; B58788
 R:Wozney, J.M.; Rosen, V.; Celeste, A.J.; Mittleman, L.M.; Whitters, M.J.; Kriz, R.W.; Hew
 Science 242, 1528-1534, 1988
 A:Title: Novel regulators of bone formation: molecular clones and activities.
 A:Reference number: A37278; MUID:89072730; PMID:3201241
 A:Accession: A37278
 A:Molecule type: mRNA
 A:Residues: 1-730 <MOZ>
 A:Cross-references: GB:M22488; NID:G179499; PIDN:AA51833.1; PID:G179500
 C:Genetics:
 A:Gene: GDB:BMP1
 A:Cross-references: GDB:125203; OMIM:112264
 A:Map position: 8p21-8p21

C:Function:
 A:Description: catalyzes hydrolysis of the carboxyl-terminal propeptide of collagen type
 C:Superfamily: procollagen C-endopeptidase; ascatin homology; C1r/C1s repeat homology;
 C:Keywords: alternative splicing; beta-hydroxyasparagine; bone; calcium; duplication; g1
 F:1-22/Domain: signal sequence #status predicted <SIG>
 F:23-730/Product: procollagen C-endopeptidase splice form BMP1 #status predicted <MAT>
 F:130-321/Domain: ascatin homology <AST>
 F:1322-431/Domain: C1r/C1s repeat homology <C1R1>
 F:1435-544/Domain: C1r/C1s repeat homology <C1R2>
 F:551-587/Domain: EGF homology <EGF>
 F:591-700/Domain: C1r/C1s repeat homology <C1R3>
 F:91,142,332,363,599/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:163-319,185-205,322-348,375-397,435-461,488-510,551-563,559-572,574-587,591-617,644-66
 F:213,217,223,272/Binding site: zinc (His, His, Tyr) #status predicted
 F:214/Active site: Glu #status predicted
 F:565/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted

Query Match 1.2%; Score 9; DB 1; Length 730;
 Best Local Similarity 100.0%; Pred. No. 1.3;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 179 YDYVEVRDG 187
 |||||
 DB 377 YDYVEVRDG 385

RESULT 5

A58788
 procollagen C-endopeptidase (EC 3.4.24.19) precursor, splice form HIS - human
 N:Alternate names: bone morphogenic protein splice form BMP-1/HIS
 C:Species: Homo sapiens (man)
 C:Date: 28-Mar-1998 #sequence_revision 09-Apr-1998 #text_change 18-Jun-1999
 C:Accession: A37278; A58788
 R:Wozney, J.M.; Rosen, V.; Celeste, A.J.; Mittleman, L.M.; Whitters, M.J.; Kriz, R.W.; Hew
 Science 242, 1528-1534, 1988
 A:Title: Novel regulators of bone formation: molecular clones and activities.
 A:Reference number: A37278; MUID:89072730; PMID:3201241
 A:Accession: A37278
 A:Molecule type: mRNA
 A:Residues: 1-702; EKRPAQPPGRPHQKFRVQKRNTPQ <MOZ>
 A:Cross-references: GB:M22488; NID:G179499; PIDN:AA51833.1; PID:G179500
 R:Takahara, K.; Lyons, G.E.; Greenspan, D.S.
 J. Biol. Chem. 269, 32572-32578, 1994
 A:Title: Bone morphogenetic protein-1 and a mammalian tollid homologue (MT1d) are encode

A:Reference number: A58788; MUID:95096114; PMID:7798260
 A:Accession: A58788
 A:Molecule type: mRNA
 A:Residues: 703-823 <TKA>
 A:Cross-references: GB:J35278; NID:G619423; PIDN:AA41703.1; PID:G619424
 C:Genetics:
 A:Gene: GDB:BMP-1
 A:Cross-references: GDB:125203; OMIM:112264
 A:Map position: 8p21-8p21

C:Function:
 A:Description: catalyzes hydrolysis of the carboxyl-terminal propeptide of collagen type
 C:Superfamily: procollagen C-endopeptidase; ascatin homology; C1r/C1s repeat homology; g1
 C:Keywords: alternative splicing; beta-hydroxyasparagine; bone; calcium; duplication; g1
 F:1-22/Domain: signal sequence #status predicted <SIG>
 F:23-823/Product: procollagen C-endopeptidase splice form HIS #status predicted <MAT>
 F:130-321/Domain: C1r/C1s repeat homology <C1R1>
 F:322-431/Domain: C1r/C1s repeat homology <C1R2>
 F:435-544/Domain: C1r/C1s repeat homology <C1R3>
 F:551-587/Domain: EGF homology <EGF>
 F:591-700/Domain: C1r/C1s repeat homology <C1R3>
 F:738-752/Region: histidine-rich
 F:91,142,332,363,599/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:163-319,185-205,322-348,375-397,435-461,488-510,551-563,559-572,574-587,591-617,644-66
 F:213,217,223,272/Binding site: zinc (His, His, Tyr) #status predicted
 F:214/Active site: Glu #status predicted
 F:565/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted

Query Match 1.2%; Score 9; DB 1; Length 823;
 Best Local Similarity 100.0%; Pred. No. 1.4;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 179 YDYVEVRDG 187
 |||||
 DB 377 YDYVEVRDG 385

RESULT 6

B58788
 procollagen C-endopeptidase (EC 3.4.24.19) precursor, tollid-like splice form - human
 N:Alternate names: bone morphogenic protein 1, tollid-like splice form
 C:Species: Homo sapiens (man)
 C:Date: 28-Mar-1998 #sequence_revision 09-Apr-1998 #text_change 09-Jul-2004
 C:Accession: A37278; B58788
 R:Wozney, J.M.; Rosen, V.; Celeste, A.J.; Mittleman, L.M.; Whitters, M.J.; Kriz, R.W.; Hew
 Science 242, 1528-1534, 1988
 A:Title: Novel regulators of bone formation: molecular clones and activities.
 A:Reference number: A37278; MUID:89072730; PMID:3201241
 A:Accession: A37278
 A:Molecule type: mRNA
 A:Residues: 1-702; EKRPAQPPGRPHQKFRVQKRNTPQ <MOZ>

A:Cross-references: UNIPROT:P13197; GB:M22488; NID:g179499; PIDN:AAA51833.1; PID:g179500
 R,Takahara, K.; Lyons, G.E.; Greenpan, D.S.
 J. Biol. Chem. 269, 32572-32578, 1994
 A:Title: Bone morphogenetic protein-1 and a mammalian tollid homologue (mtld) are encoded
 A:Reference number: A58788; MUID:95096114; PMID:7798260
 A:Accession: B58788
 A:Molecule type: mRNA
 A:Residues: 703-966 <TR>
 A:Cross-references: GB:L5279; NID:g619860; PIDN:AAC41710.1; PID:g619861
 C:Genetics:
 A:Gene: GDB:BMP1; BMP-1
 A:Cross-references: GDB:125203; OMTM:112264
 A:Map position: 8p21-8p21
 C:Function:
 A:Description: catalyzes hydrolysis of the carboxyl-terminal propeptide of collagen type
 C:Superfamily: procollagen C-endopeptidase; ascatin homology; C1r/C1s repeat homology; E
 C:Keywords: alternative splicing; beta-hydroxyasparagine; bone; calcium; duplication; gl
 F:1-22/Domains: signal sequence #status predicted <SIG>
 F:123-986/Product: procollagen C-endopeptidase tollid-like splice form #status predicted
 F:130-331/Domains: ascatin homology <AST>
 F:132-431/Domains: C1r/C1s repeat homology <C1R1>
 F:135-544/Domains: C1r/C1s repeat homology <C1R2>
 F:151-587/Domains: EGF homology <EG1>
 F:151-700/Domains: C1r/C1s repeat homology <C1R3>
 F:1707-742/Domains: EGF homology <EG2>
 F:1747-856/Domains: C1r/C1s repeat homology <C1R4>
 F:1860-973/Domains: C1r/C1s repeat homology <C1R5>
 F:91,147,332,363,599/Binding site: carboxylate (Asn) (covalent) #status predicted
 F:163-319,185-205,322-348,375-397,435-461,488-510,551-563,559-572,574-587,591-617,644-66
 F:123,217,423,272/Binding site: zinc (His, His, His, Tyr) #status predicted
 F:214/Active site: Glu #status predicted
 F:565,720/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted

Query Match 1.2% Score 9; DB 1; Length 986;
 Best Local Similarity 100.0%; Pred. No. 1.7;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 179 YDYVEVRDG 187
 |||||
 Db 377 YDYVEVRDG 385

RESULT 7
 149540
 C:Procollagen C-endopeptidase (EC 3.4.24.19) precursor, tollid-like splice form - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
 C:Accession: 149540
 R,Fukagawa, M.; Noboru, S.; Hogan, B.L.M.; Jones, C.M.
 Dev. Biol. 163, 175-183, 1994
 A:Title: Embryonic expression of mouse bone morphogenetic protein-1 (BMP-1) which is rel
 A:Reference number: 149540; MUID:9422342; PMID:8174772
 A:Accession: 149540
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-991 <RES>
 A:Cross-references: UNIPROT:P98063; GB:L24755; NID:g439606; PIDN:AAA37306.1; PID:g439607
 C:Genetics:
 A:Gene: BMP-1
 C:Superfamily: procollagen C-endopeptidase; ascatin homology; C1r/C1s repeat homology; E
 C:Keywords: hydrolyase; metalloproteinase; zinc
 F:135-326/Domains: ascatin homology <AST>
 F:156-592/Domains: EGF homology <EG1>
 F:1596-705/Domains: C1r/C1s repeat homology <C1R>
 F:1712-747/Domains: EGF homology <EG2>
 F:218,222,228,277/Binding site: zinc (His, His, His, Tyr) #status predicted
 F:219/Active site: Glu #status predicted

Query Match 1.2% Score 9; DB 2; Length 991;
 Best Local Similarity 100.0%; Pred. No. 1.7;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 179 YDYVEVRDG 187

Db 382 YDYVEVRDG 390
 |||||
 |||||

RESULT 8
 558984
 development protein tolkin (EC 3.4.24.-) - fruit fly (Drosophila melanogaster)
 C:Species: Drosophila melanogaster
 C:Date: 19-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
 C:Accession: S58984
 R,Finelli, A.L.; Xie, T.; Bossie, C.A.; Blackman, R.K.; Padgett, R.W.
 Genetics 141, 271-281, 1995
 A:Title: The tolkin gene is a tollid/BMP-1 homologue that is essential for Drosophila d
 A:Reference number: S58984; MUID:96042912; PMID:8536976
 A:Accession: S58984
 A:Molecule type: mRNA
 A:Residues: 1-1464 <FIN>
 A:Cross-references: UNIPROT:Q24132; EMBL:U34777; NID:g1002985; PIDN:AAC47015.1; PID:g100
 A:Note: the authors did not translate the codon for residue 722
 C:Genetics:
 A:Gene: tolkin
 A:Cross-references: FlyBase:FBgn0004885
 C:Keywords: hydrolyase; metalloproteinase; zinc
 F:523-722/Domains: ascatin homology <AST>
 F:958-993/Domains: EGF homology <EGF>
 F:1118-1153/Domains: EGF homology <EGF1>
 F:614,618,624,673/Binding site: zinc (His, His, His, Tyr) #status predicted
 F:615/Active site: Glu #status predicted

Query Match 1.2% Score 9; DB 2; Length 1464;
 Best Local Similarity 100.0%; Pred. No. 2.4;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 179 YDYVEVRDG 187
 |||||
 Db 897 YDYVEVRDG 905

RESULT 9
 T31070
 notch homolog - sea urchin (Lytechinus variegatus)
 C:Species: Lytechinus variegatus (variegated urchin)
 C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 31-Jan-2000
 C:Accession: T31070
 R,Sherwood, D.R.; McClay, D.R.
 Development 124, 3363-3374, 1997
 A:Title: Identification and localization of a sea urchin Notch homologue: insights into v
 A:Reference number: Z20966; MUID:97454256; PMID:9310331
 A:Accession: T31070
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-2531 <SHE>
 A:Cross-references: EMBL:AF00634; NID:g2570350; PID:g2570351; PIDN:AB82088.1
 C:Superfamily: notch protein; ankyrin repeat homology; EGF homology

Query Match 1.2% Score 9; DB 2; Length 2531;
 Best Local Similarity 100.0%; Pred. No. 4;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 260 CACIAGYTG 268
 |||||
 Db 537 CACIAGYTG 545

RESULT 10
 S00996
 IG kappa chain precursor V region (A10) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 23-Jul-1999
 C:Accession: S00996
 R,Strandinger, E.; Thiebe, R.; Huber, C.; Osterholzer, E.; Zachau, H.G.
 Biol. Chem. Hoppe-Seyler 369, 601-607, 1988
 A:Title: Two unusual human immunoglobulin V-kappa genes.

A:Reference number: S00996; MUID:89134397; PMID:2852016
 A:Accession: S00996
 A:Molecule type: DNA
 A:Residues: 1-114 <STR>
 A:Cross-references: EMBL:W2750; NID:q185914; PIDN:AAAS8912.1; PID:q553479
 A:Note: this sequence was determined from the germ-line gene
 C:Genetics:
 A:Intron: 16/1
 C:Superfamily: Immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-114/Product: Ig kappa chain V region #status predicted <MAT>
 F:42-107/Diulfide bonds: #status predicted

Query Match 1.1%; Score 8; DB 2; Length 114;
 Best Local Similarity 100.0%; Pred. No. 2.8;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 208 QSIGSSLH 215
 DB 46 QSIGSSLH 53

RESULT 11
 G70323
 conserved hypothetical protein aq_260 - Aquifex aeolicus
 C:Species: Aquifex aeolicus
 C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
 C:Accession: G70323
 R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Oy
 V.
 Nature 392, 353-358, 1998
 A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
 A:Reference number: A70300; MUID:98196666; PMID:9537320
 A:Accession: G70323
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-158 <AQF>
 A:Cross-references: UNIPROT:Q66619; GB:AE00681; NID:g2982963; PIDN:AAC0688.1; PID:g298
 A:Experimental source: strain VFS
 C:Genetics:
 A:Gene: aq_260
 C:Superfamily: nus operon 15K protein

Query Match 1.1%; Score 8; DB 2; Length 158;
 Best Local Similarity 100.0%; Pred. No. 3.7;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 57 GREVVGY 64
 DB 114 GREVVGY 121

RESULT 12
 D42696
 thrombin (EC 3.4.21.5) B chain - chicken (fragment)
 C:Species: Gallus gallus (chicken)
 C:Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 09-Jul-2004
 C:Accession: D42696
 R:Bantfield, D.K.; MacGillivray, R.T.A.
 Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992
 A:Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and seq
 A:Reference number: A42696; MUID:92212913; PMID:1557383
 A:Accession: D42696
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-235 <BAN>
 A:Cross-references: UNIPROT:Q91001; GB:M81391
 C:Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology
 C:Keywords: hydrolase; serine proteinase
 F:1-226/Domain: trypsin homology (fragment) <TRY>

Query Match 1.1%; Score 8; DB 2; Length 235;
 Best Local Similarity 100.0%; Pred. No. 5.4;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 643 VTDMNPCA 650
 DB 158 VTDMNPCA 164

RESULT 13
 H42696
 thrombin (EC 3.4.21.5) B chain - white sturgeon (fragment)
 C:Species: Acipenser transmontanus (white sturgeon)
 C:Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 09-Jul-2004
 C:Accession: H42696
 R:Bantfield, D.K.; MacGillivray, R.T.A.
 Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992
 A:Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and seq
 A:Reference number: A42696; MUID:92212913; PMID:1557383
 A:Accession: H42696
 A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
 A:Molecule type: mRNA
 A:Residues: 1-235 <BAN>
 A:Cross-references: UNIPROT:Q90244; GB:M81399
 C:Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology
 C:Keywords: hydrolase; serine proteinase
 F:1-226/Domain: trypsin homology (fragment) <TRY>

Query Match 1.1%; Score 8; DB 2; Length 235;
 Best Local Similarity 100.0%; Pred. No. 5.4;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 643 VTDMNPCA 650
 DB 157 VTDMNPCA 164

RESULT 14
 C42696
 thrombin (EC 3.4.21.5) B chain - rabbit (fragment)
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 09-Jul-2004
 C:Accession: C42696
 R:Bantfield, D.K.; MacGillivray, R.T.A.
 Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992
 A:Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and seq
 A:Reference number: A42696; MUID:92212913; PMID:1557383
 A:Accession: C42696
 A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
 A:Molecule type: mRNA
 A:Residues: 1-236 <BAN>
 A:Cross-references: UNIPROT:Q28731; GB:M81396
 C:Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology
 C:Keywords: hydrolase; serine proteinase
 F:1-227/Domain: trypsin homology (fragment) <TRY>

Query Match 1.1%; Score 8; DB 2; Length 236;
 Best Local Similarity 100.0%; Pred. No. 5.4;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 643 VTDMNPCA 650
 DB 158 VTDMNPCA 165

RESULT 15
 A80338
 probable membrane protein dedd [imported] - Yersinia pestis (strain CO92)
 C:Species: Yersinia pestis
 C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
 C:Accession: A80338
 R:Packhill, J.; Wren, B.W.; Thomson, N.R.; Tibbali, R.W.; Holden, M.T.G.; Prentice, M.B.
 deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, P.; Dougan, G.;
 11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,

Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:1158360
A;Accession: AB0338
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-240 <KUR>
A;Cross-references: UNIPROT:Q8ZD23; GB:AL590842; PIDN:CAC93009.1; PID:G15980748; GSPDB:C
C;Genetics:
A;Gene: dedd
C;Superfamily: dedd protein

Query Match 1.1%; Score 8; DB 2; Length 240;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 380 SKOKLQSA 387
Db 212 SKOKLQSA 219

Search completed: July 12, 2005, 17:23:21
Job time : 63 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 12, 2005, 17:20:13 ; Search time 176 Seconds
(without alignments)
2094.869 Million cell updates/sec

Title: US-10-063-546-38

Perfect score: 720
Sequence: 1 MELGCWTOGLTFLQLLLIS.....LSTAFKVLPEKMIERNKK 720

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1612378 seqs, 512079187 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1500 summaries

Database : UniProt_03 :
1: uniProt_sprot :
2: uniProt_trembl :*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	720	100.0	720	2 Q6UXH9	Q6UXH9 homo sapien
2	563	78.2	720	2 Q6N062	Q6N062 homo sapien
3	446	61.9	737	2 Q9JWM2	Q9JWM2 homo sapien
4	386	53.6	417	2 Q71R93	Q71R93 homo sapien
5	178	24.7	181	2 Q9Y432	Q9Y432 homo sapien
6	61	8.5	720	2 Q8BU25	Q8BU25 m mus muscu
7	41	5.7	720	2 Q8K2B8	Q8K2B8 mus muscu
8	24	3.3	722	2 Q6DIV5	Q6DIV5 xenopus tro
9	9	1.2	232	2 Q91WZ0	Q91WZ0 rattus norv
10	9	1.2	232	1 Y836_AQUAE	Y836_AQUAE aquifex aeo
11	9	1.2	276	2 Q86553	Q86553 streptomyce
12	9	1.2	593	2 Q6PUN5	Q6PUN5 homo sapien
13	9	1.2	639	1 BMPH_STRPU	BMPH_STRPU strongyloce
14	9	1.2	691	2 Q57658	Q57658 gallus gall
15	9	1.2	775	2 Q6P550	Q6P550 mus muscu
16	9	1.2	860	2 Q7QAH1	Q7QAH1 anopheles g
17	9	1.2	923	1 NRPI_BRARE	NRPI_BRARE brachydanio
18	9	1.2	923	2 Q69DB8	Q69DB8 brachydanio
19	9	1.2	986	1 BMP1_HUMAN	BMP1_HUMAN homo sapien
20	9	1.2	991	1 BMP1_MOUSE	BMP1_MOUSE mus muscu
21	9	1.2	991	1 Q6NZM2	Q6NZM2 mus muscu
22	9	1.2	1015	2 Q9Y6L7	Q9Y6L7 homo sapien
23	9	1.2	1078	2 Q9UQ00	Q9UQ00 homo sapien
24	9	1.2	1464	2 Q23995	Q23995 drosophila
25	9	1.2	1464	2 Q24132	Q24132 drosophila
26	9	1.2	1464	2 Q9VC47	Q9VC47 drosophila
27	9	1.2	2531	2 Q16004	Q16004 lytechinus
28	8	1.1	81	2 Q79204	Q79204 human immun
29	8	1.1	133	2 Q6LTX4	Q6LTX4 photobacter
30	8	1.1	136	2 Q8CEX5	Q8CEX5 mus muscu
31	8	1.1	152	2 Q924X1	Q924X1 mus muscu

32	8	1.1	158	1 Y260_AQUAE	Y260_AQUAE aquifex aeo
33	8	1.1	235	2 Q90244	Q90244 acipenser c
34	8	1.1	234	2 Q28731	Q28731 oryctolagus
35	8	1.1	240	2 Q668X3	Q668X3 yerania ps
36	8	1.1	240	2 Q8ZD23	Q8ZD23 yerania ps
37	8	1.1	242	2 Q8D0T9	Q8D0T9 yerania ps
38	8	1.1	360	1 MTSB_LACLC	MTSB_LACLC laccococcus
39	8	1.1	367	2 Q9XUN6	Q9XUN6 caenorhabdi
40	8	1.1	385	2 Q90WS2	Q90WS2 elaphie sp.
41	8	1.1	395	1 VIBC_VIBCH	VIBC_VIBCH vibrio chol
42	8	1.1	407	1 FA7_BOVIN	FA7_BOVIN bos taurus
43	8	1.1	411	2 Q67UT3	Q67UT3 oryza sativ
44	8	1.1	413	2 Q7X370	Q7X370 uncultured
45	8	1.1	466	1 YDBH_SCHPO	YDBH_SCHPO schizosacch
46	8	1.1	556	2 Q7UXI2	Q7UXI2 rhodospirell
47	8	1.1	569	2 Q62XZ6	Q62XZ6 burkholderi
48	8	1.1	569	2 Q63TF6	Q63TF6 burkholderi
49	8	1.1	607	2 Q91001	Q91001 gallus gall
50	8	1.1	608	2 Q9PTW7	Q9PTW7 struthio ca
51	8	1.1	611	2 Q94RU9	Q94RU9 oryza sativ
52	8	1.1	611	2 Q7XG00	Q7XG00 oryza sativ
53	8	1.1	719	2 Q9PVY2	Q9PVY2 triakis scy
54	8	1.1	737	2 Q8YTB7	Q8YTB7 anabaena sp.
55	8	1.1	740	1 CATB_STRRE	CATB_STRRE streptomyce
56	8	1.1	752	2 Q42374	Q42374 brachydanio
57	8	1.1	764	2 Q8XTM0	Q8XTM0 ralestonia oc
58	8	1.1	963	2 Q44393	Q44393 pisaaster oc
59	8	1.1	1019	1 LFC_CARRO	LFC_CARRO carinococ
60	8	1.1	1019	1 LFC_TACTR	LFC_TACTR tachypleus
61	8	1.1	1019	2 Q8T5S1	Q8T5S1 tachypleus
62	8	1.1	1070	2 Q91972	Q91972 aplysia cal
63	8	1.1	1083	2 Q26423	Q26423 carinococ
64	8	1.1	1238	2 Q9N614	Q9N614 drosophila
65	8	1.1	1238	2 Q9VCD8	Q9VCD8 drosophila
66	8	1.1	1316	2 Q96JU7	Q96JU7 homo sapien
67	8	1.1	36	2 Q7UD51	Q7UD51 rhodospirell
68	7	1.0	37	2 Q8F0D9	Q8F0D9 leptospira
69	7	1.0	47	2 Q75GQ9	Q75GQ9 oryza sativ
70	7	1.0	50	2 Q6Z6D5	Q6Z6D5 oryza sativ
71	7	1.0	54	2 Q8N087	Q8N087 corynebacte
72	7	1.0	55	2 Q768X9	Q768X9 uncultured
73	7	1.0	59	2 Q931M9	Q931M9 staphylococ
74	7	1.0	59	2 Q99SV1	Q99SV1 staphylococ
75	7	1.0	59	2 Q7A0F7	Q7A0F7 staphylococ
76	7	1.0	59	2 Q6G7Z5	Q6G7Z5 staphylococ
77	7	1.0	59	2 Q6GFR7	Q6GFR7 staphylococ
78	7	1.0	61	2 Q8GRP5	Q8GRP5 arabidopsis
79	7	1.0	61	2 Q8GRP6	Q8GRP6 arabidopsis
80	7	1.0	61	2 Q8GZP3	Q8GZP3 arabidopsis
81	7	1.0	61	2 Q8GZP4	Q8GZP4 arabidopsis
82	7	1.0	61	2 Q8GZP5	Q8GZP5 arabidopsis
83	7	1.0	61	2 Q8GZP7	Q8GZP7 arabidopsis
84	7	1.0	61	2 Q8GZP8	Q8GZP8 arabidopsis
85	7	1.0	61	2 Q8GZP9	Q8GZP9 arabidopsis
86	7	1.0	62	2 Q7PIZ1	Q7PIZ1 anopheles g
87	7	1.0	67	2 Q9EWT6	Q9EWT6 amaseta moo
88	7	1.0	81	2 Q9EWT8	Q9EWT8 amaseta moo
89	7	1.0	75	2 Q9C8P3	Q9C8P3 mycobacteri
90	7	1.0	81	2 Q7R3F2	Q7R3F2 giardia lam
91	7	1.0	81	2 Q9EWT8	Q9EWT8 amaseta moo
92	7	1.0	81	2 Q79209	Q79209 human immun
93	7	1.0	81	2 Q79303	Q79303 human immun
94	7	1.0	82	2 Q90D16	Q90D16 human immun
95	7	1.0	86	2 Q7X3H3	Q7X3H3 chioceps r
96	7	1.0	91	2 Q9M3B7	Q9M3B7 arabidopsis
97	7	1.0	106	2 Q87074	Q87074 suid herpes
98	7	1.0	108	2 Q62QF8	Q62QF8 bacillus li
99	7	1.0	109	2 Q966A7	Q966A7 caenorhabdi
100	7	1.0	112	2 P91967	P91967 trichinella
101	7	1.0	114	2 Q9YCT9	Q9YCT9 aeropyrum p
102	7	1.0	120	2 Q8T6A0	Q8T6A0 aplysia cal
103	7	1.0	123	2 Q6W1F1	Q6W1F1 rhizobium s
104	7	1.0	124	2 Q7WC39	Q7WC39 bordetella

105	7	1.0	124	2	081G20	081g20 bacillus ce	178	7	1.0	211	2	08ZEh2	08zeh2 yersinia pe
106	7	1.0	124	2	08G3X3	08g3x3 bifidobacte	179	7	1.0	211	2	08d4T7	08d4t7 erwilia car
107	7	1.0	126	2	06N0G5	06ng5 arabidopsis	180	7	1.0	212	1	06PW_ECOLI	p21364 escherichia
108	7	1.0	129	2	08TF33	08tf33 vibrio para	181	7	1.0	212	1	06PW_SALTI	08z762 salmonella
109	7	1.0	132	2	08MG97	08mg97 apatania zo	182	7	1.0	212	1	06PW_SALTI	08zps0 salmonella
110	7	1.0	132	2	08L158	08l158 streptomyce	183	7	1.0	212	2	0708A2	07z882 anopheles g
111	7	1.0	132	2	06SV41	06sv41 metathizium	184	7	1.0	212	2	08XC86	08x86 escherichia
112	7	1.0	136	2	06A6E6	06a6e6 propionibac	185	7	1.0	213	2	09CF55	09cf55 lactococcus
113	7	1.0	141	2	06S9X5	06s9x5 arabidopsis	186	7	1.0	214	2	087K02	087k02 vibrio para
114	7	1.0	143	2	08MG98	08mg98 moropsysche	187	7	1.0	215	2	074TX0	074tx0 yersinia pe
115	7	1.0	146	2	06R6N1	06r6n1 sus scrofa	188	7	1.0	215	2	08D0J8	08d0j8 yersinia pe
116	7	1.0	146	2	07S0S0	07s0s0 bartigiola	189	7	1.0	215	2	09RKP8	09rkp8 streptomyce
117	7	1.0	146	2	07S0Q3	07s0q3 rhopalomyia	190	7	1.0	221	2	09S5Z4	09s5z4 dirosophila
118	7	1.0	146	2	07S0F4	07s0f4 rhopalomyia	191	7	1.0	221	2	09VW77	09vw77 dirosophila
119	7	1.0	146	2	07S0F5	07s0f5 rhopalomyia	192	7	1.0	222	2	0871A9	0871a9 neurospora
120	7	1.0	146	2	07S0F6	07s0f6 rhopalomyia	193	7	1.0	222	2	06ESR8	06esr8 oryza sativ
121	7	1.0	146	2	07S0F7	07s0f7 rhopalomyia	194	7	1.0	222	2	08KQM4	08kqm4 saccharopol
122	7	1.0	146	2	07S0F8	07s0f8 rhopalomyia	195	7	1.0	223	2	07Z7Z4	07z7z4 inocybe sie
123	7	1.0	146	2	07S0F9	07s0f9 rhopalomyia	196	7	1.0	225	2	08MOX1	08mox1 synodiastyl
124	7	1.0	146	2	07S0G0	07s0g0 rhopalomyia	197	7	1.0	225	2	08W5L0	08w5l0 oryza sativ
125	7	1.0	146	2	07S0G1	07s0g1 rhopalomyia	198	7	1.0	225	2	07XH60	07xh60 oryza sativ
126	7	1.0	146	2	07S0G2	07s0g2 rhopalomyia	199	7	1.0	226	2	06J2M1	06j2m1 bacillus ce
127	7	1.0	146	2	07S0G3	07s0g3 rhopalomyia	200	7	1.0	226	2	0816L1	0816l1 bacillus ce
128	7	1.0	146	2	07S0G4	07s0g4 rhopalomyia	201	7	1.0	226	2	081KC5	081kc5 bacillus an
129	7	1.0	146	2	07S0G5	07s0g5 rhopalomyia	202	7	1.0	226	2	06HC61	06hc61 bacillus th
130	7	1.0	146	2	06Y7E3	06y7e3 oryza sativ	203	7	1.0	227	2	02S675	02s675 archaeoglob
131	7	1.0	147	2	067MY5	067my5 symbiobacte	204	7	1.0	227	2	07Z8D8	07z8d8 inocybe ada
132	7	1.0	154	2	050211	050211 mycobacteri	205	7	1.0	227	2	088QI8	088qi8 pseudomonas
133	7	1.0	156	2	06EU04	06eu04 oryza sativ	206	7	1.0	228	2	07Z8Z5	07z8z5 inocybe che
134	7	1.0	156	2	08PFR6	08pfr6 xanthomonas	207	7	1.0	228	2	0889S0	0889s0 pseudomonas
135	7	1.0	157	2	09SW21	09sw21 anthomonas	208	7	1.0	231	2	07NBZ8	07nbz8 mycoplasma
136	7	1.0	158	2	09AV48	09av48 oryza sativ	209	7	1.0	231	2	09Z795	09z795 chlamydia p
137	7	1.0	158	2	06S4W6	06s4w6 oryza sativ	210	7	1.0	232	2	09HWM1	09hwm1 pseudomonas
138	7	1.0	163	2	07S1L20	07s1l20 oryza sativ	211	7	1.0	233	2	07Z8Z4	07z8z4 inocybe che
139	7	1.0	164	2	0960K6	0960k6 homo sapien	212	7	1.0	235	2	08LD25	08ld25 arabidopsis
140	7	1.0	167	1	YPA2_ASCIM	P23375 ascobolus i	213	7	1.0	235	2	08VY63	08vy63 arabidopsis
141	7	1.0	168	2	08DUFO	08djfo synecococc	214	7	1.0	235	2	06YTS3	06yts3 oryza sativ
142	7	1.0	168	2	09Z8U3	09z8j3 chlamydia p	215	7	1.0	235	2	091004	091004 gecko gecko
143	7	1.0	169	2	087NK8	087nk8 vibrio para	216	7	1.0	236	2	09HQG1	09hqg1 halobacteri
144	7	1.0	170	2	084RT8	084rt8 chamaemelum	217	7	1.0	237	2	07ZWL3	07zwl3 xenopus lae
145	7	1.0	170	2	084SG4	084sg4 chamaemelum	218	7	1.0	238	2	07Z7Z1	07z7z1 inocybe ste
146	7	1.0	171	2	09R0P0	09rcp0 vibrio chol	219	7	1.0	238	2	08CW43	08cw43 escherichia
147	7	1.0	171	2	09K279	09k279 chlamydia p	220	7	1.0	239	2	09KQD6	09kqd6 vibrio chol
148	7	1.0	172	2	09CLY6	09cl1y6 pasteurella	221	7	1.0	239	2	0912I8	0912i8 oncorhynch
149	7	1.0	172	2	09DFD1	09dfd1 oncorhynch	222	7	1.0	240	2	0891B3	0891b3 bradyrhizob
150	7	1.0	175	2	07NK23	07nk23 gloeobacter	223	7	1.0	241	2	08FRK8	08frk8 corynebacte
151	7	1.0	176	2	09PUC7	09puc7 gallus gall	224	7	1.0	242	2	07Z9K7	07z9k7 desulfovibr
152	7	1.0	178	2	091MH2	091mh2 arabidopsis	225	7	1.0	243	2	07MAI3	07mai3 megabombus
153	7	1.0	181	2	087NZ6	087nz6 vibrio para	226	7	1.0	244	2	07X990	07x990 oryza sativ
154	7	1.0	185	2	09KMW2	09kwm2 salmoneila	227	7	1.0	244	2	06DIS2	06dis2 xenopus tro
155	7	1.0	186	2	06BL42	06bl42 debaryomyce	228	7	1.0	247	2	08FCQ3	08fcq3 escherichia
156	7	1.0	187	2	084SJO	084sj0 matricaria	229	7	1.0	247	2	08X6U7	08x6u7 escherichia
157	7	1.0	187	2	06WTT3	06wtc3 mycoplasma	230	7	1.0	247	2	083PUB	083p8 shigella fl
158	7	1.0	189	2	084SJI	084sj1 matricaria	231	7	1.0	248	2	049138	049138 arabidopsis
159	7	1.0	190	2	YRI5_GLOVI	07nh22 gloeobacter	232	7	1.0	249	2	06IE63	06ie63 retus norv
160	7	1.0	190	2	06BSX0	06bsx0 debaryomyce	233	7	1.0	249	2	08CI08	08ci08 mus muscul
161	7	1.0	191	1	MAF_BACAN	081ld6 bacillus an	234	7	1.0	250	2	08ZFK6	08zfk6 yersinia pe
162	7	1.0	191	2	0633Y9	0633y9 bacillus ce	235	7	1.0	253	2	089UG6	089ug6 bradyrhizob
163	7	1.0	191	2	09RS42	09rsa2 deinococcus	236	7	1.0	254	2	074MW1	074mw1 nanoarchaeu
164	7	1.0	191	2	06HD71	06hd71 bacillus th	237	7	1.0	254	2	06N3W7	06n3w7 rhodospseudo
165	7	1.0	193	1	Y317_MYCGE	P47617 mycoplasma	238	7	1.0	255	1	V29K_PEBV	P14850 pea early b
166	7	1.0	195	2	06AMIS	06amis desulfotale	239	7	1.0	255	2	09Y7A9	09y7a9 metathizium
167	7	1.0	196	1	CRBD_CHICK	P49152 gallus gall	240	7	1.0	255	2	084700	084700 pea early b
168	7	1.0	198	2	08XR75	08xrt75 ralscinia s	241	7	1.0	259	2	069EZ7	069ez7 homo sapien
169	7	1.0	201	1	ABP1_MAIZE	P13689 zea mays (m	242	7	1.0	259	2	08UDJ2	08udj2 agrobacteri
170	7	1.0	202	2	06ZSF8	06zsf8 homo sapien	243	7	1.0	260	1	COLI_RANRI	P22923 r corticotr
171	7	1.0	203	2	07Z2X1	07z2x1 bacillus ce	244	7	1.0	263	1	COLI_RANCA	P11885 r corticotr
172	7	1.0	204	2	08JIS7	08jis7 xenopus lae	245	7	1.0	263	2	06LJ06	06lj06 photobacter
173	7	1.0	208	2	09Z315	09z315 breadyrhizob	246	7	1.0	265	2	007812	007812 mycobacteri
174	7	1.0	209	1	NODS_BRAJA	P26026 breadyrhizob	247	7	1.0	265	2	068AV7	068av7 uncultured
175	7	1.0	210	2	07SC67	07sc67 aeshya goes	248	7	1.0	265	2	007181	007181 mycobacteri
176	7	1.0	211	2	06ESR9	06esr9 oryza sativ	249	7	1.0	266	2	07U190	07u190 mycobacteri
177	7	1.0	211	2	066AK7	066ak7 yersinia ps	250	7	1.0	266	2	081916	081916 biomia trop

251	7	1.0	266	2	06JYE6	06JYE6 elasmobranch	324	7	1.0	355	2	047485	047485 carabus cia
252	7	1.0	266	2	073QA7	073QA7 treponema d	325	7	1.0	355	2	047486	047486 carabus sic
253	7	1.0	266	2	09QU80	09QU80 tt vitruv. o	326	7	1.0	355	2	047487	047487 carabus lat
254	7	1.0	268	2	09XY56	09XY56 ctenocephal	327	7	1.0	355	2	078724	078724 carabus bla
255	7	1.0	268	2	06N9D3	06N9D3 rhodopsin	328	7	1.0	355	2	079585	079585 carabus tit
256	7	1.0	271	2	09NPM7	09NPM7 homo sapien	329	7	1.0	355	2	079586	079586 carabus aut
257	7	1.0	272	2	0510J3	0510J3 neisseria g	330	7	1.0	355	2	099052	099052 carabus por
258	7	1.0	273	2	083DM2	083DM2 coxiella bu	331	7	1.0	355	2	099053	099053 carabus por
259	7	1.0	278	2	084C08	084C08 pseudomonas	332	7	1.0	355	2	099054	099054 carabus por
260	7	1.0	280	2	087X78	087X78 pseudomonas	333	7	1.0	355	2	092098	092098 carabus mar
261	7	1.0	281	2	08U4H8	08U4H8 pyrococcus	334	7	1.0	355	2	092100	092100 carabus wag
262	7	1.0	281	2	06JYN8	06JYN8 laetonia ha	335	7	1.0	355	2	092101	092101 carabus lep
263	7	1.0	282	2	08UXE9	08UXE9 roselinia	336	7	1.0	355	2	092102	092102 carabus lud
264	7	1.0	284	2	096089	096089 haemaphysal	337	7	1.0	355	2	092103	092103 carabus bor
265	7	1.0	286	2	09H7G9	09H7G9 homo sapien	338	7	1.0	355	2	037388	037388 carabus geh
266	7	1.0	291	1	PCAR_PSEBU	052154 pseudomonas	339	7	1.0	355	2	037389	037389 carabus geh
267	7	1.0	291	1	09R9T0	09R9T0 pseudomonas	340	7	1.0	355	2	037428	037428 carabus fru
268	7	1.0	291	2	088N41	088N41 pseudomonas	341	7	1.0	355	2	037441	037441 carabus van
269	7	1.0	292	2	054441	054441 bacillus ps	342	7	1.0	355	2	037443	037443 carabus bla
270	7	1.0	294	1	PEPM_MYTEB	056839 mytilus edu	343	7	1.0	355	2	037444	037444 carabus bla
271	7	1.0	295	2	069E28	069E28 homo sapien	344	7	1.0	355	2	037445	037445 carabus bla
272	7	1.0	295	2	06D6J3	06D6J3 erwinia car	345	7	1.0	355	2	037446	037446 carabus bla
273	7	1.0	299	2	08T8D9	08T8D9 trypanosoma	346	7	1.0	355	2	037447	037447 carabus bla
274	7	1.0	299	2	07PMA7	07PMA7 anopheles g	347	7	1.0	355	2	037448	037448 carabus bla
275	7	1.0	300	2	08IN70	08IN70 dirosophila	348	7	1.0	355	2	037449	037449 carabus bla
276	7	1.0	301	2	07ZSX7	07ZSX7 figu rubrip	349	7	1.0	355	2	037453	037453 carabus bla
277	7	1.0	303	1	LEPC_XANNC	08P283 xanthomonas	350	7	1.0	355	2	037454	037454 carabus bla
278	7	1.0	303	2	074ZD4	074ZD4 ashyia goss	351	7	1.0	355	2	037457	037457 carabus bla
279	7	1.0	303	2	06V039	06V039 tetradodon n	352	7	1.0	355	2	037459	037459 carabus bla
280	7	1.0	304	2	08XRF6	08XRF6 ralsconia s	353	7	1.0	355	2	037465	037465 carabus por
281	7	1.0	305	1	LEPC_RALSO	09JHL6 ralsconia s	354	7	1.0	355	2	037518	037518 carabus mae
282	7	1.0	306	2	08L5B0	08L5B0 cryza sativ	355	7	1.0	355	2	037542	037542 carabus mae
283	7	1.0	307	2	07Q528	07Q528 anopheles g	356	7	1.0	355	2	085A26	085A26 carabus sac
284	7	1.0	307	2	09KVB9	09KVB9 vibrio chol	357	7	1.0	355	2	085BA4	085BA4 carabus cha
285	7	1.0	308	1	T2RC_MOUSE	059532 mus musculu	358	7	1.0	355	2	085GL4	085GL4 carabus sma
286	7	1.0	308	2	07MT04	07MT04 mus musculu	359	7	1.0	355	2	085GL5	085GL5 carabus sma
287	7	1.0	312	2	012125	012125 baccharomyc	360	7	1.0	355	2	085GL6	085GL6 carabus kub
288	7	1.0	314	2	06FUP3	06FUP3 candida gla	361	7	1.0	355	2	085GL7	085GL7 carabus for
289	7	1.0	315	1	Y001_CAUCR	09AC59 caulobacter	362	7	1.0	355	2	085GL8	085GL8 carabus jan
290	7	1.0	315	2	055Z30	055Z30 streptomyce	363	7	1.0	355	2	085GL9	085GL9 carabus oea
291	7	1.0	317	2	09KMA7	09KMA7 agrobacteri	364	7	1.0	355	2	085GM0	085GM0 carabus nan
292	7	1.0	318	2	06CP66	06CP66 Kluyveromyc	365	7	1.0	355	2	085GM1	085GM1 carabus kas
293	7	1.0	321	2	067LRF3	067LRF3 symbiobacte	366	7	1.0	355	2	085GM2	085GM2 carabus rem
294	7	1.0	324	2	090Z55	090Z55 acophilalmu	367	7	1.0	355	2	085GM3	085GM3 carabus alp
295	7	1.0	329	2	08U2M3	08U2M3 pyrococcus	368	7	1.0	355	2	085GM4	085GM4 carabus wag
296	7	1.0	329	2	08UMG1	08UMG1 bradyrhizob	369	7	1.0	355	2	085GM5	085GM5 carabus lam
297	7	1.0	330	2	030523	030523 vibrio shil	370	7	1.0	355	2	085GM6	085GM6 carabus dra
298	7	1.0	332	2	08NX19	08NX19 staphylococ	371	7	1.0	355	2	085GM7	085GM7 carabus ben
299	7	1.0	333	2	09KX77	09KX77 bacillus ha	372	7	1.0	355	2	085GM8	085GM8 carabus wen
300	7	1.0	336	2	069510	069510 mycobacteri	373	7	1.0	355	2	085GM9	085GM9 carabus gan
301	7	1.0	336	2	08PRA2	08PRA2 xanthomonas	374	7	1.0	355	2	085GN0	085GN0 carabus lam
302	7	1.0	336	2	06MS16	06MS16 mycoplasma	375	7	1.0	355	2	085GN1	085GN1 carabus cra
303	7	1.0	336	2	07WL07	07WL07 bordetella	376	7	1.0	355	2	085GN2	085GN2 carabus cra
304	7	1.0	337	2	09YDH3	09YDH3 aetopyrum p	377	7	1.0	355	2	085GN3	085GN3 carabus vir
305	7	1.0	338	2	08PE85	08PE85 xanthomonas	378	7	1.0	355	2	085GN4	085GN4 carabus vir
306	7	1.0	342	2	07XE33	07XE33 cryza sativ	379	7	1.0	355	2	085GN5	085GN5 carabus sun
307	7	1.0	343	2	07VVI3	07VVI3 bordetella	380	7	1.0	355	2	085GN6	085GN6 carabus bus
308	7	1.0	343	2	08D7G2	08D7G2 vibrio vuln	381	7	1.0	355	2	085GN7	085GN7 carabus erv
309	7	1.0	344	2	084QA9	084QA9 cryza sativ	382	7	1.0	355	2	085GN8	085GN8 carabus bur
310	7	1.0	344	2	092M18	092M18 rhizobium m	383	7	1.0	355	2	085GN9	085GN9 carabus tal
311	7	1.0	345	2	07W7L8	07W7L8 bordetella	384	7	1.0	355	2	085GN9	085GN9 carabus pun
312	7	1.0	346	2	06JY16	06JY16 eupolemus s	385	7	1.0	355	2	085GN5	085GN5 carabus mul
313	7	1.0	347	2	06EJZC2	06EJZC2 escherichia	386	7	1.0	355	2	085GN6	085GN6 carabus imp
314	7	1.0	347	2	07P022	07P022 chromobacte	387	7	1.0	355	2	085GN7	085GN7 carabus hen
315	7	1.0	348	1	RTCA_PYRAE	08A8E4 pyrobaculum	388	7	1.0	355	2	085GN8	085GN8 carabus mul
316	7	1.0	349	2	09YBV1	09YBV1 aetopyrum p	389	7	1.0	355	2	085GN9	085GN9 carabus mul
317	7	1.0	350	2	06NDF7	06NDF7 rhodopseudo	390	7	1.0	355	2	085GN0	085GN0 carabus syr
318	7	1.0	350	2	018122	018122 cenorhobadi	391	7	1.0	355	2	085GN1	085GN1 carabus pio
319	7	1.0	351	1	MS52_YEAST	040990 saccharomyc	392	7	1.0	355	2	085GN2	085GN2 carabus pio
320	7	1.0	352	2	08GC9H0	08GC9H0 mus musculu	393	7	1.0	355	2	085GN5	085GN5 carabus tor
321	7	1.0	354	2	099Q08	099Q08 bradyrhizob	394	7	1.0	355	2	085GN6	085GN6 carabus ere
322	7	1.0	354	2	099Q80	099Q80 bradyrhizob	395	7	1.0	355	2	085GN7	085GN7 carabus nor
323	7	1.0	355	2	047484	047484 carabus vir	396	7	1.0	355	2	085GN8	085GN8 carabus nor

397	1.0	355	2	Q85GT9	carabus tor	470	7	1.0	355	2	Q9MR78	carabus por
398	1.0	355	2	Q85GU0	carabus tor	471	7	1.0	355	2	Q9MR79	carabus por
399	1.0	355	2	Q85GU1	carabus tor	472	7	1.0	355	2	Q9MR80	carabus por
400	1.0	355	2	Q85GU2	carabus cha	473	7	1.0	355	2	Q9MR81	carabus por
401	1.0	355	2	Q85GU3	carabus tor	474	7	1.0	355	2	Q9T227	carabus bla
402	1.0	355	2	Q85GU4	carabus pra	475	7	1.0	355	2	Q9T391	carabus bla
403	1.0	355	2	Q8HAX6	carabus lit	476	7	1.0	355	2	Q9T392	carabus bla
404	1.0	355	2	Q8HDX2	carabus asc	477	7	1.0	355	2	Q9T393	carabus bla
405	1.0	355	2	Q8HDX3	carabus mas	478	7	1.0	355	2	Q9T3V1	carabus bla
406	1.0	355	2	Q8HDX4	carabus mas	479	7	1.0	355	2	Q9T3V2	carabus bla
407	1.0	355	2	Q8HDX5	carabus inf	480	7	1.0	355	2	Q9T3V3	carabus bla
408	1.0	355	2	Q8HDX6	carabus inf	481	7	1.0	355	2	Q9T3V4	carabus bla
409	1.0	355	2	Q8HDX8	carabus min	482	7	1.0	355	2	Q9T3V5	carabus bla
410	1.0	355	2	Q8HE25	carabus lit	483	7	1.0	355	2	Q9T327	carabus bla
411	1.0	355	2	Q8B9L8	carabus hum	484	7	1.0	355	2	Q9T4D6	carabus bla
412	1.0	355	2	Q8B9L9	carabus hum	485	7	1.0	355	2	Q9T4K2	carabus bla
413	1.0	355	2	Q8B9M0	carabus hum	486	7	1.0	355	2	Q9T4R4	carabus bla
414	1.0	355	2	Q8B9M0	carabus hum	487	7	1.0	355	2	Q9T4R5	carabus bla
415	1.0	355	2	Q8B9R6	carabus ruf	488	7	1.0	355	2	Q9T4R5	carabus bla
416	1.0	355	2	Q8B9R7	carabus bal	489	7	1.0	355	2	Q9T4V4	carabus bla
417	1.0	355	2	Q8B9R8	carabus str	490	7	1.0	355	2	Q9TDX8	carabus cia
418	1.0	355	2	Q8B9R9	carabus lat	491	7	1.0	355	2	Q9TDX9	carabus mao
419	1.0	355	2	Q8B9S0	carabus aen	492	7	1.0	355	2	Q9TDX0	carabus cie
420	1.0	355	2	Q8B9S1	carabus aen	493	7	1.0	355	2	Q9TDX1	carabus cie
421	1.0	355	2	Q8B9S2	carabus sac	494	7	1.0	355	2	Q9TDX2	carabus art
422	1.0	355	2	Q8B9S3	carabus lin	495	7	1.0	355	2	Q9TDX3	carabus lao
423	1.0	355	2	Q8B9S4	carabus kad	496	7	1.0	355	2	Q9TDX4	carabus lao
424	1.0	355	2	Q8B9S5	carabus str	497	7	1.0	355	2	Q9TDX5	carabus cya
425	1.0	355	2	Q8B9S6	carabus str	498	7	1.0	355	2	Q9TDX6	carabus tou
426	1.0	355	2	Q8B9S6	carabus con	499	7	1.0	355	2	Q9TDX7	carabus lux
427	1.0	355	2	Q8B9S5	carabus con	500	7	1.0	355	2	Q9TDX8	carabus ton
428	1.0	355	2	Q8B9K6	carabus gly	501	7	1.0	355	2	Q9TDX9	carabus ton
429	1.0	355	2	Q8B9K7	carabus gly	502	7	1.0	355	2	Q9TE01	carabus tru
430	1.0	355	2	Q8B9K8	carabus sma	503	7	1.0	355	2	Q9TE02	carabus can
431	1.0	355	2	Q8B9K9	carabus sma	504	7	1.0	355	2	Q9TE03	carabus can
432	1.0	355	2	Q8B9L0	carabus ale	505	7	1.0	355	2	Q9TE04	carabus can
433	1.0	355	2	Q8B9L1	carabus hae	506	7	1.0	355	2	Q9TE05	carabus can
434	1.0	355	2	Q8B9L2	carabus pot	507	7	1.0	355	2	Q9TE06	carabus sei
435	1.0	355	2	Q8B9L3	carabus pot	508	7	1.0	355	2	Q9TE07	carabus sei
436	1.0	355	2	Q8B9L4	carabus pot	509	7	1.0	355	2	Q9TE08	carabus sei
437	1.0	355	2	Q8B9L5	carabus arl	510	7	1.0	355	2	Q9TE09	carabus sei
438	1.0	355	2	Q8B9L6	carabus arl	511	7	1.0	355	2	Q9TE10	carabus sei
439	1.0	355	2	Q8B9L7	carabus exi	512	7	1.0	355	2	Q9TE11	carabus sei
440	1.0	355	2	Q8B9L8	carabus cra	513	7	1.0	355	2	Q9TE12	carabus sei
441	1.0	355	2	Q8B9L9	carabus cra	514	7	1.0	355	2	Q9TE13	carabus sei
442	1.0	355	2	Q8B9M0	carabus uen	515	7	1.0	355	2	Q9TE14	carabus sei
443	1.0	355	2	Q8B9M1	carabus uen	516	7	1.0	355	2	Q9TE15	carabus sei
444	1.0	355	2	Q8B9M2	carabus bra	517	7	1.0	355	2	Q9TE16	carabus sei
445	1.0	355	2	Q8B9M3	carabus bra	518	7	1.0	355	2	Q9TE17	carabus sei
446	1.0	355	2	Q8B9M4	carabus ign	519	7	1.0	355	2	Q9TE18	carabus sei
447	1.0	355	2	Q8B9M5	carabus mir	520	7	1.0	355	2	Q9TE19	carabus sei
448	1.0	355	2	Q8B9M6	carabus oia	521	7	1.0	355	2	Q9TE20	carabus sei
449	1.0	355	2	Q8B9M7	carabus oia	522	7	1.0	355	2	Q9TE21	carabus sei
450	1.0	355	2	Q8B9M8	carabus oia	523	7	1.0	355	2	Q9TE22	carabus sei
451	1.0	355	2	Q8B9M9	carabus oia	524	7	1.0	355	2	Q9TE23	carabus sei
452	1.0	355	2	Q8B9M0	carabus oia	525	7	1.0	355	2	Q9TE24	carabus sei
453	1.0	355	2	Q8B9M1	carabus oia	526	7	1.0	355	2	Q9TE25	carabus sei
454	1.0	355	2	Q8B9M2	carabus oia	527	7	1.0	355	2	Q9TE26	carabus sei
455	1.0	355	2	Q8B9M3	carabus oia	528	7	1.0	355	2	Q9TE27	carabus sei
456	1.0	355	2	Q8B9M4	carabus oia	529	7	1.0	355	2	Q9TE28	carabus sei
457	1.0	355	2	Q8B9M5	carabus oia	530	7	1.0	355	2	Q9TE29	carabus sei
458	1.0	355	2	Q8B9M6	carabus oia	531	7	1.0	355	2	Q9TE30	carabus sei
459	1.0	355	2	Q8B9M7	carabus oia	532	7	1.0	355	2	Q9TE31	carabus sei
460	1.0	355	2	Q8B9M8	carabus oia	533	7	1.0	355	2	Q9TE32	carabus sei
461	1.0	355	2	Q8B9M9	carabus oia	534	7	1.0	355	2	Q9TE33	carabus sei
462	1.0	355	2	Q8B9M0	carabus oia	535	7	1.0	355	2	Q9TE34	carabus sei
463	1.0	355	2	Q8B9M1	carabus oia	536	7	1.0	355	2	Q9TE35	carabus sei
464	1.0	355	2	Q8B9M2	carabus oia	537	7	1.0	355	2	Q9TE36	carabus sei
465	1.0	355	2	Q8B9M3	carabus oia	538	7	1.0	355	2	Q9TE37	carabus sei
466	1.0	355	2	Q8B9M4	carabus oia	539	7	1.0	355	2	Q9TE38	carabus sei
467	1.0	355	2	Q8B9M5	carabus oia	540	7	1.0	355	2	Q9TE39	carabus sei
468	1.0	355	2	Q8B9M6	carabus oia	541	7	1.0	355	2	Q9TE40	carabus sei
469	1.0	355	2	Q8B9M7	carabus oia	542	7	1.0	355	2	Q9TE41	carabus sei

543	7	1.0	355	2	Q9TEA6	Q9TEA6 carabus bla	616	7	1.0	446	2	Q6FCC9	Q6FCC9 acinetobact
544	7	1.0	355	2	Q9TEA7	Q9TEA7 carabus bla	617	7	1.0	447	2	Q8TAB5	Q8TAB5 homo sapien
545	7	1.0	355	2	Q9TEA8	Q9TEA8 carabus bla	618	7	1.0	449	2	Q8BI18	Q8BI18 mus musculi
546	7	1.0	355	2	Q9TEA9	Q9TEA9 carabus bla	619	7	1.0	453	2	Q6CVL9	Q6CVL9 kluyveromyc
547	7	1.0	355	2	Q9TEB0	Q9TEB0 carabus bla	620	7	1.0	453	2	Q6VAT4	Q6VAT4 umbraeculm
548	7	1.0	355	2	Q9TEB1	Q9TEB1 carabus bla	621	7	1.0	453	2	Q8P704	Q8P704 xanthomonas
549	7	1.0	355	2	Q9TEB2	Q9TEB2 carabus bla	622	7	1.0	453	2	Q8P1B8	Q8P1B8 xanthomonas
550	7	1.0	355	2	Q9TEB3	Q9TEB3 carabus bla	623	7	1.0	455	2	Q6LEF3	Q6LEF3 photobacter
551	7	1.0	357	2	Q6ZSC3	Q6ZSC3 homo sapien	624	7	1.0	459	2	Q6K349	Q6K349 brassica na
552	7	1.0	357	2	Q6ZSC3	Q6ZSC3 homo sapien	625	7	1.0	459	2	Q67110	Q67110 symbiobacte
553	7	1.0	359	1	MANR_PSEBU	MANR_PSEBU pseudomonas	626	7	1.0	461	2	Q7D565	Q7D565 mycobacteri
554	7	1.0	359	1	MANR_PSEBU	MANR_PSEBU pseudomonas	627	7	1.0	461	2	Q7D565	Q7D565 mycobacteri
555	7	1.0	359	2	Q6JY13	Q6JY13 amphiaceae sp	628	7	1.0	461	2	Q7D4A5	Q7D4A5 mycobacteri
556	7	1.0	359	2	Q6JY13	Q6JY13 amphiaceae sp	629	7	1.0	461	2	Q7D4A5	Q7D4A5 mycobacteri
557	7	1.0	360	1	AROB_BUCAP	AROB_BUCAP oryza sativ	630	7	1.0	462	2	Q7SEJ7	Q7SEJ7 ashbya gos
558	7	1.0	363	2	Q8MP22	Q8MP22 macaca fasc	631	7	1.0	462	2	Q6PAC2	Q6PAC2 xenopus lae
559	7	1.0	364	2	Q7MEH3	Q7MEH3 vibrio vuln	632	7	1.0	463	1	FMNL_HUMAN	FMNL_HUMAN
560	7	1.0	367	2	Q8N7F6	Q8N7F6 homo sapien	633	7	1.0	463	2	Q8N6T1	Q8N6T1 homo sapien
561	7	1.0	367	2	Q8N7F6	Q8N7F6 homo sapien	634	7	1.0	465	2	Q84X18	Q84X18 xerophyta h
562	7	1.0	368	2	Q32860	Q32860 mycobacteri	635	7	1.0	465	2	Q8GW44	Q8GW44 arabidopsis
563	7	1.0	372	2	Q9H2B5	Q9H2B5 pseudomonas	636	7	1.0	468	2	Q6K2N9	Q6K2N9 oryza sativ
564	7	1.0	373	2	Q704D8	Q704D8 thermoprote	637	7	1.0	469	2	Q8LEG9	Q8LEG9 arabidopsis
565	7	1.0	373	2	Q803F1	Q803F1 brachydanio	638	7	1.0	469	2	Q81NR2	Q81NR2 bacillus ce
566	7	1.0	374	1	TCT_ANASP	TCT_ANASP anabaena sp	639	7	1.0	471	2	Q6DQ98	Q6DQ98 nicotiana t
567	7	1.0	375	1	Q6JX36	Q6JX36 neisseria m	640	7	1.0	472	2	Q09657	Q09657 caenorhabd
568	7	1.0	375	2	Q9K1G5	Q9K1G5 neisseria m	641	7	1.0	475	1	GID_BRAJA	GID_BRAJA
569	7	1.0	376	2	Q9K1G5	Q9K1G5 neisseria m	642	7	1.0	476	2	Q6HMS5	Q6HMS5 bacillus an
570	7	1.0	377	2	Q7NY19	Q7NY19 chromobacte	643	7	1.0	476	2	Q735G8	Q735G8 bacillus ce
571	7	1.0	378	2	Q8X0S5	Q8X0S5 ralstonia s	644	7	1.0	476	2	Q81B16	Q81B16 bacillus ce
572	7	1.0	382	2	Q88BC3	Q88BC3 pseudomonas	645	7	1.0	476	2	Q6HGR8	Q6HGR8 bacillus th
573	7	1.0	382	2	Q90MT4	Q90MT4 crocodylus	646	7	1.0	478	2	Q6FPY7	Q6FPY7 candida gla
574	7	1.0	383	2	Q65Q28	Q65Q28 manheimia	647	7	1.0	479	2	Q99RL5	Q99RL5 staphylococ
575	7	1.0	383	2	Q7MSV6	Q7MSV6 bordetella	648	7	1.0	479	2	Q7A384	Q7A384 staphylococ
576	7	1.0	383	2	Q7WGX8	Q7WGX8 bordetella	649	7	1.0	483	2	Q89BC3	Q89BC3 bradyrhizob
577	7	1.0	387	2	Q8GJM2	Q8GJM2 synecococc	650	7	1.0	484	2	Q7PMP7	Q7PMP7 anopheles g
578	7	1.0	387	2	Q73853	Q73853 synecocyst	651	7	1.0	487	2	Q8ETV6	Q8ETV6 oceanobacil
579	7	1.0	387	2	Q8Z0N9	Q8Z0N9 anabaena sp	652	7	1.0	489	1	MEP3_YEAST	MEP3_YEAST
580	7	1.0	387	2	Q7U897	Q7U897 synecococc	653	7	1.0	489	2	Q6B2F5	Q6B2F5 saccharomyc
581	7	1.0	387	2	Q7V6M7	Q7V6M7 proclostricc	654	7	1.0	489	2	Q91Q01	Q91Q01 soybean dwa
582	7	1.0	387	2	Q8DGX2	Q8DGX2 synecococc	655	7	1.0	490	2	Q74135	Q74135 lactobacill
583	7	1.0	388	2	Q44330	Q44330 manduca rex	656	7	1.0	490	2	Q7VH13	Q7VH13 helicobacte
584	7	1.0	389	1	PTRC_SULTO	PTRC_SULTO sulfobius	657	7	1.0	491	1	MURC_PHOL	MURC_PHOL photorhabd
585	7	1.0	391	2	Q91V12	Q91V12 mus musculi	658	7	1.0	492	1	MEP1_YEAST	MEP1_YEAST
586	7	1.0	392	2	Q63W65	Q63W65 burkholderi	659	7	1.0	492	2	Q45659	Q45659 caenorhabd
587	7	1.0	394	2	P91817	P91817 tachypleus	660	7	1.0	492	2	Q88Z15	Q88Z15 lactobacill
588	7	1.0	396	2	Q7XT04	Q7XT04 oryza sativ	661	7	1.0	493	1	CAMA_CHICK	CAMA_CHICK
589	7	1.0	397	2	Q94U66	Q94U66 oryza sativ	662	7	1.0	493	2	Q972W0	Q972W0 sulfobius
590	7	1.0	397	2	Q8RJW1	Q8RJW1 xanthomonas	663	7	1.0	493	2	Q90XP7	Q90XP7 brachydanio
591	7	1.0	398	2	Q91374	Q91374 pseudomonas	664	7	1.0	494	1	CD5_MOUSE	CD5_MOUSE
592	7	1.0	399	2	Q7RY56	Q7RY56 neurospora	665	7	1.0	494	2	Q8VDV0	Q8VDV0 mus musculi
593	7	1.0	407	2	Q6Z7S5	Q6Z7S5 oryza sativ	666	7	1.0	494	2	Q91X69	Q91X69 mus musculi
594	7	1.0	408	2	Q9VMA6	Q9VMA6 dirosophila	667	7	1.0	494	2	Q8BMS0	Q8BMS0 mus musculi
595	7	1.0	408	2	Q8XWX2	Q8XWX2 ralstonia s	668	7	1.0	494	2	Q9ER20	Q9ER20 mus musculi
596	7	1.0	410	2	Q6E824	Q6E824 umbonia gra	669	7	1.0	497	2	Q54706	Q54706 streptococc
597	7	1.0	410	2	Q6E826	Q6E826 umbonia gra	670	7	1.0	497	2	Q54749	Q54749 streptococc
598	7	1.0	410	2	Q6E838	Q6E838 platycotis	671	7	1.0	497	2	Q51503	Q51503 boerella bu
599	7	1.0	410	2	Q6E840	Q6E840 platycotis	672	7	1.0	497	2	Q9A1S4	Q9A1S4 streptococc
600	7	1.0	413	2	Q29192	Q29192 archaeoglob	673	7	1.0	497	2	Q73VS8	Q73VS8 mycobacteri
601	7	1.0	413	2	Q6LYH5	Q6LYH5 methanococc	674	7	1.0	498	2	Q6C1F0	Q6C1F0 yarrowia li
602	7	1.0	414	2	Q6UDM0	Q6UDM0 palitacid h	675	7	1.0	501	2	Q9NDD6	Q9NDD6 riftia pach
603	7	1.0	416	2	Q88RT5	Q88RT5 pseudomonas	676	7	1.0	504	1	GPMI_RHOPA	GPMI_RHOPA
604	7	1.0	420	1	Q63A_DROME	Q63A_DROME treponema d	677	7	1.0	505	1	GMAT_MYCPU	GMAT_MYCPU
605	7	1.0	421	2	Q73XB7	Q73XB7 treponema d	678	7	1.0	505	1	GMAT_MYCPU	GMAT_MYCPU
606	7	1.0	426	2	Q6BX74	Q6BX74 debaryomyce	679	7	1.0	505	2	Q95EA3	Q95EA3 symnocalyct
607	7	1.0	429	2	Q7SYF9	Q7SYF9 acipenser b	680	7	1.0	507	1	MATK_BROHE	MATK_BROHE
608	7	1.0	432	2	Q73AL5	Q73AL5 bacillus ce	681	7	1.0	507	2	Q94NC4	Q94NC4 streptococ
609	7	1.0	436	2	Q67N05	Q67N05 symbiobacte	682	7	1.0	507	2	Q94P31	Q94P31 haaseocereu
610	7	1.0	437	2	Q51640	Q51640 burkholderi	683	7	1.0	507	2	Q94P34	Q94P34 erioseyce na
611	7	1.0	437	2	Q7UDY7	Q7UDY7 rhodospirill	684	7	1.0	507	2	Q94PY9	Q94PY9 acanthocally
612	7	1.0	439	2	Q9LY67	Q9LY67 arabidopsis	685	7	1.0	507	2	Q95EB7	Q95EB7 neoverderma
613	7	1.0	441	2	Q62LB1	Q62LB1 burkholderi	686	7	1.0	507	2	Q95EB8	Q95EB8 erioseyce bu
614	7	1.0	442	2	Q804X1	Q804X1 figu rubrip	687	7	1.0	507	2	Q95EB9	Q95EB9 erioseyce is
615	7	1.0	445	2	Q67RK6	Q67RK6 symbiobacte	688	7	1.0	507	2	Q95EB9	Q95EB9 erioseyce au

689	7	1.0	507	2	Q9SE93	Q9SE93	parodia maa	762	7	1.0	544	2	Q8TFN9	Q8TFN9	emericella
690	7	1.0	507	2	Q9SE96	Q9SE96	matucana in	763	7	1.0	545	2	Q67LM0	Q67LM0	symbiobacte
691	7	1.0	507	2	Q9SE97	Q9SE97	rauhocereus	764	7	1.0	549	2	Q9DM53	Q9DM53	rat cytoMeg
692	7	1.0	507	2	Q9SEAO	Q9SEAO	trichocereus	765	7	1.0	553	2	Q97S10	Q97S10	streptococc
693	7	1.0	507	2	Q9SEAI	Q9SEAI	uebelmannia	766	7	1.0	553	2	Q8DOR3	Q8DOR3	streptococc
694	7	1.0	507	2	Q9SEAA	Q9SEAA	coleocephal	767	7	1.0	556	1	NU2M_PODAN	PI5578	podopora a
695	7	1.0	507	2	Q9SEEA	Q9SEEA	browningia	768	7	1.0	556	2	Q6DEK7	Q6DEK7	brachydania
696	7	1.0	507	2	Q9SECA	Q9SECA	copiapa la	769	7	1.0	560	2	Q49141	Q49141	arabidopsis
697	7	1.0	507	2	Q9SECS	Q9SECS	copiapa br	770	7	1.0	560	2	Q50057	Q50057	arabidopsis
698	7	1.0	507	2	Q9SECE	Q9SECE	copiapa so	771	7	1.0	561	2	Q9KY69	Q9KY69	streptomyc
699	7	1.0	507	2	Q9SEDE	Q9SEDE	pereskiopti	772	7	1.0	561	2	Q9RX81	Q9RX81	deinococcus
700	7	1.0	507	2	Q7HFB7	Q7HFB7	parodia mag	773	7	1.0	563	2	Q74JC6	Q74JC6	lactobacill
701	7	1.0	507	2	Q7HFB8	Q7HFB8	oreocereus	774	7	1.0	568	2	Q88M64	Q88M64	lactobacill
702	7	1.0	507	2	Q7HFB9	Q7HFB9	samaltapice	775	7	1.0	576	2	Q6YID6	Q6YID6	panaeus mon
703	7	1.0	507	2	Q7HFC0	Q7HFC0	micranthoce	776	7	1.0	579	2	Q65X75	Q65X75	oryza sativ
704	7	1.0	507	2	Q7HFC1	Q7HFC1	cereus alac	777	7	1.0	580	2	Q9ZOP6	Q9ZOP6	arabidopsis
705	7	1.0	508	2	Q9SEB2	Q9SEB2	pfieffera m	778	7	1.0	581	1	YD15_SCHPO	Q10238	schizosacch
706	7	1.0	508	2	Q9JSM9	Q9JSM9	staphylococ	779	7	1.0	581	2	Q91KH1	Q91KH1	mesembryant
707	7	1.0	508	2	Q6GB44	Q6GB44	staphylococ	780	7	1.0	581	2	Q8D7C1	Q8D7C1	vibrio vuln
708	7	1.0	509	2	Q9SEB3	Q9SEB3	leptismilum c	781	7	1.0	582	2	Q23492	Q23492	arabidopsis
709	7	1.0	509	2	Q9SEB5	Q9SEB5	rhypsalis f	782	7	1.0	584	2	Q9SQZ0	Q9SQZ0	arabidopsis
710	7	1.0	509	2	Q9SEB6	Q9SEB6	haciara sal	783	7	1.0	584	2	Q67RH6	Q67RH6	symbiobacte
711	7	1.0	509	2	Q9SE91	Q9SE91	parodia oct	784	7	1.0	585	2	Q17491	Q17491	caenorhabdi
712	7	1.0	509	2	Q9SE92	Q9SE92	parodia mic	785	7	1.0	585	2	Q8SZY4	Q8SZY4	caenorhabdi
713	7	1.0	509	2	Q9SEAE	Q9SEAE	disocactus	786	7	1.0	600	2	Q93GX8	Q93GX8	streptomyc
714	7	1.0	509	2	Q9SEAE7	Q9SEAE7	selenicereu	787	7	1.0	600	2	Q6AZT2	Q6AZT2	xenopus lae
715	7	1.0	509	2	Q9SEAE8	Q9SEAE8	hylocereus	788	7	1.0	602	2	Q65DM0	Q65DM0	bacillus 1i
716	7	1.0	509	2	Q9SEAE9	Q9SEAE9	echinocereus	789	7	1.0	607	2	Q6DFJ5	Q6DFJ5	xenopus lae
717	7	1.0	509	2	Q9SEBA1	Q9SEBA1	pachycereus	790	7	1.0	608	2	Q9GMB0	Q9GMB0	sus scrofa
718	7	1.0	509	2	Q9SEBA3	Q9SEBA3	pfieffera m	791	7	1.0	611	2	Q7MEC8	Q7MEC8	vibrio vuln
719	7	1.0	509	2	Q9SEBA4	Q9SEBA4	pfieffera l	792	7	1.0	612	2	Q804W7	Q804W7	fugu rubrip
720	7	1.0	509	2	Q9SEB5	Q9SEB5	corryocactu	793	7	1.0	614	1	SPAS_MOUSE	Q949Y7	mus musculu
721	7	1.0	509	2	Q9SEB6	Q9SEB6	eulychmia l	794	7	1.0	615	1	Q6GNK4	Q6GNK4	xenopus lae
722	7	1.0	509	2	Q9SEB7	Q9SEB7	neoraimondi	795	7	1.0	616	1	SPAS_HUMAN	Q9UBP0	homo saplen
723	7	1.0	509	2	Q9SEB8	Q9SEB8	autrocactu	796	7	1.0	617	1	THRB_RAT	PI8292	ratius norv
724	7	1.0	509	2	Q9SEB9	Q9SEB9	caecellanos	797	7	1.0	617	2	Q97UG5	Q97UG5	sulfolobus
725	7	1.0	509	2	Q9SECO	Q9SECO	leptocereus	798	7	1.0	618	1	CTR3_MOUSE	P70423	mus musculu
726	7	1.0	509	2	Q9SECI	Q9SECI	armatocereus	799	7	1.0	618	1	THRB_MOUSE	P19221	mus musculu
727	7	1.0	509	2	Q9SECI2	Q9SECI2	acanthocere	800	7	1.0	620	2	Q38940	Q38940	arabidopsis
728	7	1.0	509	2	Q9SECI3	Q9SECI3	calymmanchi	801	7	1.0	622	1	THRB_HUMAN	P00734	homo saplen
729	7	1.0	509	2	Q9SEEC7	Q9SEEC7	aztekium ri	802	7	1.0	622	2	Q7Z7F3	Q7Z7F3	homo saplen
730	7	1.0	509	2	Q9SEEC8	Q9SEEC8	astrophytum	803	7	1.0	624	2	Q94CP4	Q94CP4	arabidopsis
731	7	1.0	509	2	Q9SEED0	Q9SEED0	echinocactu	804	7	1.0	625	1	THRB_BOVIN	P00735	bos taurus
732	7	1.0	509	2	Q9SEED1	Q9SEED1	fireilea pha	805	7	1.0	629	1	THIC_PSES	Q87V91	pseudomonas
733	7	1.0	509	2	Q9SEED2	Q9SEED2	fireilea gra	806	7	1.0	633	2	Q90Z56	Q90Z56	scophthalmu
734	7	1.0	509	2	Q9SEED3	Q9SEED3	bloufeldia	807	7	1.0	648	2	Q9NKD7	Q9NKD7	drosophila
735	7	1.0	509	2	Q9SEED4	Q9SEED4	bloufeldia	808	7	1.0	651	2	Q7NGA4	Q7NGA4	gloeobacter
736	7	1.0	509	2	Q9SEED5	Q9SEED5	opuntia qui	809	7	1.0	658	2	Q65466	Q65466	arabidopsis
737	7	1.0	509	2	Q9SEED9	Q9SEED9	pereskia gu	810	7	1.0	663	2	Q8U2H8	Q8U2H8	pyrococcus
738	7	1.0	509	2	Q9SEED0	Q9SEED0	autrococylln	811	7	1.0	674	2	Q9C559	Q9C559	arabidopsis
739	7	1.0	509	2	Q9SEED2	Q9SEED2	pereskia st	812	7	1.0	678	2	Q9A4E2	Q9A4E2	caulobacter
740	7	1.0	509	2	Q9SEED3	Q9SEED3	pereskia gu	813	7	1.0	680	2	Q8GX18	Q8GX18	arabidopsis
741	7	1.0	509	2	Q9SEED4	Q9SEED4	talium pan	814	7	1.0	682	2	Q6DKG5	Q6DKG5	homo saplen
742	7	1.0	510	1	MARK_GABR	Q9SEED5	grahania br	815	7	1.0	682	2	Q8EWR4	Q8EWR4	mycoplasma
743	7	1.0	510	2	Q7SEH0	Q7SEH0	neurospora	816	7	1.0	684	2	Q80709	Q80709	arabidopsis
744	7	1.0	517	2	Q67SM0	Q67SM0	synbiobacte	817	7	1.0	700	2	Q8ECU0	Q8ECU0	shewanella
745	7	1.0	521	1	GM12_METAC	GM12_METAC	mechanosarc	818	7	1.0	703	2	Q8R917	Q8R917	thermoanaer
746	7	1.0	521	1	GPMI_METMA	GPMI_METMA	debaryomyce	819	7	1.0	705	2	Q7RSY9	Q7RSY9	giardia lam
747	7	1.0	524	2	Q7SXH8	Q7SXH8	brachydania	820	7	1.0	707	1	BMP1_XENLA	P98070	xenopus lae
748	7	1.0	525	2	Q6BJI7	Q6BJI7	homo saplen	821	7	1.0	708	2	Q872J9	Q872J9	lactococcus
749	7	1.0	526	2	Q96AV5	Q96AV5	debaromyce	822	7	1.0	713	2	Q62A36	Q62A36	burkholderi
750	7	1.0	527	2	Q8P606	Q8P606	xanthomonas	823	7	1.0	720	2	Q63NR2	Q63NR2	burkholderi
751	7	1.0	529	2	Q17403	Q17403	caenorhabdi	824	7	1.0	732	2	Q65QI8	Q65QI8	mannheimia
752	7	1.0	529	2	Q7ND04	Q7ND04	gloeobacter	825	7	1.0	735	2	Q57381	Q57381	xenopus lae
753	7	1.0	530	2	Q94900	Q94900	homo saplen	826	7	1.0	735	2	Q66K13	Q66K13	xenopus lae
754	7	1.0	532	2	Q9YDB4	Q9YDB4	aeropyrum p	827	7	1.0	746	2	Q6M7J3	Q6M7J3	corynebacte
755	7	1.0	533	2	Q9B147	Q9B147	caenorhabdi	828	7	1.0	746	2	Q97R74	Q97R74	streptococc
756	7	1.0	535	2	Q9JP77	Q9JP77	thermomonas	829	7	1.0	749	2	Q9YGB8	Q9YGB8	oncorhynch
757	7	1.0	535	2	Q6MR14	Q6MR14	bdellovibri	830	7	1.0	754	2	Q49144	Q49144	arabidopsis
758	7	1.0	541	2	Q7P546	Q7P546	fusobacteri	831	7	1.0	754	2	Q7G196	Q7G196	arabidopsis
759	7	1.0	541	2	Q8RFL3	Q8RFL3	fusobacteri	832	7	1.0	765	2	Q8XY74	Q8XY74	ralstonia s
760	7	1.0	541	2	Q7WPA4	Q7WPA4	botryocella	833	7	1.0	778	2	Q6CP63	Q6CP63	kluveromyc
761	7	1.0	542	1	MODU_DROME	PI3469	drosophila	834	7	1.0	783	1	YX11_PSEAE	Q9HYT3	pseudomonas

835	7	1.0	783	2	Q7R5Y0	Q75Y0 giardia lam	908	7	1.0	1450	2	Q6BCK1	Q6bck1 tetrahymena
836	7	1.0	783	2	Q6BLI3	Q6b113 giardia lam	909	7	1.0	1506	2	Q6NS59	Q6ns59 mus musculus
837	7	1.0	783	2	Q6DWL6	Q6dw76 glycine max	910	7	1.0	1522	1	DNA2_YEAST	P38859 saccharomyc
838	7	1.0	783	2	Q9E1Z6	Q9e1z6 cercopithec	911*	7	1.0	1527	2	Q6F1I8	Q6f1i8 candida gla
839	7	1.0	786	2	Q6DMW4	Q6dm74 locus japon	912	7	1.0	1544	2	Q6E2B3	Q6e2b3 botrytis ci
840	7	1.0	787	2	Q9V1E8	Q9vie8 drosophila	913	7	1.0	1569	2	Q9FHD0	Q9fhd0 arabidopsis
841	7	1.0	790	1	CADI_HUMAN	Q1634 homo sapien	914	7	1.0	1608	2	Q9SVAS	Q9svas drosophila
842	7	1.0	790	2	Q8N5Z2	Q8n5z2 homo sapien	915	7	1.0	1631	2	Q8D237	Q8d237 streptococc
843	7	1.0	791	2	Q49137	Q49137 arabidopsis	916	7	1.0	1640	2	Q86291	Q86291 gibberella
844	7	1.0	791	2	Q49139	Q49139 arabidopsis	917	7	1.0	1660	2	Q947Z9	Q947z9 oryza sativ
845	7	1.0	791	2	Q50073	Q50073 arabidopsis	918	7	1.0	1660	2	Q7XFK3	Q7xfk3 oryza sativ
846	7	1.0	793	2	Q7QUH8	Q7qub8 giardia lam	919	7	1.0	1666	2	Q8LPE8	Q8lpe8 chlamydomon
847	7	1.0	799	2	Q7SAU1	Q7sau1 aethya goss	920	7	1.0	1755	2	Q7RVJ1	Q7rvj1 neurospora
848	7	1.0	799	2	Q8NSU9	Q8nsu9 corynebacte	921	7	1.0	1768	2	Q9N8K7	Q9nbk7 trypanosoma
849	7	1.0	803	2	Q6FV15	Q6fv15 candida gla	922	7	1.0	1822	1	SC72_SCHPO	Q9pxw1 schizosacch
850	7	1.0	805	2	Q9SRK7	Q9srk7 drosophila	923	7	1.0	1826	2	Q7RXK8	Q7rxk8 neurospora
851	7	1.0	805	2	Q636U8	Q636u8 bacillus ce	924	7	1.0	1831	2	Q86T77	Q86t77 homo sapien
852	7	1.0	805	2	Q733A2	Q733a2 bacillus ce	925	7	1.0	1863	2	Q81VX2	Q81vx2 homo sapien
853	7	1.0	805	2	Q81WV6	Q81wv6 bacillus an	926	7	1.0	1865	2	Q7Z401	Q7z401 homo sapien
854	7	1.0	805	2	Q6HF81	Q6hf81 bacillus th	927	7	1.0	1877	2	Q9XKW1	Q9xkw1 plasmodium
855	7	1.0	806	2	Q81A60	Q81a60 bacillus ce	928	7	1.0	1879	2	Q7PDP1	Q7pdp1 plasmodium
856	7	1.0	808	2	Q9S7D1	Q9s7d1 arabidopsis	929	7	1.0	1903	2	Q9UON7	Q9uon7 plasmodium
857	7	1.0	826	2	Q8BPUR4	Q8bup4 methanobact	930	7	1.0	1952	2	Q9S5N5	Q9s5n5 drosophila
858	7	1.0	826	2	Q8TQX6	Q8tqx6 methanobact	931	7	1.0	1961	2	Q6WGB9	Q6wgb9 ratius norv
859	7	1.0	826	2	Q9T041	Q9t041 arabidopsis	932	7	1.0	1966	2	Q81QA6	Q81qa6 drosophila
860	7	1.0	841	1	TRK1_SCHPO	P47946 schizosacch	933	7	1.0	1966	2	Q9NHX6	Q9nhx6 neurospora
861	7	1.0	842	2	Q9LSB8	Q9lsb8 arabidopsis	934	7	1.0	1968	2	Q8XOC5	Q8xoc5 drosophila
862	7	1.0	859	1	ALR1_YEAST	Q08269 saccharomyc	935	7	1.0	1985	2	Q8T9N4	Q8t9n4 drosophila
863	7	1.0	864	2	Q6BVK4	Q6bvk4 arabidopsis	936	7	1.0	1985	2	Q7KUN8	Q7kun8 drosophila
864	7	1.0	867	2	Q211B6	Q211b6 caenorhabdi	937	7	1.0	1985	2	Q9VSK5	Q9vsk5 drosophila
865	7	1.0	869	2	Q8IG55	Q8ig55 caenorhabdi	938	7	1.0	1988	2	Q86BH2	Q86bh2 drosophila
866	7	1.0	873	2	Q9S0Z4	Q9s0z4 escherichia	939	7	1.0	2381	2	Q7R4R8	Q7r4r8 giardia lam
867	7	1.0	917	2	Q9V4B8	Q9v4b8 drosophila	940	7	1.0	2393	2	Q81461	Q81461 plasmodium
868	7	1.0	921	2	Q9VJ29	Q9vj29 drosophila	941	7	1.0	2549	2	Q7PPU7	Q7ppu7 anopheles g
869	7	1.0	921	2	Q9BDU0	Q9bdu0 dendrotyrax	942	7	1.0	2605	2	Q50B58	Q50b58 myxococcus
870	7	1.0	922	2	Q6BTU4	Q6btu4 debaryomyce	943	7	1.0	2906	2	Q9WUH9	Q9wuh9 ratius norv
871	7	1.0	950	2	Q8RZX0	Q8rxz0 oryza sativ	944	7	1.0	2907	1	FBN2_MOUSE	Q61555 mus musculu
872	7	1.0	955	2	Q7Z6R1	Q7z6r1 desulfovibr	945	7	1.0	2911	1	FBN2_HUMAN	P35556 homo sapien
873	7	1.0	961	2	Q8SVH3	Q8svh3 encephalito	946	7	1.0	3306	2	Q9FT44	Q9ft44 arabidopsis
874	7	1.0	970	2	Q7XFE2	Q7xf23 oryza sativ	947	7	1.0	3446	2	Q86AC8	Q86ac8 dictyosteli
875	7	1.0	970	2	Q9AYF2	Q9ayf2 oryza sativ	948	7	1.0	3523	2	Q7QCP4	Q7qcp4 anopheles g
876	7	1.0	977	2	Q919Z5	Q919z5 xenopus lae	949	7	1.0	3564	1	CSM1_MOUSE	Q92313 mus musculu
877	7	1.0	980	2	Q22088	Q22088 caenorhabdi	950	7	1.0	3666	2	Q6UDX0	Q6udx0 plasmodium
878	7	1.0	982	2	Q6CWM6	Q6cwm6 kluyveromyc	951	7	1.0	3972	2	Q9S0R8	Q9s0r8 streptomyc
879	7	1.0	991	2	Q8TDM1	Q8tdh1 homo sapien	952	7	1.0	3996	2	Q7KTP2	Q7ktp2 drosophila
880	7	1.0	995	1	YPD1_CAEEL	P49053 caenorhabdi	953	7	1.0	4547	2	Q9W3J3	Q9w3j3 drosophila
881	7	1.0	1007	2	Q6CJZ8	Q6cjz8 xenopus lae	954	7	1.0	4569	2	Q7FS35	Q7f353 anopheles g
882	7	1.0	1013	2	Q6MFE7	Q6mf67 parachlamyd	955	7	1.0	4899	2	Q9V8J1	Q9v8j1 drosophila
883	7	1.0	1022	1	TLD_BRARE	Q57460 brachydantio	956	7	1.0	23015	2	Q81QI8	Q81qi8 drosophila
884	7	1.0	1031	2	Q8GSK2	Q8gsk2 bifidobacte	957	7	0.8	27	1	ANF_ANGJA	P18144 anguilla ja
885	7	1.0	1046	2	Q6C1R8	Q6c1r8 yarrowia li	958	7	0.8	27	1	Q8FZ50	Q8fz50 bruceella su
886	7	1.0	1047	2	Q9FKM9	Q9fkw9 arabidopsis	959	7	0.8	33	2	Q8B9R2	Q8b9r2 emilliantia h
887	7	1.0	1048	2	Q9NA71	Q9na71 caenorhabdi	960	7	0.8	33	2	Q8B9R3	Q8b9r3 emilliantia h
888	7	1.0	1074	2	Q831Z5	Q831z5 enterococcu	961	7	0.8	33	2	Q8B9R4	Q8b9r4 emilliantia h
889	7	1.0	1079	2	Q6MLZ8	Q6mlz8 bdellovibri	962	7	0.8	33	2	Q8B9R5	Q8b9r5 emilliantia h
890	7	1.0	1081	2	Q8BZL9	Q8bz19 mus musculu	963	7	0.8	33	2	Q8B9R6	Q8b9r6 emilliantia h
891	7	1.0	1100	2	Q86UD1	Q86uh1 homo sapien	964	7	0.8	33	2	Q8B9R7	Q8b9r7 emilliantia h
892	7	1.0	1111	2	Q8S5Z2	Q8s5z2 mycobacteri	965	7	0.8	33	2	Q8B9R8	Q8b9r8 emilliantia h
893	7	1.0	1120	2	Q8FP57	Q8fp57 corynebacte	966	7	0.8	33	2	Q8B9R9	Q8b9r9 emilliantia h
894	7	1.0	1135	2	Q7Q1J7	Q7q1j7 anopheles g	967	7	0.8	35	2	Q9KSL5	Q9ksl5 vibrio chol
895	7	1.0	1136	2	Q81JDB	Q81jdb plasmodium	968	7	0.8	36	2	Q96WJ6	Q96wv6 ophiostoma
896	7	1.0	1158	2	Q7Q2S3	Q7q2s3 anopheles g	969	7	0.8	36	2	Q72CQ3	Q72cq3 desulfovibr
897	7	1.0	1201	2	Q71RU0	Q71ru0 nitrobacter	970	7	0.8	37	2	Q9DPR2	Q9dpr2 human immun
898	7	1.0	1233	2	Q6CAC2	Q6cac2 yarrowia li	971	7	0.8	38	2	Q7VM96	Q7vm96 haemophilus
899	7	1.0	1240	2	Q7SF30	Q7sf30 neurospora	972	7	0.8	39	2	Q29360	Q29360 sus scrofa
900	7	1.0	1243	1	DLT_DROME	Q8f626 drosophila	973	7	0.8	39	2	Q6IEB9	Q6ieb9 macaca mula
901	7	1.0	1240	2	Q55468	Q55468 arabidopsis	974	7	0.8	40	2	Q9RAD0	Q9rad0 thermus aqu
902	7	1.0	1243	2	Q35954	Q35954 mus musculu	975	7	0.8	40	2	Q735I0	Q735i0 bacillus ce
903	7	1.0	1300	2	Q8XOV5	Q8xov5 neurospora	976	7	0.8	40	2	Q9KLT1	Q9klt1 vibrio chol
904	7	1.0	1327	2	Q6C4U5	Q6c4j5 yarrowia li	977	7	0.8	40	2	Q8UM87	Q8um87 human immun
905	7	1.0	1340	2	Q9GYW4	Q9gyw4 anopheles g	978	7	0.8	40	2	Q8USM4	Q8usm4 human immun
906	7	1.0	1346	2	Q9ZG12	Q9zgl2 streptomyc	979	7	0.8	41	2	Q9OSM4	Q9osm4 human immun
907	7	1.0	1355	2	Q7Q7S9	Q7q7s9 anopheles g	980	7	0.8	41	2	Q9OSM5	Q9osm5 human immun

981	6	0.8	41	2	Q90SM6	Q96n6 human immun	1054	6	0.8	56	2	Q97A0	Q97a0 thermoplasm
982	6	0.8	41	2	Q78226	Q78226 human immun	1055	6	0.8	56	2	Q81P7	Q81p7 bacillus an
983	6	0.8	41	2	Q9G37	Q9G37 human immun	1056	6	0.8	56	2	Q9CB3	Q9cb3 mycobacteri
984	6	0.8	42	2	Q85WV3	Q85WV3 pinus korae	1057	6	0.8	57	2	Q38990	Q38990 arabidopsis
985	6	0.8	42	2	Q67PK6	Q67PK6 symbiodace	1058	6	0.8	57	2	Q38991	Q38991 arabidopsis
986	6	0.8	43	2	Q704X0	Q704X0 bos taurus	1059	6	0.8	57	2	Q38992	Q38992 arabidopsis
987	6	0.8	44	2	Q8F2Y9	Q8F2Y9 leptospira	1060	6	0.8	57	2	Q8D59	Q8d59 vibrio vuln
988	6	0.8	44	2	Q8F9N3	Q8F9N3 leptospira	1061	6	0.8	59	2	Q81Z30	Q81z30 bacillus an
989	6	0.8	45	2	Q80HK8	Q80HK8 hepatitis c	1062	6	0.8	59	2	Q9HYB3	Q9hyb3 pseudomonas
990	6	0.8	45	2	Q80I53	Q80I53 hepatitis c	1063	6	0.8	60	2	Q6ZGX7	Q6zgx7 oryza sativ
991	6	0.8	45	2	Q80I54	Q80I54 hepatitis c	1064	6	0.8	60	2	Q62963	Q62963 rattus norv
992	6	0.8	45	2	Q80I55	Q80I55 hepatitis c	1065	6	0.8	60	2	Q6SPV9	Q6spv9 human immun
993	6	0.8	45	2	Q80I56	Q80I56 hepatitis c	1066	6	0.8	61	2	Q6Z4I9	Q6z4i9 oryza sativ
994	6	0.8	45	2	Q80I57	Q80I57 hepatitis c	1067	6	0.8	61	2	Q45045	Q45045 borellia bu
995	6	0.8	45	2	Q80I58	Q80I58 hepatitis c	1068	6	0.8	61	2	Q75577	Q75577 human immun
996	6	0.8	45	2	Q80I59	Q80I59 hepatitis c	1069	6	0.8	62	1	CX51_CONIM	Q96z5 conus imper
997	6	0.8	45	2	Q80I60	Q80I60 hepatitis c	1070	6	0.8	63	2	Q6BK44	Q6bk44 debaryomyce
998	6	0.8	45	2	Q80I61	Q80I61 hepatitis c	1071	6	0.8	63	2	Q19260	Q19260 pongo pygma
999	6	0.8	45	2	Q80I62	Q80I62 hepatitis c	1072	6	0.8	63	2	Q841B5	Q841b5 metohermus
1000	6	0.8	45	2	Q9G3F1	Q9G3F1 human immun	1073	6	0.8	63	2	Q8K6X6	Q8k6x6 streptococ
1001	6	0.8	47	2	Q71IY3	Q71IY3 lactobacill	1074	6	0.8	63	2	Q6OK44	Q6ok44 classisal s
1002	6	0.8	48	2	Q9P1I5	Q9P1I5 homo sapien	1075	6	0.8	63	2	Q6OK45	Q6ok45 classisal s
1003	6	0.8	48	2	Q9B8D3	Q9B8D3 candida alb	1076	6	0.8	63	2	Q6OK46	Q6ok46 classisal s
1004	6	0.8	48	2	Q9K201	Q9K201 chlamydia p	1077	6	0.8	63	2	Q6OK47	Q6ok47 classisal s
1005	6	0.8	49	2	P74885	P74885 salmonella	1078	6	0.8	63	2	Q6OLN6	Q6oln6 classisal s
1006	6	0.8	49	2	Q9F800	Q9F800 erwina amy	1079	6	0.8	63	2	Q6OK44	Q6ok44 classisal s
1007	6	0.8	50	2	Q18986	Q18986 canis fami	1080	6	0.8	63	2	Q7BE63	Q7be63 classisal s
1008	6	0.8	50	2	Q72YX1	Q72YX1 bacillus ce	1081	6	0.8	63	2	Q7BE64	Q7be64 classisal s
1009	6	0.8	51	2	Q9G3E5	Q9G3E5 human immun	1082	6	0.8	63	2	Q7BE65	Q7be65 classisal s
1010	6	0.8	51	2	Q9G3E7	Q9G3E7 human immun	1083	6	0.8	63	2	Q7BE66	Q7be66 classisal s
1011	6	0.8	51	2	Q9G3E9	Q9G3E9 human immun	1084	6	0.8	63	2	Q7BE67	Q7be67 classisal s
1012	6	0.8	51	2	Q9G3F3	Q9G3F3 human immun	1085	6	0.8	63	2	Q7BE68	Q7be68 classisal s
1013	6	0.8	51	2	Q9G3F5	Q9G3F5 human immun	1086	6	0.8	63	2	Q7BE69	Q7be69 classisal s
1014	6	0.8	51	2	Q9G3F7	Q9G3F7 human immun	1087	6	0.8	63	2	Q7BE73	Q7be73 classisal s
1015	6	0.8	51	2	Q9G3G1	Q9G3G1 human immun	1088	6	0.8	63	2	Q7BE74	Q7be74 classisal s
1016	6	0.8	51	2	Q9G3G3	Q9G3G3 human immun	1089	6	0.8	63	2	Q7BE75	Q7be75 classisal s
1017	6	0.8	51	2	Q9G3G5	Q9G3G5 human immun	1090	6	0.8	63	2	Q7BE76	Q7be76 classisal s
1018	6	0.8	52	2	Q76YQ6	Q76YQ6 bacterioph	1091	6	0.8	63	2	Q7BE77	Q7be77 classisal s
1019	6	0.8	52	2	Q77369	Q77369 human immun	1092	6	0.8	63	2	Q7BE78	Q7be78 classisal s
1020	6	0.8	53	2	Q9PGC6	Q9PGC6 xyella fas	1093	6	0.8	63	2	Q7BE79	Q7be79 classisal s
1021	6	0.8	54	2	Q6JLK6	Q6JLK6 penicillium	1094	6	0.8	64	2	Q7TE80	Q7te80 classisal s
1022	6	0.8	54	2	Q6JLK9	Q6JLK9 penicillium	1095	6	0.8	64	2	Q9V2B1	Q9v2b1 pyrococcus
1023	6	0.8	54	2	Q6JLL1	Q6JLL1 penicillium	1096	6	0.8	64	2	Q7S0P1	Q7sup1 patinopete
1024	6	0.8	54	2	Q6JLL2	Q6JLL2 penicillium	1097	6	0.8	64	2	Q9SV44	Q9sv44 arabidopsis
1025	6	0.8	54	2	Q6JLL3	Q6JLL3 penicillium	1098	6	0.8	64	2	Q09527	Q09527 human immun
1026	6	0.8	54	2	Q6JLL5	Q6JLL5 penicillium	1099	6	0.8	64	2	P88426	P88426 human immun
1027	6	0.8	54	2	Q6JLL6	Q6JLL6 penicillium	1100	6	0.8	65	2	Q7PCU9	Q7pcu9 plasmodium
1028	6	0.8	54	2	Q6JLL7	Q6JLL7 penicillium	1101	6	0.8	65	2	Q8NW16	Q8nw16 straphylococ
1029	6	0.8	54	2	Q6JLL9	Q6JLL9 penicillium	1102	6	0.8	66	2	Q98GK0	Q98gk0 rhizobium l
1030	6	0.8	54	2	Q6JLM1	Q6JLM1 penicillium	1103	6	0.8	66	2	Q87Q04	Q87q04 vibrio para
1031	6	0.8	54	2	Q6JLM2	Q6JLM2 penicillium	1104	6	0.8	66	2	Q8DNS2	Q8dns2 streptococ
1032	6	0.8	54	2	Q6JLM3	Q6JLM3 penicillium	1105	6	0.8	66	2	Q91Q04	Q91q04 human herpe
1033	6	0.8	54	2	Q6JLM4	Q6JLM4 penicillium	1106	6	0.8	66	2	Q91Q06	Q91q06 human herpe
1034	6	0.8	54	2	Q6JLM5	Q6JLM5 penicillium	1107	6	0.8	66	2	Q91Q24	Q91q24 carcopithec
1035	6	0.8	54	2	Q6JLM6	Q6JLM6 penicillium	1108	6	0.8	67	2	Q01676	Q01676 pneumocyti
1036	6	0.8	54	2	Q6JLM7	Q6JLM7 penicillium	1109	6	0.8	67	2	Q9U8X3	Q9u8x3 tachypleus
1037	6	0.8	54	2	Q6JLM8	Q6JLM8 penicillium	1110	6	0.8	67	2	Q63N90	Q63n90 burkholderi
1038	6	0.8	54	2	Q6JLM9	Q6JLM9 penicillium	1111	6	0.8	67	2	Q8YXN0	Q8yxno anabaena sp
1039	6	0.8	54	2	Q6JLN1	Q6JLN1 penicillium	1112	6	0.8	68	2	Q80094	Q80094 straphylococ
1040	6	0.8	54	2	Q6JLN2	Q6JLN2 penicillium	1113	6	0.8	68	2	Q92UC5	Q92uc5 rhizobium m
1041	6	0.8	54	2	Q6JLN3	Q6JLN3 penicillium	1114	6	0.8	68	2	Q7MTX3	Q7mtx3 vibrio vuln
1042	6	0.8	54	2	Q9XCE2	Q9xce2 micromonosp	1115	6	0.8	68	2	Q91Q51	Q91q51 pongine her
1043	6	0.8	54	2	Q8NUN5	Q8nun5 staphylococ	1116	6	0.8	68	2	Q38492	Q38492 human immun
1044	6	0.8	54	2	Q97P43	Q97P43 streptococ	1117	6	0.8	69	2	Q8UBZ2	Q8ubz2 agrobacteri
1045	6	0.8	54	2	Q7UTY8	Q7uty8 rhodopirell	1118	6	0.8	70	1	RL31_ECOLI	RL31 ecoceria
1046	6	0.8	54	2	Q8PYT6	Q8pyt6 brucella su	1119	6	0.8	70	2	Q7MTV4	Q7mtv4 porphyromon
1047	6	0.8	54	2	Q9JLC3	Q9jlc3 neisseria m	1120	6	0.8	70	2	Q7VAV4	Q7vav4 prochloromon
1048	6	0.8	54	2	Q6G5Y7	Q6g5y7 staphylococ	1121	6	0.8	70	2	Q813J7	Q813j7 bacillus ce
1049	6	0.8	55	1	FER_CLOAC	P00198 clostridium	1122	6	0.8	70	2	Q9PBR4	Q9pb4 xyella fas
1050	6	0.8	55	2	P76555	P76555 escherichia	1123	6	0.8	70	2	Q83PD4	Q83pd4 shigella fl
1051	6	0.8	55	2	Q6TPA6	Q6tpa6 aeromonas h	1124	6	0.8	71	2	Q91Q53	Q91q53 pongine her
1052	6	0.8	55	2	Q8V9P1	Q8v9p1 sulfolobus	1125	6	0.8	71	2	Q13969	Q13969 homo sapien
1053	6	0.8	55	2	Q6EPW5	Q6epw5 human immun	1126	6	0.8	71	2	Q38272	Q38272 lactococcus

1127	6	0.8	71	2	Q77JLS	Q77JLS bacterioph	1200	6	0.8	81	2	Q10811	Q10811 human immu
1128	6	0.8	71	2	Q77JMS	Q77JMS bacterioph	1201	6	0.8	81	2	Q10893	Q10893 human immu
1129	6	0.8	71	2	Q9XJEB	Q9XJEB lactococcus	1202	6	0.8	81	2	Q04271	Q04271 human immu
1130	6	0.8	71	2	Q75161	Q75161 oryza sativ	1203	6	0.8	81	2	Q90MJ9	Q90MJ9 human immu
1131	6	0.8	71	2	Q6FCLO	Q6FCLO acinetobact	1204	6	0.8	81	2	Q90VH8	Q90VH8 human immu
1132	6	0.8	71	2	Q6ZEJ3	Q6ZEJ3 synechocyst	1205	6	0.8	81	2	Q6JN14	Q6JN14 human immu
1133	6	0.8	71	2	Q7MYC6	Q7MYC6 photorhabdu	1206	6	0.8	81	2	Q6JN11	Q6JN11 human immu
1134	6	0.8	71	2	Q83NLS	Q83NLS tropheryma	1207	6	0.8	81	2	Q6JN14	Q6JN14 human immu
1135	6	0.8	71	2	Q9CB16	Q9CB16 lactococcus	1208	6	0.8	81	2	Q6JN11	Q6JN11 human immu
1136	6	0.8	71	2	Q79955	Q79955 human immu	1209	6	0.8	81	2	Q6Q461	Q6Q461 human immu
1137	6	0.8	71	2	Q79957	Q79957 human immu	1210	6	0.8	81	2	Q78324	Q78324 human immu
1138	6	0.8	71	2	Q79959	Q79959 human immu	1211	6	0.8	81	2	Q79289	Q79289 human immu
1139	6	0.8	71	2	Q79965	Q79965 human immu	1212	6	0.8	81	2	Q7SKG5	Q7SKG5 human immu
1140	6	0.8	71	2	Q79967	Q79967 human immu	1213	6	0.8	81	2	Q91G74	Q91G74 human immu
1141	6	0.8	71	2	Q79969	Q79969 human immu	1214	6	0.8	82	1	VPU HV1BN	
1142	6	0.8	71	2	Q79970	Q79970 human immu	1215	6	0.8	82	2	Q8SC64	Q8SC64 stx2 conver
1143	6	0.8	71	2	Q79971	Q79971 human immu	1216	6	0.8	82	2	Q7Y202	Q7Y202 stx2 conver
1144	6	0.8	71	2	Q79974	Q79974 human immu	1217	6	0.8	82	2	Q7Y363	Q7Y363 stx1 conver
1145	6	0.8	71	2	Q79976	Q79976 human immu	1218	6	0.8	82	2	Q8F7V5	Q8F7V5 leptospira
1146	6	0.8	71	2	Q79979	Q79979 human immu	1219	6	0.8	82	2	Q6M9U3	Q6M9U3 parachlamyd
1147	6	0.8	71	2	Q79982	Q79982 human immu	1220	6	0.8	82	2	Q9D2H1	Q9D2H1 m musc musc
1148	6	0.8	72	2	Q9PIH3	Q9PIH3 homo sapien	1221	6	0.8	82	2	Q9Q313	Q9Q313 hepatitis c
1149	6	0.8	72	2	Q26687	Q26687 trypanosoma	1222	6	0.8	82	2	Q90M11	Q90M11 human immu
1150	6	0.8	72	2	Q49229	Q49229 mycoplasma	1223	6	0.8	83	2	Q8NW72	Q8NW72 corynebacte
1151	6	0.8	72	2	Q64PI1	Q64PI1 bacteroides	1224	6	0.8	83	2	Q90VF3	Q90VF3 human immu
1152	6	0.8	72	2	Q8K7S9	Q8K7S9 streptococc	1225	6	0.8	84	2	Q8R7W3	Q8R7W3 thermoanaer
1153	6	0.8	72	2	Q7NLJ8	Q7NLJ8 glieobacter	1226	6	0.8	85	1	RS17 MYCGE	
1154	6	0.8	72	2	Q83214	Q83214 enterococcu	1227	6	0.8	85	2	Q9G1P8	Q9G1P8 mesembryant
1155	6	0.8	72	2	Q87XL9	Q87XL9 pseudomonas	1228	6	0.8	85	2	Q6S168	Q6S168 mesembryant
1156	6	0.8	72	2	P90297	P90297 human immu	1229	6	0.8	85	2	Q8RU69	Q8RU69 chlamydia p
1157	6	0.8	72	2	Q78261	Q78261 human immu	1230	6	0.8	85	2	Q6SKS6	Q6SKS6 arthrobacte
1158	6	0.8	72	2	Q79534	Q79534 human immu	1231	6	0.8	85	2	Q8E9J9	Q8E9J9 shewanella
1159	6	0.8	72	2	Q79551	Q79551 human immu	1232	6	0.8	86	1	DIN1 ECOLI	Q47150 escherichia
1160	6	0.8	72	2	Q79551	Q79551 human immu	1233	6	0.8	86	2	Q8TT30	Q8TT30 methanobact
1161	6	0.8	73	2	Q8RXW8	Q8RXW8 arabidopsis	1234	6	0.8	86	2	Q89S30	Q89S30 bradyrhizob
1162	6	0.8	73	2	Q69U82	Q69U82 oryza sativ	1235	6	0.8	86	2	Q8X7Q6	Q8X7Q6 escherichia
1163	6	0.8	73	2	Q97HT9	Q97HT9 clostridium	1236	6	0.8	86	2	Q9W166	Q9W166 hepatitis c
1164	6	0.8	73	2	Q8F557	Q8F557 leptospira	1237	6	0.8	87	2	Q8W1B7	Q8W1B7 oryza sativ
1165	6	0.8	73	2	Q9HY80	Q9HY80 pseudomonas	1238	6	0.8	87	2	Q9LX24	Q9LX24 arabidopsis
1166	6	0.8	74	2	Q8TKU9	Q8TKU9 methanobact	1239	6	0.8	87	2	Q69W08	Q69W08 oryza sativ
1167	6	0.8	74	2	Q8FWB5	Q8FWB5 brucella su	1240	6	0.8	87	2	Q05325	Q05325 pseudomonas
1168	6	0.8	74	2	P88432	P88432 human immu	1241	6	0.8	87	2	Q63R25	Q63R25 burkholderi
1169	6	0.8	75	1	YOR4 SMYEA	Q00848 strawberry	1242	6	0.8	88	2	Q9H316	Q9H316 homo sapien
1170	6	0.8	75	2	Q8PYR9	Q8PYR9 methanobact	1243	6	0.8	88	2	Q49249	Q49249 astroemer
1171	6	0.8	75	2	Q9P169	Q9P169 homo sapien	1244	6	0.8	88	2	Q93444	Q93444 chlamydia p
1172	6	0.8	75	2	Q7PGQ2	Q7PGQ2 anopheles g	1245	6	0.8	88	2	Q8Y1U0	Q8Y1U0 anabaena sp
1173	6	0.8	75	2	Q691W9	Q691W9 oryza sativ	1246	6	0.8	88	2	Q97F86	Q97F86 clostridium
1174	6	0.8	75	2	Q8U5R3	Q8U5R3 agrobacteri	1247	6	0.8	88	2	Q7TU28	Q7TU28 prochloroco
1175	6	0.8	75	2	Q835D8	Q835D8 enterococcu	1248	6	0.8	88	2	Q9PH80	Q9PH80 xylella fas
1176	6	0.8	75	2	Q87C72	Q87C72 xylella fas	1249	6	0.8	88	2	Q70007	Q70007 human immu
1177	6	0.8	75	2	Q9PB10	Q9PB10 xylella fas	1250	6	0.8	88	2	Q8PW30	Q8PW30 methanobact
1178	6	0.8	75	2	Q41279	Q41279 strawberry	1251	6	0.8	89	2	Q9URB8	Q9URB8 homo sapien
1179	6	0.8	76	2	Q84XF0	Q84XF0 oryza sativ	1252	6	0.8	89	2	Q9ZAF0	Q9ZAF0 thermus the
1180	6	0.8	76	2	Q09529	Q09529 human immu	1253	6	0.8	89	2	Q73824	Q73824 mycobacteri
1181	6	0.8	77	1	YCXB CYAPA	P48332 cyanophora	1254	6	0.8	89	2	Q41547	Q41547 human immu
1182	6	0.8	77	2	Q6ZD12	Q6ZD12 oryza sativ	1255	6	0.8	89	2	Q90VH2	Q90VH2 human immu
1183	6	0.8	77	2	Q9LDK3	Q9LDK3 oryza sativ	1256	6	0.8	90	2	Q8WYX0	Q8WYX0 pelliculum nu
1184	6	0.8	77	2	Q8YU14	Q8YU14 anabaena sp	1257	6	0.8	90	2	Q42020	Q42020 arabidopsis
1185	6	0.8	78	1	YVFB VACCC	P20560 vaccinia vi	1258	6	0.8	90	2	Q6M010	Q6M010 mycoplasma
1186	6	0.8	78	2	Q96HMO	Q96HMO homo sapien	1259	6	0.8	90	2	Q89ZD8	Q89ZD8 bacteroides
1187	6	0.8	78	2	Q6YL42	Q6YL42 homo sapien	1260	6	0.8	90	2	Q8V200	Q8V200 milliania h
1188	6	0.8	78	2	Q7THW1	Q7THW1 compox viru	1261	6	0.8	90	2	Q41533	Q41533 human immu
1189	6	0.8	79	1	Y476 ARCTU	Q28774 archaeoglob	1262	6	0.8	90	2	Q41538	Q41538 human immu
1190	6	0.8	79	2	Q8C3F5	Q8C3F5 mus musculu	1263	6	0.8	90	2	Q41557	Q41557 human immu
1191	6	0.8	80	1	NUSM CERCA	Q34052 ceratilis c	1264	6	0.8	90	2	Q41561	Q41561 human immu
1192	6	0.8	80	2	Q8U4J1	Q8U4J1 pyrococcus	1265	6	0.8	90	2	Q41594	Q41594 human immu
1193	6	0.8	80	2	Q8K1W5	Q8K1W5 proteus vul	1266	6	0.8	90	2	Q41645	Q41645 human immu
1194	6	0.8	80	2	Q7U3T4	Q7U3T4 synechococc	1267	6	0.8	90	2	P88528	P88528 human immu
1195	6	0.8	80	2	Q7UVG1	Q7UVG1 rhodospirill	1268	6	0.8	90	2	Q69993	Q69993 human immu
1196	6	0.8	80	2	Q8DQ12	Q8DQ12 streptococc	1269	6	0.8	90	2	Q74750	Q74750 human immu
1197	6	0.8	80	2	Q991V0	Q991V0 uncultured	1270	6	0.8	90	2	Q91QN4	Q91QN4 human immu
1198	6	0.8	80	2	Q7ZP14	Q7ZP14 human immu	1271	6	0.8	90	2	Q91QN6	Q91QN6 human immu
1199	6	0.8	81	2	Q7ULV1	Q7ULV1 rhodospirill	1272	6	0.8	90	2	Q91QN7	Q91QN7 human immu

1273	6	0.8	90	2	Q91QN8	Q91gn8 human immun	1346	6	0.8	102	2	Q87GJ3	Q87gJ3 vibrio para
1274	6	0.8	91	2	Q826F7	Q826f7 salmonella	1347	6	0.8	102	2	Q89H29	Q89h29 bradyrhizob
1275	6	0.8	91	2	Q82Pv4	Q82pv4 salmonella	1348	6	0.8	102	2	Q9K8L0	Q9K8L0 bacillus ha
1276	6	0.8	91	2	Q9JVM4	Q9Jvm4 neisseria m	1349	6	0.8	103	2	Q972J7	Q972J7 sulfolobus
1277	6	0.8	91	2	Q70004	Q70004 human immun	1350	6	0.8	103	2	Q95M89	Q95m89 equus caball
1278	6	0.8	91	2	Q70009	Q70009 human immun	1351	6	0.8	103	2	Q74G06	Q74g06 geobacter s
1279	6	0.8	91	2	Q72787	Q72787 human immun	1352	6	0.8	103	2	Q7UCU8	Q7ucU8 rhodopirell
1280	6	0.8	92	1	YLKP_BACSU	YLKP_BACSU	1353	6	0.8	103	2	Q87706	Q87706 vibrio para
1281	6	0.8	92	2	Q8HQJ5	Q8hqj5 ornithodora	1354	6	0.8	103	2	Q6D9M5	Q6d9m5 erwinia car
1282	6	0.8	92	2	Q93KE9	Q93ke9 chlamydia p	1355	6	0.8	104	2	Q9D5D6	Q9d5d6 mus musculu
1283	6	0.8	92	2	Q65J10	Q65j10 bacillus li	1356	6	0.8	104	2	Q8SQY2	Q8sqY2 enccephalito
1284	6	0.8	92	2	Q65U129	Q65u129 emilliania h	1357	6	0.8	104	2	Q8SX12	Q8sx12 drosophila
1285	6	0.8	93	2	Q85F10	Q85f10 adiantum ca	1358	6	0.8	104	2	Q61K98	Q61k98 drosophila
1286	6	0.8	93	2	Q8LML6	Q8lml6 oryza sativ	1359	6	0.8	104	2	Q7R8C5	Q7r8c5 plasmodium
1287	6	0.8	93	2	Q42278	Q42278 arabidopsis	1360	6	0.8	104	2	Q38556	Q38556 bacteriopho
1288	6	0.8	93	2	Q629K2	Q629K2 haemophilus	1361	6	0.8	104	2	Q6V8N3	Q6v8n3 malus domes
1289	6	0.8	93	2	Q41565	Q41565 human immun	1362	6	0.8	104	2	Q65117	Q65117 bacteroides
1290	6	0.8	94	2	Q61L90	Q61l90 drosophila	1363	6	0.8	104	2	Q73139	Q73139 wolbachia p
1291	6	0.8	94	2	Q7QWNL	Q7qwnl giardia lam	1364	6	0.8	104	2	Q7POH7	Q7poh7 chromobacte
1292	6	0.8	94	2	Q9BDR2	Q9bdr2 bos taurus	1365	6	0.8	104	2	Q88594	Q88594 mus musculu
1293	6	0.8	94	2	Q94MT3	Q94mt3 bacteriopho	1366	6	0.8	105	2	Q27553	Q27553 methanobact
1294	6	0.8	94	2	Q49475	Q49475 mycoplasma	1367	6	0.8	105	2	Q97C63	Q97c63 thermoplas
1295	6	0.8	94	2	Q9ZBM8	Q9zbm8 mycobacteri	1368	6	0.8	105	2	Q23899	Q23899 dictyosteli
1296	6	0.8	94	2	Q8V1Z6	Q8v1z6 emilliania h	1369	6	0.8	105	2	Q8S005	Q8s005 oryza sativ
1297	6	0.8	94	2	Q8V1Z8	Q8v1z8 emilliania h	1370	6	0.8	105	2	Q6ZLD9	Q6zld9 oryza sativ
1298	6	0.8	94	2	Q8V202	Q8v202 emilliania h	1371	6	0.8	105	2	Q91HNL	Q91hnl arabidopsis
1299	6	0.8	94	2	Q8V203	Q8v203 emilliania h	1372	6	0.8	105	2	Q7N4V8	Q7n4v8 photorhabd
1300	6	0.8	94	2	Q8V204	Q8v204 emilliania h	1373	6	0.8	105	2	Q7NTJ2	Q7ntj2 chromobacte
1301	6	0.8	94	2	Q41599	Q41599 human immun	1374	6	0.8	105	2	Q8BP51	Q8bp51 mus musculu
1302	6	0.8	94	2	Q70001	Q70001 human immun	1375	6	0.8	106	1	RNP4_SUSO	RNP4_sulfolobus
1303	6	0.8	95	2	Q914U5	Q914u5 pseudomonas	1376	6	0.8	106	2	Q74K55	Q74k55 lactobacill
1304	6	0.8	95	2	Q80XZ8	Q80xz8 mus musculu	1377	6	0.8	107	1	RL21_CHLTR	RL21_chlamydia t
1305	6	0.8	95	2	Q61EC0	Q61ec0 ictalurus p	1378	6	0.8	107	2	Q61GL6	Q61gl6 drosophila
1306	6	0.8	96	2	Q7PEFK0	Q7pEfk0 anopheles g	1379	6	0.8	107	2	Q8E7H9	Q8e7h9 streptococc
1307	6	0.8	96	2	Q7QSG2	Q7qsg2 giardia lam	1380	6	0.8	107	2	Q9C8P1	Q9c8p1 mycobacteri
1308	6	0.8	96	2	Q9MPY9	Q9mpy9 anopheles c	1381	6	0.8	107	2	Q6AKO7	Q6akO7 desulfotale
1309	6	0.8	96	2	Q9C7L8	Q9c7l8 arabidopsis	1382	6	0.8	108	1	Q8BM14	Q8bm14 mus musculu
1310	6	0.8	96	2	Q7NWN1	Q7wnj1 chromobacte	1383	6	0.8	108	1	PT05_STYPL	PT05_styela plic
1311	6	0.8	96	2	Q7UGN6	Q7ugn6 rhodopirell	1384	6	0.8	108	2	Q6UAT7	Q6uat7 bacteriopho
1312	6	0.8	97	2	Q7RLM5	Q7rlm5 giardia lam	1385	6	0.8	108	2	Q8K3Z8	Q8k3z8 arabidopsis
1313	6	0.8	97	2	Q7YVGA	Q7yvga trypanosoma	1386	6	0.8	108	2	Q6K4F7	Q6k4f7 oryza sativ
1314	6	0.8	98	2	Q884H1	Q884h1 pseudomona	1387	6	0.8	108	2	Q7NMK6	Q7nmk6 gloeobacter
1315	6	0.8	98	2	Q8R0E3	Q8r0e3 methanosarc	1388	6	0.8	108	2	Q10826	Q10826 human immun
1316	6	0.8	98	2	Q6R2Z3	Q6r2z3 endoxyla sp	1389	6	0.8	108	2	Q9QN58	Q9qn58 human immun
1317	6	0.8	98	2	Q25731	Q25731 plasmodium	1390	6	0.8	108	2	Q9QN68	Q9qn68 human immun
1318	6	0.8	98	2	Q9NFM0	Q9nfh0 plasmodium	1391	6	0.8	109	1	TCMI_STRGA	TCMI_streptomyce
1319	6	0.8	98	2	Q6SEGO	Q6sego lactobacill	1392	6	0.8	109	2	Q9M272	Q9m272 arabidopsis
1320	6	0.8	98	2	Q52096	Q52096 pseudomonas	1393	6	0.8	109	2	Q9ZLFS	Q9zlf5 rhizobium m
1321	6	0.8	98	2	Q69509	Q69509 mycobacteri	1394	6	0.8	110	1	M280_ARATH	M280_arabidopsis
1322	6	0.8	98	2	Q7TUT9	Q7tut9 prochloroco	1395	6	0.8	110	2	Q462D7	Q462d7 clostridium
1323	6	0.8	98	2	Q9KMT4	Q9kmt4 vibrio chol	1396	6	0.8	110	2	Q925A8	Q925a8 rhizobium m
1324	6	0.8	98	2	Q65PM7	Q65pm7 lactobacill	1397	6	0.8	110	2	Q9F5I4	Q9f5i4 bradyrhizob
1325	6	0.8	98	2	Q6D5N1	Q6d5n1 erwinia car	1398	6	0.8	110	2	Q8CDY6	Q8cdy6 mus musculu
1326	6	0.8	99	1	YQJ2_CAEEL	YQJ2_CAEEL	1399	6	0.8	110	2	Q69141	Q69141 human herpe
1327	6	0.8	99	2	Q91S64	Q91s64 arabidopsis	1400	6	0.8	111	2	Q8TOS6	Q8tos6 methanosarc
1328	6	0.8	99	2	Q82VDS	Q82vds nitrosomona	1401	6	0.8	111	2	Q6IH26	Q6ih26 drosophila
1329	6	0.8	99	2	Q89H95	Q89h95 bradyrhizob	1402	6	0.8	111	2	Q6DND4	Q6dnd4 streptomyce
1330	6	0.8	99	2	Q924W3	Q924w3 ractus norv	1403	6	0.8	111	2	Q725M5	Q725m5 deulfovibr
1331	6	0.8	99	2	P88433	P88433 human immun	1404	6	0.8	111	2	Q8FLI7	Q8fli7 corynebacte
1332	6	0.8	99	2	P84DE3	P84de3 uncultured	1405	6	0.8	111	2	Q9JHB8	Q9jhb8 spodoptera
1333	6	0.8	100	2	Q50101	Q50101 pyrococcus	1406	6	0.8	112	1	PT17_STYPL	PT17_styela plic
1334	6	0.8	100	2	Q6VYV4	Q6vyv4 oryza sativ	1407	6	0.8	112	2	Q9GLK5	Q9glk5 felis silve
1335	6	0.8	100	2	Q7MS23	Q7me23 wolfinella s	1408	6	0.8	112	2	PT2474	PT2474 streptococc
1336	6	0.8	101	2	Q979B6	Q979b6 thermoplas	1409	6	0.8	112	2	Q62J69	Q62j69 burkholderi
1337	6	0.8	101	2	Q94JPF2	Q94jpf2 neisseria m	1410	6	0.8	112	2	Q63SW1	Q63sw1 burkholderi
1338	6	0.8	101	2	Q91Z64	Q91z64 sigmodon hi	1411	6	0.8	112	2	Q684B5	Q684b5 sulfolobus
1339	6	0.8	101	2	Q8BTY4	Q8bty4 mus musculu	1412	6	0.8	112	2	Q9PSU2	Q9psu2 xenopus lae
1340	6	0.8	101	2	Q8K3D7	Q8k3d7 mus musculu	1413	6	0.8	113	2	Q8LSR1	Q8lsr1 pecunia hyb
1341	6	0.8	102	2	Q14278	Q14278 homo sapien	1414	6	0.8	113	2	Q84YV8	Q84yv8 crypthecodi
1342	6	0.8	102	2	Q7R3J1	Q7r3j1 giardia lam	1415	6	0.8	113	2	Q49970	Q49970 mycobacteri
1343	6	0.8	102	2	Q67N07	Q67n07 oryza sativ	1416	6	0.8	113	2	Q925X2	Q925x2 frankia sp.
1344	6	0.8	102	2	Q925K2	Q925k2 mycobacteri	1417	6	0.8	113	2	Q64GA6	Q64ga6 cylindrope
1345	6	0.8	102	2	Q65RK9	Q65r99 mannheimia	1418	6	0.8	113	2	Q87DR0	Q87d0 xyella fas

1419	6	0.8	113	2	OBFJZ5	OBFJZ5	escherichia
1420	6	0.8	114	2	OEGUR2	OEGUR2	axonopus co
1421	6	0.8	114	2	OEMWV6	OEMWV6	bdellovibri
1422	6	0.8	114	2	O8BDL1	O8BDL1	bradyrhizob
1423	6	0.8	114	2	O8G6K9	O8G6K9	human immun
1424	6	0.8	115	1	C7E9_MOUSE	O9CRJ7	mus musculu
1425	6	0.8	115	2	O9YD49	O9YD49	aeropyrum p
1426	6	0.8	115	2	O9BTD1	O9BTD1	homo sapien
1427	6	0.8	115	2	O8LTU8	O8LTU8	lactococcus
1428	6	0.8	115	2	O38I32	O38I32	bacteriopho
1429	6	0.8	115	2	O8DA10	O8DA10	vibrio vuln
1430	6	0.8	115	2	O6PB12	O6PB12	brachydanio
1431	6	0.8	115	2	O67ZS7	O67ZS7	human immun
1432	6	0.8	116	1	RL22_GLOVI	O7NEF7	gloeobacter
1433	6	0.8	116	2	O9HLT4	O9HLT4	thermoplasm
1434	6	0.8	116	2	O6B883	O6B883	ixodes paci
1435	6	0.8	116	2	O6B8C4	O6B8C4	ixodes paci
1436	6	0.8	116	2	O6B8E6	O6B8E6	ixodes paci
1437	6	0.8	116	2	O8HA82	O8HA82	salmomella
1438	6	0.8	116	2	O9XIA6	O9XIA6	arabidopsis
1439	6	0.8	116	2	O67R66	O67R66	symbiobacte
1440	6	0.8	116	2	O7MFI1	O7MFI1	vibrio vuln
1441	6	0.8	116	2	P87922	P87922	human immun
1442	6	0.8	116	2	O9Q2G8	O9Q2G8	human immun
1443	6	0.8	116	2	O6Q453	O6Q453	human immun
1444	6	0.8	117	1	RL22_STAM	O99892	staphylococ
1445	6	0.8	117	1	RL22_STAM	O74460	staphylococ
1446	6	0.8	117	1	RL22-STAW	O74079	staphylococ
1447	6	0.8	117	1	RL22-STAP	O8CR95	staphylococ
1448	6	0.8	117	2	O9YA74	O9YA74	aeropyrum p
1449	6	0.8	117	2	O7SO13	O7SO13	neurospora
1450	6	0.8	117	2	O7QON3	O7QON3	anopheles g
1451	6	0.8	117	2	O7OKI5	O7OKI5	anopheles g
1452	6	0.8	117	2	O7RPA0	O7RPA0	plasmodium g
1453	6	0.8	117	2	O6G776	O6G776	staphylococ
1454	6	0.8	117	2	O6GEI8	O6GEI8	staphylococ
1455	6	0.8	118	2	O44226	O44226	drosophila
1456	6	0.8	118	2	O6IGT2	O6IGT2	drosophila
1457	6	0.8	118	2	O7OIG7	O7OIG7	anopheles g
1458	6	0.8	118	2	O69UD4	O69UD4	coryza bati
1459	6	0.8	118	2	O6ZAR7	O6ZAR7	coryza bati
1460	6	0.8	118	2	O7BTW1	O7BTW1	yersinia pe
1461	6	0.8	118	2	O84040	O84040	chlamydia t
1462	6	0.8	118	2	O72MY2	O72MY2	leptospira
1463	6	0.8	118	2	O8FB09	O8FB09	leptospira
1464	6	0.8	119	2	O9MG34	O9MG34	calitrix
1465	6	0.8	119	2	O9WG25	O9WG25	calitrix
1466	6	0.8	119	2	O46457	O46457	chlamydia t
1467	6	0.8	119	2	O53469	O53469	mycobacteri
1468	6	0.8	119	2	O7TZ50	O7TZ50	mycobacteri
1469	6	0.8	119	2	O35755	O35755	rattus norv
1470	6	0.8	120	2	O05715	O05715	saccharomyc
1471	6	0.8	120	2	O74LTI	O74LTI	lactobacilli
1472	6	0.8	120	2	O8C3D7	O8C3D7	mus musculu
1473	6	0.8	120	2	O6DJ28	O6DJ28	xenopus tro
1474	6	0.8	121	2	O6BN47	O6BN47	debaromyces
1475	6	0.8	121	2	O7XXC5	O7XXC5	caenorhabdi
1476	6	0.8	121	2	O867A3	O867A3	proctolagus
1477	6	0.8	121	2	O7V633	O7V633	proctolotoco
1478	6	0.8	121	2	O91450	O91450	salvelliinus
1479	6	0.8	121	2	O79786	O79786	human immun
1480	6	0.8	122	1	RL14_MYCGB	P47407	mycoplasma
1481	6	0.8	122	1	RL14_MYCPN	O50308	mycoplasma
1482	6	0.8	122	2	O9MPZ1	O9MPZ1	anopheles f
1483	6	0.8	122	2	O9TGJ5	O9TGJ5	taenia hyda
1484	6	0.8	122	2	P96093	P96093	thiobacilli
1485	6	0.8	123	1	NEF_HV1B1	P03404	human immun
1486	6	0.8	123	1	NEF_HV1H2	P04601	human immun
1487	6	0.8	123	2	O58242	O58242	pyrococcus
1488	6	0.8	123	2	P95954	P95954	bulfitobius
1489	6	0.8	123	2	O9TGK1	O9TGK1	taenia soli
1490	6	0.8	123	2	O47794	O47794	enterococcu
1491	6	0.8	123	2	O63DY7	O63DY7	bacillus ce

1492	6	0.8	123	2	Q7VUW2	Q7VUW2	borderetella
1493	6	0.8	123	2	Q7W3Z5	Q7W3Z5	borderetella
1494	6	0.8	123	2	Q7WFC7	Q7WFC7	borderetella
1495	6	0.8	123	2	O8IT77	O8IT77	bacillus an
1496	6	0.8	123	2	O89103	O89103	bradyrhizob
1497	6	0.8	123	2	O6D7P8	O6D7P8	erwinia car
1498	6	0.8	123	2	O6HLG2	O6HLG2	bacillus th
1499	6	0.8	124	1	VNS1_IATXR	P08276	influenza a
1500	6	0.8	124	2	O8ZYTL	O8ZYTL	pyrobaculum

ALIGNMENTS

RESULT 1

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Db 361 PMOVQSETEPLHOLYSAAFSKQKQASAPTKKRALPFQGLDPMGVGHULTOLOECISPFYR 420
 Qy 421 RLSSRRRTCLRTGKMSGRAPSCIPICGKIENITAPKTQGLRMVQQAIIYRTSGVHDGSL 480
 Db 421 RLSSRRRTCLRTGKMSGRAPSCIPICGKIENITAPKTQGLRMVQQAIIYRTSGVHDGSL 480
 Qy 481 HKGAMFLVCGSALNERTVVAACVTDLGKVTMTKADLKVYLGGKYRDDDEKTIQS 540
 Db 481 HKGAMFLVCGSALNERTVVAACVTDLGKVTMTKADLKVYLGGKYRDDDEKTIQS 540
 Qy 541 LQISAILLHPYVDIILLDADIAIKLIDKARISTRVOPICLAASRDSTSPQESHITVAG 600
 Db 541 LRISAILLHPYVDIILLDADIAIKLIDKARISTRVOPICLAASRDSTSPQESHITVAG 600
 Qy 601 MNVLADVRSPGKNDTLRSQVSVVDSLLCEQHEHDGIPVSVTDNMFCAWEPAPSDI 660
 Db 601 MNVLADVRSPGKNDTLRSQVSVVDSLLCEQHEHDGIPVSVTDNMFCAWEPAPSDI 660
 Qy 661 CTAAE 664
 Db 661 CTAAE 664
 RESULT 3
 ID 096JW2 PRELIMINARY; PRT; 737 AA.
 AC 096JW2;
 DT 01-DEC-2001 (TReMBLrel. 19, Created)
 DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
 DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
 DE Hypothetical protein FLJ14935.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Eumetazoa; Euteleostomi; Primates; Catarrhini; Hominoidea; Homo.
 NX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX PubMed=14702039; DOI=10.1038/ng1285;
 RA Ota T., Suzuki Y., Nishikawa T., Ohtsuki T., Sugiyama T., Irie R.,
 Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
 Sekine M., Ohtsuka M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
 Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahara K.,
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 Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
 Okumura K., Nagase T., Nomura N., Kikuchi H., Maehuo Y., Yamashita R.,
 Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
 RT "Complete sequencing and characterization of 21,243 full-length human
 cDNAs";
 RL Nat. Genet. 36:40-45(2004).
 CC - SIMILARITY: Belongs to peptidase family S1.
 CC - SIMILARITY: Contains 1 EGF-like domain.
 DR EMBL; AK027841; BAB55404.1; -.

DR HSP, P00736, 1GPZ.
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0004295; F:trypsin activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR000859; CUB.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR006209; EGF-like.
 DR InterPro; IPR006210; IEGF.
 DR InterPro; IPR001254; Peptidase S1.
 DR InterPro; IPR001314; Peptidase S1A.
 DR InterPro; IPR009003; Pept. Ser. Cys.
 DR InterPro; IPR00436; Sushi_SCR_CCP.
 DR Pfam; PF00431; CUB; 1.
 DR Pfam; PF00008; EGF; 1.
 DR Pfam; PF00084; Sushi; 1.
 DR Pfam; PF00089; Trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00032; CCP; 2.
 DR SMART; SM00042; CUB; 1.
 DR SMART; SM00181; EGF; 2.
 DR SMART; SM00020; Tryp. SPC; 1.
 DR PROSITE; PS01180; CUB; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS50026; EGF_3; 1.
 DR PROSITE; PS50923; SUSH; 2.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR EGF-like domain; Hydroxylase; Protease; Serine protease.
 KW EGF-like domain; Hydroxylase; Protease; Serine protease.
 SQ SEQUENCE 737 AA; 81952 MW; 4F51689C5EB32B44 CRC64;
 Query Match 61.9%; Score 446; DB 2; Length 737;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 446; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 275 LEBRNCSDPGCPVNGYOKITGGRLNGRAKIGTVSPFCNNSYVLSGNEKRTQONGE 334
 Db 292 LEBRNCSDPGCPVNGYOKITGGRLNGRAKIGTVSPFCNNSYVLSGNEKRTQONGE 351
 Qy 335 WSGKOPICIRACBPKISDILVRRVLPMOVQSETEPLHOLYSAAFSKQKQASAPTKKRAL 394
 Db 352 WSGKOPICIRACBPKISDILVRRVLPMOVQSETEPLHOLYSAAFSKQKQASAPTKKRAL 411
 Qy 395 PFQGLPMGVGHULTOLOECISPFYRLGSSRRCTCLRTGKMSGRAPSCIPICGKIENITA 454
 Db 412 PFQGLPMGVGHULTOLOECISPFYRLGSSRRCTCLRTGKMSGRAPSCIPICGKIENITA 471
 Qy 455 PTKQGLRMPQQAIIYRTSGVHDGSLHKGAMFLVCGSALNERTVVAACVTDLGKVTM 514
 Db 472 PTKQGLRMPQQAIIYRTSGVHDGSLHKGAMFLVCGSALNERTVVAACVTDLGKVTM 531
 Qy 515 IKTADLKVYLGKYYRDDDEKTIQSIQISAILLHPYVDIILLDADIAIKLIDKARIST 574
 Db 532 IKTADLKVYLGKYYRDDDEKTIQSIQISAILLHPYVDIILLDADIAIKLIDKARIST 591
 Qy 575 RVOPICLAASRDSTSPQESHITVAGMNVADVRSPGKNDTLRSQVSVVDSLLCEQHE 634
 Db 592 RVOPICLAASRDSTSPQESHITVAGMNVADVRSPGKNDTLRSQVSVVDSLLCEQHE 651
 Qy 635 EDHGIPVSVTDNMFCAWEPAPSDICTAETGGIAAVSPGRASPFRMHLMGVSNYSYD 694
 Db 652 EDHGIPVSVTDNMFCAWEPAPSDICTAETGGIAAVSPGRASPFRMHLMGVSNYSYD 711
 Qy 695 KTCSHRLSTAFYTLVLPKDWIERNMK 720
 Db 712 KTCSHRLSTAFYTLVLPKDWIERNMK 737
 RESULT 4
 ID 071RE9 PRELIMINARY; PRT; 417 AA.
 AC 071RE9;
 DT 05-JUL-2004 (TReMBLrel. 27, Created)

DT 05-JUL-2004 (TRENBLREL. 27, Last sequence update)
 DT 05-JUL-2004 (TRENBLREL. 27, Last annotation update)
 DE FP938.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 NC NCB1_TaxID=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Huang Y., Zhou X.M., Zhang P.P., Jiang H.Q., Qin W.X., Zhao X.T.,
 Wan D.F., Gu J.R.;
 RL Submitted (APR-2001) to the EMBL/Genbank/DBJ databases.
 CC -1- SIMILARITY: belongs to peptidase family S1.
 DR EMBL; AF370388; AAQ15224.1; -.
 DR HSSP; P00734; 1B00.
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.
 DR GO; GO:0004295; F:trypsin activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR001254; Peptidase_S1.
 DR InterPro; IPR009003; Pept_Ser_Cys.
 DR InterPro; IPR000436; Sushi_SCR_CCP.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00020; TRYP_SPC; 1.
 DR PROSITE; PS50923; SUSHI; 1.
 DR PROSITE; PS50240; TRYP_SIN_DOM; 1.
 KW Hydroxylase; Protease; Serine protease.
 SQ SEQUENCE 417 AA; 46703 MW; 2546A52A3697C1C4 CRC64;

Query Match 53.6%; Score 386; DB 2; Length 417;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 386; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 335 MSGKOPITKACREPKISDVARRVLPQVOSRETEHLQVLSAARSKQKLSAPTKPKAL 394
 DB 32 MSGKOPITKACREPKISDVARRVLPQVOSRETEHLQVLSAARSKQKLSAPTKPKAL 91
 QY 395 PFGDLPMGYOHLHTQLOECISPFYRRLGSSRRCTLRGKMSGRAPSCIPICGKIENTA 454
 DB 92 PFGDLPMGYOHLHTQLOECISPFYRRLGSSRRCTLRGKMSGRAPSCIPICGKIENTA 151
 QY 455 PRTQGLRMPQWAAIYRRTSGVHDSGLHKGAMFLVCSGALVNERIVVAACHVTDLGKTM 514
 DB 152 PRTQGLRMPQWAAIYRRTSGVHDSGLHKGAMFLVCSGALVNERIVVAACHVTDLGKTM 211
 QY 515 IKTADLKVVLGKFEYDDDDDEKTIQSLQISATILHPNVDPIILLDDIALILKLDKARIST 574
 DB 212 IKTADLKVVLGKFEYDDDDDEKTIQSLQISATILHPNVDPIILLDDIALILKLDKARIST 271
 QY 575 RVQPICLAASRDLSFQESHITTVAGMNVLDVRSFGFNKDTLRSGVSVVDSLLCEBQH 634
 DB 272 RVQPICLAASRDLSFQESHITTVAGMNVLDVRSFGFNKDTLRSGVSVVDSLLCEBQH 331
 QY 635 EDHGIPVSVTDNMFCAWEPPTAPSDICTAETGIAVSPFGASPEPRWHLGLVSWSYD 694
 DB 332 EDHGIPVSVTDNMFCAWEPPTAPSDICTAETGIAVSPFGASPEPRWHLGLVSWSYD 391
 QY 695 KTCSHRLSTAFTKVLPRKDWIERNNK 720
 DB 392 KTCSHRLSTAFTKVLPRKDWIERNNK 417

RESULT 5

QY432 PRELIMINARY; PRT; 181 AA.
 AC QY432;
 DT 01-NOV-1999 (TRENBLREL. 12, Created)
 DT 01-NOV-1999 (TRENBLREL. 12, Last sequence update)
 DT 01-MAR-2004 (TRENBLREL. 26, Last annotation update)
 DE Hypothetical protein DKFZps56H2123 (Fragment).
 GN Name=DKFZps56H2123;
 OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 NC NCB1_TaxID=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Ansoorge W., Winkler U., Mewes H.W., Gassenhuber J., Wiemann S.;
 RL Submitted (MAY-1999) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AL050214; CAB43317.1; -.
 DR PIR; T08805; T08805.
 DR HSSP; P00736; 1MD7.
 DR MEROPS; S01.998; -.
 DR GO; GO:0004295; F:trypsin activity; IEA.
 DR GO; GO:0004295; F:trypsin activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR001254; Peptidase_S1.
 DR InterPro; IPR009003; Pept_Ser_Cys.
 DR Pfam; PF00089; Trypsin; 1.
 DR SMART; SM00020; TRYP_SPC; 1.
 DR PROSITE; PS50240; TRYP_SIN_DOM; 1.
 KW Hydroxylase; Hypothetical protein; Protease; Serine protease.
 FT NON TER
 SQ SEQUENCE 181 AA; 19962 MW; ABC793BB682D439 CRC64;

Query Match 24.7%; Score 178; DB 2; Length 181;
 Best Local Similarity 100.0%; Pred. No. 2,5e-181;
 Matches 178; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 543 ISATILHPNVDPIILLDDIALILKLDKARISTRVQPICLAASRDLSFQESHITTVAGM 602
 DB 4 ISATILHPNVDPIILLDDIALILKLDKARISTRVQPICLAASRDLSFQESHITTVAGM 63
 QY 603 VLADVRSPGFNDTLRSGVSVVDSLLCEBQEDHGIPVSVTDNMFCAWEPPTAPSDICT 662
 DB 64 VLADVRSPGFNDTLRSGVSVVDSLLCEBQEDHGIPVSVTDNMFCAWEPPTAPSDICT 123
 QY 663 AETGIAVSPFGASPEPRWHLGLVSWSYDTCSSRLSTAFTKVLPRKDWIERNNK 720
 DB 124 AETGIAVSPFGASPEPRWHLGLVSWSYDTCSSRLSTAFTKVLPRKDWIERNNK 181

RESULT 6

Q88U25 PRELIMINARY; PRT; 720 AA.
 AC Q88U25;
 DT 01-MAR-2003 (TRENBLREL. 23, Created)
 DT 01-MAR-2003 (TRENBLREL. 23, Last sequence update)
 DT 01-MAR-2004 (TRENBLREL. 26, Last annotation update)
 DE Mus musculus 2 days neonate thymus thymic cells cDNA, RIKEN full-length enriched library, clone:R43002G05 product:hypothetical BGF-like domain, CUB domain, Sushi domain / SCR repeat / CCP module and DE Serine proteases, trypsin family domain containing protein, full insert sequence.
 GN Name=B43002G05R1k;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NC NCB1_TaxID=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA STRAIN=NOD; TISSUE=Thymus;
 RC MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44(1999).
 RN (2)
 RP SEQUENCE FROM N.A.
 RA STRAIN=NOD; TISSUE=Thymus;
 RC MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN (3)

RP SEQUENCE FROM N.A.
 RC STRAIN=NOD; TISSUE=Thymus;
 RA The FANTOM Consortium;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs."
 RL Nature 420:563-573(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NOD; TISSUE=Thymus;
 RX MEDLINE=2049374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes."
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NOD; TISSUE=Thymus;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama J., Nishi K., Kitamura T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanishi M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multiplexed capillary sequencer."
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NOD; TISSUE=Thymus;
 RA Araiuchi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,
 RA Horii F., Imclanti K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Kato H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
 RA Kuribara C., Maruyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohnato N., Okazaki Y.,
 RA Saito R., Satoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to peptidase family S1.
 CC -1- SIMILARITY: Contains 1 EGF-like domain.
 CC HSSP; AK088017; BAC40098.1; -.
 DR HSSP; P00736; IGPZ.
 DR MGD; MGI:2445082; E430002G05R1K.
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR InterPro; IPR000859; CUB.
 DR InterPro; IPR007442; EGF_2.
 DR InterPro; IPR006209; EGF_1like.
 DR InterPro; IPR006210; IEGF.
 DR InterPro; IPR001254; Peptidase_S1.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR InterPro; IPR009003; Pept_Ser_Cys.
 DR InterPro; IPR000436; Sushi_SCR_CCP.
 DR Pfam; PF00431; CUB; 1.
 DR Pfam; PF00008; EGF; 1.
 DR Pfam; PF00084; Sushi; 1.
 DR Pfam; PF00089; Trypsin; 1.
 DR PRINTS; PRO0722; CHYMOTRYPSIN.
 DR SMART; SM00032; CCP; 2.
 DR SMART; SM00042; CUB; 1.
 DR SMART; SM00181; EGF; 2.
 DR SMART; SM00020; Tryp_SPC; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS50026; EGF_3; 1.
 DR PROSITE; PS50923; Sushi; 2.

DR PROSITE; PS50240; TRYPsin_DOM; 1.
 KW EGF-like domain; Hydroxylase; Hypothetical protein; Protease;
 KM Serine protease.
 SQ SEQUENCE 720 AA; 80300 MW; C098E076D903A5A0 CRC64;
 Query Match 8.5%; Score 61; DB 2; Length 720;
 Best Local Similarity 100.0%; Pred. No. 1.6e-55;
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 74 NECDSCILHPGCTIFENKSCRNAGMGTDFYVKGFCACERAGWYGGDCRCQVLR 133
 DB 74 NECDSCILHPGCTIFENKSCRNAGMGTDFYVKGFCACERAGWYGGDCRCQVLR 133
 QY 134 A 134
 DB 134 A 134
 RESULT 7
 Q8K2B8 PRELIMINARY; PRT; 720 AA.
 AC Q8K2B8;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Regeneration associated muscle protease.
 GN Name=E430002G05R1K;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CZECH II; TISSUE=Mammary tumor;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heile F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Tohiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butcherfield Y.S.,
 RA Krzywicki M.I., Skalka U., Smalins D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CZECH II; TISSUE=Mammary tumor;
 RA Straubberg R.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CZECH II; TISSUE=Mammary tumor;
 RA Straubberg R.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to peptidase family S1.
 DR EMBL; BC031841; AA31841.1; -.
 DR EMBL; BC057685; AA57685.1; -.
 DR HSSP; P00736; IGPZ.
 DR MGD; MGI:2445082; E430002G05R1K.
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR InterPro; IPR000859; CUB.
 DR InterPro; IPR007442; EGF_2.

DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR InterPro; IPR000436; Sush1_SCR_CCP.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF00084; Sush1; 1.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS50026; EGF_3; 1.
DR PROSITE; PS50923; SUSH1; 2.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 720 AA; 80377 MW; 7172B7F1E690FD0E CRC64;

Query Match 5.7%; Score 41; DB 2; Length 720;
Best Local Similarity 100.0%; Pred. No. 4,2e-34;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 13 FLOLLISLPREYVINEACPGAMNIMCECEYDIEC 53
Db 13 FLOLLISLPREYVINEACPGAMNIMCECEYDIEC 53

RESULT 8

06DIV5 PRELIMINARY; PRT; 722 AA.

ID 06DIV5;
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE MG889196 protein.
GN Name=MG889196;
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoes; Pipidae;
OC Xenopodine; Xenopus.
OX NCBI_TaxID=8364;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=whole body;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Schmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Bueow K.H., Scheefel C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Cavaletti T.L., Schetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carinci P., Prange C.,
RA Rane S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Boeck S.A., McKean P.J., McKernan K.V., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kerteman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalish D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=whole body;
RA Klein S., Gerhard D.S.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 EGF-like domain.
EMBL; BC075430; AAH75430.1; -.

DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR InterPro; IPR000436; Sush1_SCR_CCP.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF00084; Sush1; 2.
DR Pfam; PF00089; Trypsin; 1.
DR SMART; SM00042; CCP; 2.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00181; EGF; 2.
DR SMART; SM00179; EGF_Ca; 1.
DR SMART; SM00020; TRYP_SPC; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS50026; EGF_3; 1.
DR PROSITE; PS50923; SUSH1; 2.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
KW EGF-like domain; Hydrolase; Protease; Serine protease.
KW EGF-like domain; Hydrolase; Protease; Serine protease.
SQ SEQUENCE 722 AA; 80366 MW; F173563206D1A82 CRC64;

Query Match 3.3%; Score 24; DB 2; Length 722;
Best Local Similarity 100.0%; Pred. No. 6.7e-16;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 62 VGYTIPCCRNENECDSCLIHPCG 85
Db 64 VGYTIPCCRNENECDSCLIHPCG 87

RESULT 9

091WZ0 PRELIMINARY; PRT; 222 AA.

ID 091WZ0;
AC 091WZ0;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Bone morphogenetic protein 1 (Fragment).
GN Name=Bmp-1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=Mistar; TISSUE=E18 whole embryo;
RA Kataoka H., Enomoto K.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB073100; BAB69961.1; -.
DR HSSP; Q9UCV4; INZI.
DR GO; GO:0008533; F:actin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR Pfam; PF01400; Actacin; 1.
DR Pfam; PF00431; CUB; 2.
DR PROSITE; PS01180; CUB; 2.
FT NON_TER 1 1
FT TER 222 222
SQ SEQUENCE 222 AA; 25426 MW; F6A9052DA98B57A CRC64;

Query Match 1.2%; Score 9; DB 2; Length 222;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 179 YDYEVVRDG 187
|||||||

Db 80 YDYEVNRDGS 88

RESULT 10

Y836_AQUAE STANDARD; PRT; 232 AA.

ID 067008;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Hypothetical protein AQ_836.

GN OrderedLocustNames=AQ_836;

OS Aquifex aeolicus.

OC Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.

OX NCBI_TaxID=63363;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=VF5;

RX MEDLINE=98196666; PubMed=9537320; DOI=10.1038/32831;

RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Graham D.E., Overbeek R., Sneed M.A., Keller M., Aulay M., Huber R., Feldman R.A., Short J.M., Olsen G.J., Swanson M.V.;

RT "The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.";

RL Nature 392:353-358(1998).

CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).

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CC -----

CC EMBL; AE000709; AAC06970.1; -

DR PIR; E70372; E70372.

KW Complete proteome; Hypothetical protein; Transmembrane.

FT TRANSMEM 4 24 Potential.

FT TRANSMEM 42 62 Potential.

FT TRANSMEM 100 120 Potential.

FT TRANSMEM 145 165 Potential.

FT TRANSMEM 171 191 Potential.

FT TRANSMEM 232 AA; 26317 MW; B934B56FEA35B183 CRC64;

SO SEQUENCE

Query Match 1.2%; Score 9; DB 1; Length 232;

Best Local Similarity 100.0%; Pred. No. 2.7;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 88 FENCKSCRN 96

DB 23 FENCKSCRN 31

RESULT 11

086553 PRELIMINARY; PRT; 276 AA.

ID 086553;

AC 086553;

DT 01-NOV-1998 (TRENBLrel. 08, Created)

DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)

DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)

DE Putative dehydrogenase.

GN ORFNames=SCIP2.16c;

OS Streptomyces coelicolor.

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

OC Streptomycinae; Streptomycetaceae; Streptomycetes.

OX NCBI_TaxID=1902;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=A3(2) / M145;

RX MEDLINE=21996410; PubMed=12000953; DOI=10.1038/41714a;

RA Bentley S.D., Chater K.F., Cardeno-Tarrazaga A.-M., Challis G.L., Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleeer H.,

RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M., Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S., Huang C.-H., Kleser T., Larke L., Murphy L.D., Oliver K., O'Neill S., Rabinowitz E., Rajendram M.A., Rutherford K.M., Rutter S., Seeger K., Sanders D., Sharp S., Squares R., Squares S., Taylor K., Warren T., Wierorrek A., Woodward J.R., Barrell B.G., Parkhill J., Hopwood D.A.;

RT "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2)."

RL Nature 417:141-147(2002).

CC -1- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases (SDR) family.

CC EMBL; AL939128; CA920507.1; -

DR PIR; T29125; T29125.

DR HSSP; P08074; 1CYD.

DR GO; GO:0016491; F:oxidoreductase activity; IEA.

DR GO; GO:0008152; P:metabolism; IEA.

DR InterPro; IPR002198; ADH_short.

DR InterPro; IPR002347; Adh_short_C2.

DR Pfam; PF00106; adh_short; 1.

DR PRINTS; PR00081; GDRDH.

DR PRINTS; PR00080; SDRFAMILY.

DR PROSITE; PS00061; ADH_SHORT; 1.

KW Complete proteome; Oxidoreductase.

SO SEQUENCE 276 AA; 29010 MW; 30F0038B70D63C7C CRC64;

Query Match 1.2%; Score 9; DB 2; Length 276;

Best Local Similarity 100.0%; Pred. No. 3.2;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 670 AVSFPGRAS 678

DB 225 AVSFPGRAS 233

RESULT 12

06PUN5 PRELIMINARY; PRT; 593 AA.

ID 06PUN5;

AC 06PUN5;

DT 05-JUL-2004 (TRENBLrel. 27, Created)

DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)

DE TIL2 protein (Fragment).

GN Name=TIL2;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Ovary;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusik A.K., Farmer A.A., Rubin G.M., Hong L., Scapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loughran N.A., Peters G.J., Abramson R.D., Mullah S.J., Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchan J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

[2]

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RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RA Strauberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013871; AAH13871.1; -.
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DR GO; GO:0008533; F:actacin activity; IEA.
DR GO; GO:0008237; F:metallopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR006026; Peptidase_M.
DR InterPro; IPR001506; Peptidase_M12A.
DR InterPro; IPR006025; Pept_M_zn_BS.
DR Pfam; PF01400; Astacin; 1.
DR PRINTS; PR00480; ASTACIN.
DR SMART; SM00042; CUB; 2.
DR SMART; SM00235; ZNMC; 1.
DR PROSITE; PS01180; CUB; 2.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
DR NON_TER 593 593
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Query Match 1.2%; Score 9; DB 2; Length 593;
Best Local Similarity 100.0%; Pred. No. 6.4;
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Oy 179 YDYVEVRDG 187
Db 406 YDYVEVRDG 414

RESULT 13
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AC P98069;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Bone morphogenetic protein 1 homolog precursor (EC 3.4.24.-) (SUBMP).
OS Strongylocentrotus purpuratus (Purple sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
OC Strongylocentrotus.
OX NCBI_TaxID=7668;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=94215496; PubMed=8162855;
RA Hwang S.P.L., Partin J.S., Lennarz W.J.;
RT "Characterization of a homolog of human bone morphogenetic protein 1
in the embryo of the sea urchin, Strongylocentrotus purpuratus.";
RL Development 120:559-568(1994).
CC -1- TISSUE SPECIFICITY: Ectodermal and primary mesenchym cells in
hatched blastula.
CC -1- DEVELOPMENTAL STAGE: Embryo; highest level before epiculogenesis.
CC -1- SIMILARITY: Belongs to the peptidase M12A family.
CC -1- SIMILARITY: Contains 2 CUB domains.
CC -1- SIMILARITY: Contains 1 EGF-like domain.
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CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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or send an email to license@isb-sib.ch).
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CC EMBL; L23838; AAA30081.1; -.
DR HSSP; P35555; IEMN.
DR MEROPS; M12.005; -.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR000859; CUB.

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DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR006025; Pept_M_zn_BS.
DR InterPro; IPR006026; Peptidase_M.
DR InterPro; IPR001506; Peptidase_M12A.
DR Pfam; PF01400; Astacin; 1.
DR Pfam; PF00431; CUB; 2.
DR PRINTS; PR00008; EGF; 1.
DR PRINTS; PR00480; ASTACIN.
DR SMART; SM00042; CUB; 2.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00235; ZNMC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS01180; CUB; 2.
DR PROSITE; PS00022; EGF_1; FALSE_NEG.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS50026; EGF_3; 1.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
DR Calcium; Developmental protein; EGF-like domain; Embryo; Hydrolase;
KW Metalloprotease; Protease; Repeat; Signal; Zinc.
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FT PROPEP 24 109
FT CHAIN 110 639
FT DOMAIN 110 306
FT DOMAIN 307 419
FT DOMAIN 420 531
FT DOMAIN 532 573
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FT ACT_SITE 198 198
FT METAL 201 201
FT METAL 207 207
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FT DISULFID 544 557
FT CARBOHYD 122 122
FT CARBOHYD 140 140
FT CARBOHYD 317 317
FT CARBOHYD 455 455
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Query Match 1.2%; Score 9; DB 1; Length 639;
Best Local Similarity 100.0%; Pred. No. 6.9;
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Oy 179 YDYVEVRDG 187
Db 475 YDYVEVRDG 483

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ID 057658 PRELIMINARY; PRT; 691 AA.
AC 057658;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Bone morphogenetic protein 1 (Fragment).
GN Name=BMP1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;
OC Actinoptera; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20267865; PubMed=10806368; DOI=10.1016/S0378-1119(00)00114-1;
RA Reynolds S.D., Zhang D., Fuzas J.E., O'Keefe R.J., Rosier R.N.,
RT "Cloning of the chick BMP1/Tolloid cDNA and expression in skeletal
tissues.";
RL Gene 248:233-243(2000).

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OM protein - protein search, using SW model

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(without alignments)
1249,938 Million cell updates/sec

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Gapop 60.0 , Gapext 60.0

Searched: 513545 seqs, 74649064 residues

Word size : 0

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1500 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	16	2.2	46	4 US-10-067-422-17	Sequence 17, Appl1
3	12	1.7	12	4 US-10-067-422-16	Sequence 16, Appl1
4	9	1.2	101	3 US-09-374-135-4	Sequence 4, Appl1
5	9	1.2	110	4 US-09-341-461-28	Sequence 28, Appl1
6	9	1.2	113	4 US-09-438-046-60	Sequence 20, Appl1
7	9	1.2	730	3 US-08-872-757-2	Sequence 2, Appl1
8	9	1.2	730	3 US-09-850-048A-2	Sequence 2, Appl1
9	9	1.2	788	1 US-08-572-225-1	Sequence 1, Appl1
10	9	1.2	986	4 US-09-285-185C-19	Sequence 19, Appl1
11	9	1.2	986	4 US-09-949-016-6690	Sequence 6690, Ap
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57	7	1.0	172	4 US-09-198-452A-368	Sequence 368, App
58	7	1.0	172	4 US-09-438-185A-352	Sequence 352, App
59	7	1.0	187	4 US-09-107-532A-6736	Sequence 6736, App
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122	7	1.0	1074	4	US-09-071-035-358	Sequence 358, App	195	6	0.8	64	4	US-09-252-991A-11573	Sequence 11573, A
123	7	1.0	1096	4	US-09-071-035-394	Sequence 394, App	196	6	0.8	68	4	US-09-248-796A-24682	Sequence 24682, A
124	7	1.0	1096	4	US-09-134-000C-5764	Sequence 5764, Ap	197	6	0.8	69	4	US-08-302-756E-20	Sequence 20, Appl
125	7	1.0	1346	3	US-09-320-878-4	Sequence 4, Appl1	198	6	0.8	70	4	US-09-732-210-883	Sequence 883, App
126	7	1.0	1346	3	US-09-105-537-37	Sequence 37, Appl1	199	6	0.8	72	4	US-09-540-236-2193	Sequence 2193, Ap
127	7	1.0	1346	4	US-09-141-908-5	Sequence 5, Appl1	200	6	0.8	74	4	US-09-543-681A-8341	Sequence 8341, Ap
128	7	1.0	1346	4	US-09-657-440-4	Sequence 4, Appl1	201	6	0.8	74	4	US-09-134-000C-6316	Sequence 6316, Ap
129	7	1.0	1387	3	US-09-105-537-6	Sequence 6, Appl1	202	6	0.8	76	4	US-09-328-352-4331	Sequence 4331, Ap
130	6	0.8	11	2	US-08-464-961-2	Sequence 2, Appl1	203	6	0.8	77	3	US-08-718-904-6	Sequence 6, Appl1
131	6	0.8	11	3	US-08-957-130-17	Sequence 17, Appl	204	6	0.8	77	4	US-09-449-249-6	Sequence 6, Appl1
132	6	0.8	11	3	US-08-969-315-2	Sequence 2, Appl1	205	6	0.8	77	4	US-09-107-433-3411	Sequence 3411, Ap
133	6	0.8	11	5	PCT-US96-08233-2	Sequence 2, Appl1	206	6	0.8	80	4	US-09-583-110-2844	Sequence 2844, Ap
134	6	0.8	12	4	US-09-205-258-304	Sequence 304, App	207	6	0.8	81	4	US-09-270-767-46160	Sequence 46160, A
135	6	0.8	13	1	US-08-179-481-87	Sequence 87, Appl	208	6	0.8	84	4	US-09-248-796A-23422	Sequence 23422, A
136	6	0.8	17	1	US-08-205-938A-14	Sequence 14, Appl	209	6	0.8	85	4	US-09-732-210-1467	Sequence 1467, Ap
137	6	0.8	17	5	PCT-US95-02626-14	Sequence 14, Appl	210	6	0.8	86	1	US-07-847-743B-19	Sequence 19, Appl
138	6	0.8	20	1	US-08-205-938A-13	Sequence 13, Appl	211	6	0.8	86	1	US-08-456-201-19	Sequence 19, Appl
139	6	0.8	20	5	PCT-US95-02626-13	Sequence 13, Appl	212	6	0.8	86	2	US-08-330-161-17	Sequence 17, Appl
140	6	0.8	25	3	US-09-660-587-28	Sequence 28, Appl	213	6	0.8	86	2	US-08-456-241-19	Sequence 19, Appl
141	6	0.8	25	4	US-09-261-358A-28	Sequence 28, Appl	214	6	0.8	86	2	US-08-440-401-17	Sequence 17, Appl
142	6	0.8	25	4	US-09-201-458-20	Sequence 20, Appl	215	6	0.8	86	2	US-08-419-878B-17	Sequence 17, Appl
143	6	0.8	25	4	US-09-811-007A-28	Sequence 28, Appl	216	6	0.8	86	3	US-09-134-001C-3359	Sequence 3359, Ap
144	6	0.8	31	4	US-08-437-943D-14	Sequence 14, Appl	217	6	0.8	86	3	US-09-173-480-17	Sequence 17, Appl
145	6	0.8	35	1	US-08-145-708A-15	Sequence 15, Appl	218	6	0.8	86	4	US-09-252-991A-17535	Sequence 17535, A
146	6	0.8	35	2	US-08-331-454-15	Sequence 15, Appl	219	6	0.8	86	5	PCT-US92-04295A-19	Sequence 19, Appl
147	6	0.8	37	2	US-09-066-074-14	Sequence 14, Appl	220	6	0.8	87	4	US-09-252-991A-28740	Sequence 28740, A
148	6	0.8	37	2	US-08-555-912A-14	Sequence 14, Appl	221	6	0.8	90	4	US-09-252-991A-24674	Sequence 24674, A
149	6	0.8	37	3	US-08-348-518C-24	Sequence 24, Appl	222	6	0.8	91	4	US-09-107-433-4244	Sequence 4244, Ap
150	6	0.8	37	3	US-08-476-509B-24	Sequence 24, Appl	223	6	0.8	93	4	US-09-252-991A-117535	Sequence 117535, A
151	6	0.8	37	4	US-09-252-404A-39	Sequence 39, Appl	224	6	0.8	93	4	US-09-270-767-39947	Sequence 39947, A
152	6	0.8	37	4	US-09-275-900-14	Sequence 14, Appl	225	6	0.8	93	4	US-09-270-767-55164	Sequence 55164, A
153	6	0.8	37	4	US-09-821-861-16	Sequence 16, Appl	226	6	0.8	94	3	US-08-946-329A-79	Sequence 79, Appl
154	6	0.8	38	1	US-08-145-708A-14	Sequence 14, Appl	227	6	0.8	94	3	US-08-466-368-5	Sequence 5, Appl1
155	6	0.8	40	4	US-09-270-767-40577	Sequence 40577, A	228	6	0.8	94	4	US-08-470-998-2	Sequence 2, Appl1
156	6	0.8	40	4	US-08-424-550B-467	Sequence 467, App	229	6	0.8	94	4	US-08-328-500-10	Sequence 10, Appl
157	6	0.8	40	4	US-08-469-260A-467	Sequence 467, App	230	6	0.8	94	4	US-09-270-767-33056	Sequence 33056, A
158	6	0.8	40	4	US-08-488-446-467	Sequence 467, App	231	6	0.8	94	4	US-09-270-767-47687	Sequence 47687, A
159	6	0.8	40	4	US-08-467-344A-467	Sequence 467, App	232	6	0.8	95	4	US-09-270-767-46409	Sequence 46409, A
160	6	0.8	40	4	US-09-270-767-40577	Sequence 40577, A	233	6	0.8	95	4	US-09-248-796A-25418	Sequence 25418, A
161	6	0.8	40	4	US-09-270-767-55793	Sequence 55793, A	234	6	0.8	96	3	US-09-230-637-44	Sequence 44, Appl
162	6	0.8	41	4	US-08-168-091A-41	Sequence 41, Appl	235	6	0.8	99	4	US-09-270-767-32461	Sequence 32461, A
163	6	0.8	41	4	US-08-168-091A-41	Sequence 41, Appl	236	6	0.8	99	4	US-09-270-767-47687	Sequence 47687, A
164	6	0.8	42	4	US-09-066-330-3	Sequence 3, Appl1	237	6	0.8	100	4	US-09-270-767-35703	Sequence 35703, A
165	6	0.8	43	1	US-07-998-003A-73	Sequence 73, Appl	238	6	0.8	100	4	US-09-270-767-50920	Sequence 50920, A
166	6	0.8	43	1	US-08-453-274B-73	Sequence 73, Appl	239	6	0.8	100	4	US-09-471-276-832	Sequence 832, App
167	6	0.8	43	1	US-08-453-695A-73	Sequence 73, Appl	240	6	0.8	101	4	US-09-390-134B-42	Sequence 42, Appl
168	6	0.8	43	1	US-08-268-161A-73	Sequence 73, Appl	241	6	0.8	102	4	US-09-270-767-58844	Sequence 58844, A
169	6	0.8	43	2	US-08-453-702A-73	Sequence 73, Appl	242	6	0.8	103	3	US-09-199-637A-271	Sequence 271, App
170	6	0.8	43	2	US-08-751-305-4	Sequence 4, Appl1	243	6	0.8	103	4	US-09-252-991A-32642	Sequence 32642, A
171	6	0.8	43	3	US-09-099-639-73	Sequence 73, Appl	244	6	0.8	103	4	US-09-543-681A-88232	Sequence 88232, Ap
172	6	0.8	43	3	PCT-US93-12588-73	Sequence 73, Appl	245	6	0.8	103	4	US-09-621-976-4109	Sequence 4109, Ap
173	6	0.8	43	5	PCT-US95-08071-73	Sequence 73, Appl	246	6	0.8	103	4	US-09-513-999C-3560	Sequence 5560, Ap

247	6	0.8	106	4	US-09-087-031E-13	Sequence 13, Appl	320	6	0.8	151	3	US-08-679-493A-74	Sequence 74, Appl
248	6	0.8	106	4	US-09-248-796A-14519	Sequence 1519, A	321	6	0.8	152	4	US-09-885-723-11	Sequence 11, Appl
249	6	0.8	107	4	US-09-732-210-230	Sequence 230, App	322	6	0.8	153	4	US-09-288-143-123	Sequence 123, App
250	6	0.8	107	4	US-09-489-039A-9954	Sequence 9954, 'Ap	323	6	0.8	153	4	US-09-252-991A-22634	Sequence 2634, A
251	6	0.8	107	4	US-09-710-279-1586	Sequence 1586, Ap	324	6	0.8	153	4	US-09-134-000C-5186	Sequence 5186, Ap
252	6	0.8	108	4	US-09-489-039A-9393	Sequence 9392, Ap	325	6	0.8	154	3	US-09-387-418A-8	Sequence 8, Appl
253	6	0.8	108	4	US-09-489-039A-11679	Sequence 11679, A	326	6	0.8	156	1	US-08-469-667-20	Sequence 20, Appl
254	6	0.8	109	4	US-09-134-000C-6718	Sequence 6718, Ap	327	6	0.8	156	3	US-09-224-110-20	Sequence 20, Appl
255	6	0.8	109	4	US-09-270-767-60583	Sequence 60583, A	328	6	0.8	156	4	US-09-252-991A-24413	Sequence 24413, A
256	6	0.8	110	3	US-09-376-330-24	Sequence 24, Appl	329	6	0.8	156	4	US-09-388-292A-20	Sequence 20, Appl
257	6	0.8	111	4	US-09-252-991A-17096	Sequence 17096, A	330	6	0.8	156	5	PCT-US95-07289-20	Sequence 20, Appl
258	6	0.8	111	4	US-09-294-298A-12	Sequence 12, Appl	331	6	0.8	157	2	US-08-811-949-41	Sequence 41, Appl
259	6	0.8	112	4	US-09-107-532A-7068	Sequence 7068, Ap	332	6	0.8	157	3	US-08-872-855-6	Sequence 6, Appl
260	6	0.8	112	4	US-09-270-767-44754	Sequence 34754, A	333	6	0.8	157	3	US-08-981-392-68	Sequence 66, Appl
261	6	0.8	112	4	US-09-270-767-49971	Sequence 49971, A	334	6	0.8	157	3	US-09-071-035-446	Sequence 46, App
262	6	0.8	112	4	US-09-902-540-5940	Sequence 9940, Ap	335	6	0.8	157	4	US-09-308-322-62	Sequence 66, Appl
263	6	0.8	113	4	US-09-438-046-53	Sequence 23, Appl	336	6	0.8	159	3	US-08-796-792-8	Sequence 2, Appl
264	6	0.8	115	4	US-09-270-767-47912	Sequence 47912, A	337	6	0.8	159	4	US-09-491-795-2	Sequence 2, Appl
265	6	0.8	115	4	US-09-902-540-10750	Sequence 10750, A	338	6	0.8	162	1	US-08-266-451E-29	Sequence 29, Appl
266	6	0.8	120	4	US-09-583-110-5022	Sequence 5022, Ap	339	6	0.8	162	2	US-08-748-725-29	Sequence 29, Appl
267	6	0.8	121	1	US-08-307-499-7	Sequence 7, Appl	340	6	0.8	162	4	US-09-540-236-2636	Sequence 2636, Ap
268	6	0.8	121	4	US-09-299-268-7	Sequence 683, App	341	6	0.8	164	4	US-09-489-039A-11750	Sequence 11750, A
269	6	0.8	121	4	US-10-101-464A-683	Sequence 588, App	342	6	0.8	164	4	US-09-270-767-41274	Sequence 41274, A
270	6	0.8	122	4	US-09-732-210-598	Sequence 600, App	343	6	0.8	167	4	US-09-270-767-56490	Sequence 56490, A
271	6	0.8	122	4	US-09-732-210-600	Sequence 600, App	344	6	0.8	170	4	US-09-252-991A-22362	Sequence 22362, A
272	6	0.8	122	4	US-10-101-464A-712	Sequence 712, App	345	6	0.8	172	4	US-09-328-352-5691	Sequence 5691, Ap
273	6	0.8	122	4	US-09-424-840B-14	Sequence 14, Appl	346	6	0.8	172	4	US-09-328-352-5691	Sequence 11425, A
274	6	0.8	122	4	US-09-107-433-3697	Sequence 3697, Ap	347	6	0.8	175	4	US-09-902-540-11425	Sequence 24281, A
275	6	0.8	123	3	US-09-124-900-10	Sequence 383, Ap	348	6	0.8	176	4	US-09-252-991A-24281	Sequence 24281, A
276	6	0.8	123	3	US-09-134-001C-3283	Sequence 3283, Ap	349	6	0.8	176	4	US-09-252-991A-24805	Sequence 24805, A
277	6	0.8	124	4	US-08-311-731A-202	Sequence 202, App	350	6	0.8	176	4	US-09-489-039A-12706	Sequence 12706, A
278	6	0.8	125	4	US-09-270-767-61747	Sequence 61747, A	351	6	0.8	177	2	US-08-770-544-20	Sequence 20, Appl
279	6	0.8	125	4	US-09-543-681A-7177	Sequence 7177, Ap	352	6	0.8	177	4	US-09-579-259-20	Sequence 20, Appl
280	6	0.8	126	4	US-09-902-540-12158	Sequence 12158, A	353	6	0.8	177	4	US-09-543-681A-5159	Sequence 5159, Ap
281	6	0.8	127	3	US-09-134-001C-2936	Sequence 2936, Ap	354	6	0.8	177	4	US-09-650-324A-20	Sequence 20, Appl
282	6	0.8	127	3	US-09-809-739-10	Sequence 2937, Ap	355	6	0.8	177	4	US-09-583-110-3692	Sequence 3692, Ap
283	6	0.8	127	3	US-09-809-739-10	Sequence 10, Appl	356	6	0.8	178	4	US-09-270-767-31704	Sequence 31704, A
284	6	0.8	128	3	US-09-134-001C-2881	Sequence 2881, Ap	357	6	0.8	178	4	US-09-270-767-46921	Sequence 46921, A
285	6	0.8	128	3	US-09-134-000C-3953	Sequence 3953, Ap	358	6	0.8	179	3	US-09-612-126-11	Sequence 11, Appl
286	6	0.8	128	4	US-09-513-999C-8084	Sequence 8084, Ap	359	6	0.8	179	4	US-09-248-796A-21646	Sequence 21646, A
287	6	0.8	129	4	US-09-513-999C-5740	Sequence 5740, Ap	360	6	0.8	180	4	US-09-543-681A-7669	Sequence 7669, Ap
288	6	0.8	130	4	US-09-902-540-11601	Sequence 11601, A	361	6	0.8	180	4	US-09-270-767-37167	Sequence 37167, A
289	6	0.8	132	4	US-09-252-991A-29618	Sequence 29618, A	362	6	0.8	180	4	US-09-270-767-37167	Sequence 52384, A
290	6	0.8	132	4	US-09-311-021-162	Sequence 162, App	363	6	0.8	180	4	US-09-878-281A-14	Sequence 14, Appl
291	6	0.8	133	4	US-09-252-991A-32343	Sequence 32343, A	364	6	0.8	180	4	US-09-878-281A-16	Sequence 16, Appl
292	6	0.8	134	3	US-09-134-001C-3817	Sequence 3817, Ap	365	6	0.8	180	4	US-09-878-281A-18	Sequence 18, Appl
293	6	0.8	134	4	US-09-252-991A-24835	Sequence 24835, A	366	6	0.8	180	4	US-09-878-281A-20	Sequence 20, Appl
294	6	0.8	134	4	US-09-513-999C-8169	Sequence 8169, Ap	367	6	0.8	180	4	US-09-878-281A-22	Sequence 22, Appl
295	6	0.8	136	4	US-09-252-991A-24892	Sequence 24892, A	368	6	0.8	180	4	US-09-878-281A-24	Sequence 24, Appl
296	6	0.8	138	3	US-08-630-172-1	Sequence 1, Appl	369	6	0.8	180	4	US-09-878-281A-26	Sequence 26, Appl
297	6	0.8	138	3	US-09-375-419-1	Sequence 1, Appl	370	6	0.8	180	4	US-09-878-281A-28	Sequence 28, Appl
298	6	0.8	139	3	US-08-444-818-174	Sequence 144, App	371	6	0.8	180	4	US-09-502-540-10368	Sequence 10368, A
299	6	0.8	139	4	US-09-270-767-44805	Sequence 44805, A	372	6	0.8	181	4	US-09-252-991A-17818	Sequence 17818, A
300	6	0.8	140	4	US-09-252-991A-31623	Sequence 31623, A	373	6	0.8	181	4	US-09-134-000C-4633	Sequence 4633, Ap
301	6	0.8	140	4	US-09-270-767-11800	Sequence 11800, A	374	6	0.8	181	4	US-09-640-211A-1033	Sequence 1033, Ap
302	6	0.8	141	3	US-08-906-769-135	Sequence 135, App	375	6	0.8	183	4	US-09-621-976-4025	Sequence 4025, Ap
303	6	0.8	141	3	US-08-906-616-135	Sequence 135, App	376	6	0.8	183	4	US-09-976-451-2	Sequence 2, Appl
304	6	0.8	141	3	US-08-639-075A-135	Sequence 135, App	377	6	0.8	184	3	US-08-907-800A-2	Sequence 2, Appl
305	6	0.8	141	3	US-09-012-431-135	Sequence 135, App	378	6	0.8	184	3	US-08-969-317-7	Sequence 2, Appl
306	6	0.8	141	3	US-09-012-692-135	Sequence 135, App	379	6	0.8	184	4	US-09-270-767-4433	Sequence 4433, A
307	6	0.8	141	3	US-08-906-613-135	Sequence 135, App	380	6	0.8	184	4	US-09-107-433-4306	Sequence 4306, Ap
308	6	0.8	141	4	US-09-270-767-60471	Sequence 60471, A	381	6	0.8	185	3	US-08-975-762-11	Sequence 11, Appl
309	6	0.8	143	4	US-09-538-092-237	Sequence 237, App	382	6	0.8	185	3	US-08-821-324-11	Sequence 11, Appl
310	6	0.8	144	3	US-09-199-637A-17	Sequence 17, Appl	383	6	0.8	185	3	US-09-295-028-11	Sequence 11, Appl
311	6	0.8	144	3	US-09-134-001C-4218	Sequence 4218, Ap	384	6	0.8	185	3	US-09-106-882-11	Sequence 11, Appl
312	6	0.8	145	4	US-09-252-991A-21532	Sequence 21532, A	385	6	0.8	185	4	US-09-159-469-11	Sequence 11, Appl
313	6	0.8	146	4	US-09-252-991A-18563	Sequence 18563, A	386	6	0.8	185	4	US-09-593-542-11	Sequence 11, Appl
314	6	0.8	146	4	US-09-270-767-39779	Sequence 39779, A	387	6	0.8	186	3	US-09-612-126-8	Sequence 8, Appl
315	6	0.8	146	4	US-09-270-767-54996	Sequence 54996, A	388	6	0.8	187	4	US-08-635-886C-207	Sequence 207, App
316	6	0.8	146	4	US-09-248-796A-26332	Sequence 26332, A	389	6	0.8	187	4	US-08-635-886C-208	Sequence 208, App
317	6	0.8	149	2	US-08-039-364-18	Sequence 18, Appl	390	6	0.8	187	4	US-08-635-886C-209	Sequence 209, App
318	6	0.8	149	3	US-09-158-710-18	Sequence 18, Appl	391	6	0.8	187	4	US-08-974-690C-207	Sequence 207, App
319	6	0.8	150	4	US-09-252-991A-17720	Sequence 17720, A	392	6	0.8	187	4	US-08-974-690C-208	Sequence 208, App

393	6	0.8	187	4	US-08-974-690C-209	Sequence 209, App	466	6	0.8	209	4	US-09-693-542-71	Sequence 71, Appl
394	6	0.8	187	4	US-09-248-796A-14589	Sequence 14589, A	467	6	0.8	209	4	US-09-438-185A-949	Sequence 949, App
395	6	0.8	187	4	US-09-248-796A-16267	Sequence 16267, A	468	6	0.8	210	3	US-09-162-184-33	Sequence 33, Appl
396	6	0.8	188	4	US-09-248-796A-18153	Sequence 18153, A	469	6	0.8	210	3	US-09-489-777E-33	Sequence 33, Appl
397	6	0.8	188	4	US-10-101-464A-540	Sequence 540, App	470	6	0.8	210	4	US-09-252-991A-27171	Sequence 27171, A
398	6	0.8	189	4	US-09-270-767-46721	Sequence 46721, A	471	6	0.8	211	4	US-09-252-991A-28553	Sequence 28553, A
399	6	0.8	191	2	US-08-290-665A-187	Sequence 187, App	472	6	0.8	211	4	US-09-949-016-9913	Sequence 9913, Ap
400	6	0.8	191	2	US-08-290-665A-189	Sequence 189, App	473	6	0.8	212	3	US-08-861-774E-22	Sequence 22, Appl
401	6	0.8	191	2	US-08-290-665A-190	Sequence 190, App	474	6	0.8	212	3	US-08-861-774E-34	Sequence 34, Appl
402	6	0.8	191	5	PCT-US95-10398-187	Sequence 187, App	475	6	0.8	212	4	US-09-538-092-500	Sequence 500, App
403	6	0.8	191	5	PCT-US95-10398-189	Sequence 189, App	476	6	0.8	213	3	US-08-861-774E-60	Sequence 60, Appl
404	6	0.8	191	5	PCT-US95-10398-190	Sequence 190, App	477	6	0.8	213	3	US-08-861-774E-64	Sequence 64, Appl
405	6	0.8	192	4	US-09-196-452A-276	Sequence 276, App	478	6	0.8	213	3	US-08-861-774E-72	Sequence 72, Appl
406	6	0.8	192	4	US-09-248-796A-22528	Sequence 22528, A	479	6	0.8	213	4	US-09-902-540-13705	Sequence 13705, A
407	6	0.8	192	4	US-09-438-185A-266	Sequence 266, App	480	6	0.8	214	3	US-08-861-774E-30	Sequence 30, Appl
408	6	0.8	193	1	US-08-248-466B-14	Sequence 14, Appl	481	6	0.8	214	3	US-08-861-774E-32	Sequence 32, Appl
409	6	0.8	193	3	US-09-041-889-5	Sequence 5, Appli	482	6	0.8	214	3	US-08-861-774E-44	Sequence 44, Appl
410	6	0.8	193	3	US-08-837-058-5	Sequence 5, Appli	483	6	0.8	214	3	US-08-861-774E-48	Sequence 48, Appl
411	6	0.8	193	4	US-09-417-264-5	Sequence 5, Appli	484	6	0.8	214	3	US-08-861-774E-54	Sequence 54, Appl
412	6	0.8	193	4	US-08-635-886C-210	Sequence 210, App	485	6	0.8	214	3	US-08-861-774E-66	Sequence 66, Appl
413	6	0.8	193	4	US-08-974-690C-210	Sequence 210, App	486	6	0.8	214	3	US-08-861-774E-76	Sequence 76, Appl
414	6	0.8	194	3	US-09-516-914-9	Sequence 9, Appli	487	6	0.8	214	3	US-08-861-774E-78	Sequence 78, Appl
415	6	0.8	194	4	US-09-489-039A-8286	Sequence 8286, Ap	488	6	0.8	214	5	PCT-US96-08950-2	Sequence 2, Appli
416	6	0.8	194	4	US-09-248-796A-16995	Sequence 16995, A	489	6	0.8	214	5	PCT-US96-09127-2	Sequence 2, Appli
417	6	0.8	196	3	US-08-981-392-35	Sequence 35, Appl	490	6	0.8	215	1	US-08-266-451B-27	Sequence 27, Appl
418	6	0.8	196	4	US-09-908-322-35	Sequence 35, Appl	491	6	0.8	215	2	US-08-748-725-47	Sequence 47, Appl
419	6	0.8	198	4	US-09-252-991A-22691	Sequence 22691, A	492	6	0.8	215	3	US-08-861-774E-40	Sequence 40, Appl
420	6	0.8	199	4	US-09-252-991A-31135	Sequence 31135, A	493	6	0.8	215	4	US-09-270-767-15086	Sequence 4086, A
421	6	0.8	200	4	US-09-101-272G-73	Sequence 73, Appl	494	6	0.8	216	3	US-08-861-774E-58	Sequence 58, Appl
422	6	0.8	200	4	US-09-252-991A-28054	Sequence 28054, A	495	6	0.8	216	3	US-08-861-774E-62	Sequence 62, Appl
423	6	0.8	200	4	US-09-489-039A-1526	Sequence 7526, App	496	6	0.8	218	3	US-08-861-774E-46	Sequence 46, Appl
424	6	0.8	201	3	US-08-679-493A-190	Sequence 190, App	497	6	0.8	218	3	US-08-861-774E-50	Sequence 50, Appl
425	6	0.8	202	4	US-09-252-991A-26505	Sequence 26505, A	498	6	0.8	218	4	US-09-134-000C-3898	Sequence 3898, Ap
426	6	0.8	202	4	US-09-252-991A-27017	Sequence 27017, A	499	6	0.8	218	4	US-09-828-303-23	Sequence 23, Appl
427	6	0.8	203	2	US-08-284-391B-31	Sequence 31, Appl	500	6	0.8	219	3	US-08-861-774E-70	Sequence 70, Appl
428	6	0.8	203	3	US-09-218-950-31	Sequence 31, Appl	501	6	0.8	219	4	US-09-252-991A-28228	Sequence 28228, A
429	6	0.8	203	4	US-09-543-681A-4329	Sequence 4329, Ap	502	6	0.8	219	4	US-09-198-452A-634	Sequence 634, App
430	6	0.8	203	4	US-08-394-388A-537	Sequence 537, Appl	503	6	0.8	219	4	US-09-270-767-33084	Sequence 33084, A
431	6	0.8	203	4	US-10-101-464A-537	Sequence 537, App	504	6	0.8	219	4	US-09-270-767-8301	Sequence 8301, A
432	6	0.8	203	4	US-10-101-464A-658	Sequence 658, App	505	6	0.8	219	4	US-09-438-185A-593	Sequence 593, App
433	6	0.8	204	4	US-09-252-991A-29225	Sequence 29225, A	506	6	0.8	221	4	US-09-874-926-2	Sequence 2, Appl
434	6	0.8	204	4	US-09-543-681A-8020	Sequence 8020, Ap	507	6	0.8	222	4	US-09-252-991A-24147	Sequence 24147, A
435	6	0.8	205	3	US-09-134-001C-4766	Sequence 4766, Ap	508	6	0.8	223	4	US-09-198-452A-683	Sequence 19065, A
436	6	0.8	205	4	US-09-252-991A-29334	Sequence 29334, A	509	6	0.8	224	4	US-09-198-452A-683	Sequence 683, App
437	6	0.8	205	4	US-09-134-000C-3913	Sequence 3913, Ap	510	6	0.8	229	3	US-08-630-915A-221	Sequence 221, App
438	6	0.8	206	3	US-08-679-493A-75	Sequence 75, Appl	511	6	0.8	229	4	US-09-879-957-221	Sequence 221, App
439	6	0.8	206	4	US-09-543-681A-4763	Sequence 4763, Ap	512	6	0.8	229	4	US-09-438-185A-648	Sequence 648, App
440	6	0.8	206	4	US-09-270-767-35977	Sequence 35977, A	513	6	0.8	230	3	US-09-516-143A-6	Sequence 6, Appli
441	6	0.8	206	4	US-09-270-767-51194	Sequence 51194, A	514	6	0.8	230	4	US-09-984-205-6	Sequence 6, Appli
442	6	0.8	207	1	US-07-935-309-2	Sequence 1020, Ap	515	6	0.8	231	4	US-09-543-681A-6357	Sequence 6357, Ap
443	6	0.8	208	1	US-08-884-682-1	Sequence 2, Appli	516	6	0.8	233	3	US-09-069-023-16	Sequence 36, Appl
444	6	0.8	208	1	US-08-039-364-2	Sequence 1, Appli	517	6	0.8	233	4	US-09-270-767-16462	Sequence 36462, A
445	6	0.8	208	2	US-08-766-551-9	Sequence 9, Appli	518	6	0.8	233	4	US-09-270-767-51679	Sequence 51679, A
446	6	0.8	208	2	US-08-766-551-9	Sequence 9, Appli	519	6	0.8	234	3	US-08-861-774E-52	Sequence 52, Appl
447	6	0.8	208	2	US-09-036-082-1	Sequence 1, Appli	520	6	0.8	235	1	US-08-287-959-8	Sequence 8, Appl
448	6	0.8	208	2	US-08-718-904-5	Sequence 5, Appli	521	6	0.8	235	4	US-09-107-532A-6979	Sequence 6979, Ap
449	6	0.8	208	3	US-08-718-904-7	Sequence 7, Appli	522	6	0.8	235	4	US-09-583-110-1199	Sequence 4199, Ap
450	6	0.8	208	3	US-08-612-973-30	Sequence 30, Appl	523	6	0.8	235	4	US-09-107-433-1326	Sequence 3326, Ap
451	6	0.8	208	3	US-09-181-974-2	Sequence 2, Appli	524	6	0.8	236	4	US-09-134-000C-4896	Sequence 4896, Ap
452	6	0.8	208	3	US-09-158-710-2	Sequence 2, Appli	525	6	0.8	237	3	US-08-861-774E-68	Sequence 68, Appl
453	6	0.8	208	3	US-08-927-597-30	Sequence 30, Appl	526	6	0.8	238	4	US-09-252-991A-29406	Sequence 29406, A
454	6	0.8	208	4	US-09-518-950-2	Sequence 2, Appli	527	6	0.8	238	4	US-09-902-540-13083	Sequence 13083, A
455	6	0.8	208	4	US-09-449-249-5	Sequence 5, Appli	528	6	0.8	239	3	US-09-004-731-44	Sequence 44, Appl
456	6	0.8	208	4	US-09-449-249-7	Sequence 7, Appli	529	6	0.8	239	3	US-08-749-699-44	Sequence 44, Appl
457	6	0.8	208	4	US-09-252-991A-22641	Sequence 22641, A	530	6	0.8	239	3	US-08-679-493A-76	Sequence 76, Appl
458	6	0.8	208	4	US-10-138-158-18	Sequence 18, Appl	531	6	0.8	239	4	US-09-004-729-44	Sequence 44, Appl
459	6	0.8	208	4	US-09-949-016-6149	Sequence 6149, Ap	532	6	0.8	239	4	US-09-328-352-7328	Sequence 7328, Ap
460	6	0.8	209	3	US-08-975-762-71	Sequence 71, Appl	533	6	0.8	240	4	US-09-328-352-7253	Sequence 7253, Ap
461	6	0.8	209	3	US-09-295-028-71	Sequence 71, Appl	534	6	0.8	242	3	US-09-004-731-61	Sequence 41, Appl
462	6	0.8	209	3	US-09-106-582-71	Sequence 71, Appl	535	6	0.8	242	3	US-09-032-215-47	Sequence 47, Appl
463	6	0.8	209	3	US-09-311-311C-20	Sequence 20, Appl	536	6	0.8	242	3	US-08-749-699-41	Sequence 41, Appl
464	6	0.8	209	4	US-09-252-991A-29571	Sequence 29571, A	537	6	0.8	242	4	US-09-004-729-41	Sequence 41, Appl
465	6	0.8	209	4	US-09-159-469-71	Sequence 71, Appl	538	6	0.8	242	4	US-09-252-991A-19021	Sequence 19021, A

539	6	0.8	242	4	US-09-107-532A-6244	Sequence 6244, Ap	612	6	0.8	281	4	US-09-270-767-43839	Sequence 43839, A
540	6	0.8	242	4	US-09-583-110-3522	Sequence 3522, Ap	613	6	0.8	282	4	US-09-252-991A-25948	Sequence 25948, A
541	6	0.8	243	4	US-09-543-681A-7356	Sequence 7356, Ap	614	6	0.8	284	4	US-08-976-063E-2	Sequence 2, Appl1
542	6	0.8	244	4	US-09-461-325-463	Sequence 463, App	615	6	0.8	285	3	US-09-027-137-3	Sequence 3, Appl1
543	6	0.8	244	4	US-09-252-991A-29762	Sequence 29762, A	616	6	0.8	285	3	US-09-344-441-3	Sequence 3, Appl1
544	6	0.8	244	4	US-10-012-542-463	Sequence 463, App	617	6	0.8	285	4	US-09-248-796A-16474	Sequence 16474, A
545	6	0.8	244	4	US-10-115-123-463	Sequence 463, App	618	6	0.8	285	4	US-09-248-796A-20009	Sequence 20009, A
546	6	0.8	245	4	US-08-956-171E-5222	Sequence 5222, Ap	619	6	0.8	287	3	US-08-549-515-10	Sequence 10, Appl
547	6	0.8	245	4	US-08-781-986A-5222	Sequence 5222, Ap	620	6	0.8	288	4	US-09-489-039A-8939	Sequence 8939, Ap
548	6	0.8	245	4	US-09-640-211A-833	Sequence 833, App	621	6	0.8	288	4	US-09-248-796A-16494	Sequence 16494, A
549	6	0.8	248	1	US-08-266-451B-2	Sequence 2, Appl1	622	6	0.8	289	4	US-09-071-035-12	Sequence 71, Appl
550	6	0.8	248	2	US-08-748-725-2	Sequence 2, Appl1	623	6	0.8	289	4	US-09-252-991A-22483	Sequence 22483, A
551	6	0.8	248	3	US-08-944-483-71	Sequence 71, Appl	624	6	0.8	292	3	US-09-027-137-1	Sequence 1, Appl1
552	6	0.8	248	4	US-09-252-991A-17358	Sequence 17358, A	625	6	0.8	292	3	US-09-344-441-1	Sequence 1, Appl1
553	6	0.8	249	3	US-09-010-809-21	Sequence 21, Appl	626	6	0.8	292	4	US-09-348-352-6642	Sequence 6642, Ap
554	6	0.8	250	3	US-09-010-809-3	Sequence 3, Appl1	627	6	0.8	292	4	US-09-543-681A-7918	Sequence 7918, Ap
555	6	0.8	250	4	US-09-538-092-355	Sequence 355, App	628	6	0.8	295	4	US-09-114-000C-3737	Sequence 3737, Ap
556	6	0.8	251	3	US-08-630-915A-8	Sequence 8, Appl1	629	6	0.8	295	6	5223394-9	Patent No. 5223394
557	6	0.8	251	4	US-09-270-767-44693	Sequence 44693, A	630	6	0.8	295	6	5223394-9	Patent No. 5223394
558	6	0.8	251	4	US-09-879-957-8	Sequence 8, Appl1	631	6	0.8	296	4	US-09-252-991A-17385	Sequence 17385, A
559	6	0.8	252	3	US-08-944-483-72	Sequence 72, Appl	632	6	0.8	296	4	US-09-949-016-9495	Sequence 9495, Ap
560	6	0.8	253	2	US-09-027-337-8	Sequence 8, Appl1	633	6	0.8	297	4	US-09-543-681A-7800	Sequence 7800, Ap
561	6	0.8	253	3	US-08-975-762-52	Sequence 52, Appl	634	6	0.8	298	4	US-09-252-991A-25360	Sequence 25360, A
562	6	0.8	253	3	US-08-944-483-73	Sequence 73, Appl	635	6	0.8	298	4	US-09-270-767-41439	Sequence 41439, A
563	6	0.8	253	3	US-09-295-028-52	Sequence 52, Appl	636	6	0.8	299	4	US-09-270-767-41683	Sequence 41683, A
564	6	0.8	253	3	US-09-106-582-52	Sequence 52, Appl	637	6	0.8	300	1	US-08-148-310-1	Sequence 1, Appl1
565	6	0.8	253	4	US-09-644-600-8	Sequence 8, Appl1	638	6	0.8	300	1	US-08-448-937A-1	Sequence 1, Appl1
566	6	0.8	253	4	US-09-159-469-52	Sequence 52, Appl	639	6	0.8	300	4	US-09-252-991A-20115	Sequence 20115, A
567	6	0.8	253	4	US-09-489-039A-13739	Sequence 13739, A	640	6	0.8	301	4	US-09-252-991A-25396	Sequence 25396, A
568	6	0.8	253	4	US-09-654-600A-8	Sequence 8, Appl1	641	6	0.8	301	4	US-09-114-000C-6014	Sequence 6014, Ap
569	6	0.8	254	4	US-09-693-542-52	Sequence 52, Appl	642	6	0.8	302	4	US-09-252-991A-21331	Sequence 21331, A
570	6	0.8	254	2	US-08-560-098A-49	Sequence 49, Appl	643	6	0.8	302	4	US-09-328-352-4508	Sequence 4508, Ap
571	6	0.8	254	4	US-09-270-767-46094	Sequence 46094, A	644	6	0.8	302	4	US-09-540-236-2119	Sequence 2119, Ap
572	6	0.8	254	4	US-09-248-796A-19272	Sequence 19272, A	645	6	0.8	303	4	US-09-107-532A-5585	Sequence 5585, Ap
573	6	0.8	255	3	US-09-612-126-1	Sequence 1, Appl1	646	6	0.8	303	4	US-09-949-016-10112	Sequence 10112, A
574	6	0.8	256	3	US-09-230-637-29	Sequence 29, Appl	647	6	0.8	304	4	US-09-902-540-11322	Sequence 11322, A
575	6	0.8	256	4	US-09-489-039A-8774	Sequence 8774, Ap	648	6	0.8	304	4	US-09-489-039A-9424	Sequence 9424, Ap
576	6	0.8	257	2	US-08-467-265-16	Sequence 16, Appl	649	6	0.8	304	4	US-09-902-540-15483	Sequence 15483, A
577	6	0.8	257	3	US-08-467-265-16	Sequence 16, Appl	650	6	0.8	306	2	US-08-560-098A-45	Sequence 45, Appl
578	6	0.8	257	3	US-09-407-891-16	Sequence 16, Appl	651	6	0.8	306	4	US-09-252-991A-27054	Sequence 27054, A
579	6	0.8	257	4	US-09-375-907-5	Sequence 5, Appl1	652	6	0.8	306	4	US-09-328-352-5398	Sequence 5398, Ap
580	6	0.8	257	4	US-09-828-447-14	Sequence 14, Appl	653	6	0.8	306	4	US-09-602-787A-572	Sequence 572, App
581	6	0.8	258	4	US-09-248-796A-24697	Sequence 24697, A	654	6	0.8	307	4	US-09-393-634-53	Sequence 634, Appl
582	6	0.8	258	3	US-09-227-357-198	Sequence 198, App	655	6	0.8	308	4	US-09-107-532A-6023	Sequence 6023, Ap
583	6	0.8	258	4	US-09-252-991A-32929	Sequence 32929, A	656	6	0.8	308	4	US-09-248-796A-18392	Sequence 18392, A
584	6	0.8	261	4	US-09-252-991A-29007	Sequence 29007, A	657	6	0.8	309	2	US-08-949-016A-6	Sequence 6, Appl1
585	6	0.8	262	4	US-09-270-767-45003	Sequence 45003, A	658	6	0.8	310	3	US-08-477-460B-6	Sequence 6, Appl1
586	6	0.8	263	4	US-09-270-767-42374	Sequence 42374, A	659	6	0.8	310	3	US-08-379-516-6	Sequence 6, Appl1
587	6	0.8	263	4	US-09-270-767-47591	Sequence 47591, A	660	6	0.8	310	3	US-09-329-916-6	Sequence 6, Appl1
588	6	0.8	264	2	US-08-484-905-120	Sequence 120, App	661	6	0.8	310	3	US-08-485-372A-6	Sequence 6, Appl1
589	6	0.8	264	3	US-08-481-985B-120	Sequence 120, App	662	6	0.8	310	3	US-09-409-006A-6	Sequence 6, Appl1
590	6	0.8	264	3	US-08-370-476-120	Sequence 120, App	663	6	0.8	310	4	US-08-484-681-6	Sequence 6, Appl1
591	6	0.8	270	4	US-09-949-016-11038	Sequence 11038, A	664	6	0.8	310	4	US-09-766-995-5	Sequence 6, Appl1
592	6	0.8	272	4	US-09-252-991A-27911	Sequence 27911, A	665	6	0.8	310	5	PCT-US93-074422-6	Sequence 6, Appl1
593	6	0.8	274	4	US-09-270-767-40695	Sequence 40695, A	666	6	0.8	311	4	US-09-543-681A-5602	Sequence 5602, Ap
594	6	0.8	274	4	US-09-270-767-55911	Sequence 55911, A	667	6	0.8	311	4	US-09-489-039A-13013	Sequence 13013, A
595	6	0.8	276	3	US-08-953-326-18	Sequence 18, Appl	668	6	0.8	312	4	US-09-071-035-70	Sequence 70, Appl
596	6	0.8	276	4	US-09-553-662-18	Sequence 18, Appl	669	6	0.8	312	4	US-09-351-150A-11	Sequence 11, Appl
597	6	0.8	276	4	US-10-062-994-18	Sequence 18, Appl	670	6	0.8	312	4	US-09-539-960B-96	Sequence 96, Appl
598	6	0.8	276	4	US-09-880-503-5	Sequence 5, Appl1	671	6	0.8	313	4	US-09-148-545-233	Sequence 233, App
599	6	0.8	277	4	US-09-252-991A-17567	Sequence 17567, A	672	6	0.8	313	4	US-09-248-796A-17016	Sequence 17016, A
600	6	0.8	278	4	US-09-252-991A-28712	Sequence 28712, A	673	6	0.8	315	4	US-09-270-767-42766	Sequence 42766, A
601	6	0.8	278	4	US-09-328-352-5824	Sequence 5824, Ap	674	6	0.8	315	4	US-09-270-767-43483	Sequence 43483, A
602	6	0.8	278	4	US-09-902-540-11962	Sequence 11962, A	675	6	0.8	315	4	US-09-603-208A-212	Sequence 212, App
603	6	0.8	280	4	US-09-107-532A-6088	Sequence 6088, Ap	676	6	0.8	317	4	US-09-583-110-5279	Sequence 5279, Ap
604	6	0.8	280	4	US-09-270-767-40154	Sequence 40154, A	677	6	0.8	317	4	US-09-270-767-42650	Sequence 42650, A
605	6	0.8	280	4	US-09-270-767-55370	Sequence 55370, A	678	6	0.8	318	4	US-09-252-991A-25243	Sequence 25243, A
606	6	0.8	280	4	US-10-101-464A-511	Sequence 511, App	679	6	0.8	318	4	US-09-710-279-976	Sequence 976, App
607	6	0.8	281	3	US-09-660-587-9	Sequence 9, Appl	680	6	0.8	318	6	5223394-11	Patent No. 5223394
608	6	0.8	281	4	US-09-261-358A-9	Sequence 9, Appl1	681	6	0.8	318	6	5223394-11	Patent No. 5223394
609	6	0.8	281	4	US-09-201-458-5	Sequence 5, Appl1	682	6	0.8	320	3	US-09-114-001C-3552	Sequence 3552, Ap
610	6	0.8	281	4	US-09-314-701-2	Sequence 2, Appl1	683	6	0.8	320	3	US-09-114-001C-3823	Sequence 3823, Ap
611	6	0.8	281	4	US-09-811-007A-9	Sequence 9, Appl1	684	6	0.8	320	4	US-09-489-039A-10349	Sequence 10349, A

685	6	0.8	320	4	US-09-489-039A-13881	Sequence 13881, A	758	6	0.8	359	4	US-09-583-9110-3909	Sequence 13909, Ap
686	6	0.8	320	4	US-09-134-000C-5021	Sequence 5021, Ap	759	6	0.8	362	4	US-09-252-991A-18894	Sequence 18894, A
687	6	0.8	322	4	US-09-252-991A-29347	Sequence 29347, A	760	6	0.8	363	4	US-09-107-433-3869	Sequence 3869, Ap
688	6	0.8	322	4	US-09-949-016-8007	Sequence 8007, Ap	761	6	0.8	364	4	US-09-252-991A-19037	Sequence 19037, A
689	6	0.8	323	4	US-09-270-767-61011	Sequence 61011, A	762	6	0.8	364	4	US-09-438-185A-815	Sequence 815, Ap
690	6	0.8	323	4	US-09-880-503-7	Sequence 7, Ap	763	6	0.8	365	1	US-08-093-741-83	Sequence 83, Ap
691	6	0.8	324	4	US-09-270-767-44986	Sequence 44986, A	764	6	0.8	365	1	US-08-720-012-83	Sequence 83, Ap
692	6	0.8	325	4	US-08-311-731A-249	Sequence 249, Ap	765	6	0.8	365	3	US-09-211-529-3	Sequence 3, Ap
693	6	0.8	325	4	US-09-248-796A-14929	Sequence 14929, A	766	6	0.8	365	3	US-08-977-916-3	Sequence 3, Ap
694	6	0.8	326	3	US-09-066-046-29	Sequence 29, Ap	767	6	0.8	366	4	US-09-252-991A-24466	Sequence 24466, A
695	6	0.8	326	3	US-09-066-047-15	Sequence 15, Ap	768	6	0.8	366	4	US-09-902-540-15482	Sequence 15482, A
696	6	0.8	326	3	US-09-411-977-3	Sequence 3, Ap	769	6	0.8	367	3	US-08-895-707-6	Sequence 6, Ap
697	6	0.8	326	3	US-09-543-681A-7709	Sequence 7709, Ap	770	6	0.8	367	4	US-09-252-991A-17240	Sequence 17240, A
698	6	0.8	326	4	US-10-057-951-3	Sequence 3, Ap	771	6	0.8	367	4	US-09-328-352-7662	Sequence 7662, Ap
699	6	0.8	327	4	US-09-252-991A-33067	Sequence 33067, A	772	6	0.8	369	4	US-09-248-796A-14930	Sequence 14930, A
700	6	0.8	327	4	US-09-107-433-3331	Sequence 3331, Ap	773	6	0.8	370	4	US-09-902-540-9972	Sequence 9972, Ap
701	6	0.8	328	4	US-09-248-796A-20663	Sequence 20663, A	774	6	0.8	372	4	US-09-252-991A-28586	Sequence 28586, A
702	6	0.8	330	4	US-09-710-279-2476	Sequence 2476, Ap	775	6	0.8	372	4	US-09-973-963-4	Sequence 4, Ap
703	6	0.8	330	4	US-09-710-279-2734	Sequence 2734, Ap	776	6	0.8	372	4	US-09-949-016-6463	Sequence 6463, Ap
704	6	0.8	331	2	US-08-560-098A-46	Sequence 2734, Ap	777	6	0.8	373	4	US-09-404-296B-4	Sequence 4, Ap
705	6	0.8	332	3	US-09-134-001C-4323	Sequence 4323, Ap	778	6	0.8	374	2	US-08-820-170A-25	Sequence 25, Ap
706	6	0.8	333	4	US-09-328-352-7516	Sequence 7516, Ap	779	6	0.8	374	3	US-09-055-699-25	Sequence 25, Ap
707	6	0.8	334	3	US-09-218-363-11	Sequence 11, Ap	780	6	0.8	374	3	US-09-273-565-25	Sequence 25, Ap
708	6	0.8	336	1	US-07-904-073-2	Sequence 2, Ap	781	6	0.8	374	3	US-09-565-538-25	Sequence 25, Ap
709	6	0.8	336	1	US-07-904-071-2	Sequence 2, Ap	782	6	0.8	374	3	US-09-651-468-25	Sequence 25, Ap
710	6	0.8	336	1	US-08-442-043A-16	Sequence 16, Ap	783	6	0.8	374	4	US-09-976-165-25	Sequence 25, Ap
711	6	0.8	336	4	US-08-441-893A-16	Sequence 16, Ap	784	6	0.8	374	4	US-09-227-853A-3	Sequence 3, Ap
712	6	0.8	337	4	US-09-252-991A-26757	Sequence 26757, A	785	6	0.8	374	4	US-09-540-236-2230	Sequence 2230, Ap
713	6	0.8	337	4	US-09-252-991A-30261	Sequence 30261, A	786	6	0.8	374	5	FCT-US95-06385-2	Sequence 2, Ap
714	6	0.8	338	4	US-09-107-532A-5819	Sequence 5819, Ap	787	6	0.8	375	3	US-08-872-979-3	Sequence 3, Ap
715	6	0.8	340	4	US-09-543-681A-7850	Sequence 7850, Ap	788	6	0.8	375	4	US-09-328-352-6191	Sequence 6191, Ap
716	6	0.8	340	4	US-09-816-248-15	Sequence 15, Ap	789	6	0.8	375	4	US-09-489-039A-11560	Sequence 11560, A
717	6	0.8	341	4	US-09-543-681A-7713	Sequence 4713, Ap	790	6	0.8	377	4	US-09-679-279-3	Sequence 3, Ap
718	6	0.8	341	4	US-09-248-796A-17051	Sequence 17051, A	791	6	0.8	377	4	US-09-489-039A-12546	Sequence 12546, A
719	6	0.8	341	4	US-09-902-540-13921	Sequence 13921, A	792	6	0.8	378	3	US-09-553-498-10	Sequence 10, Ap
720	6	0.8	342	4	US-09-252-991A-30257	Sequence 30257, A	793	6	0.8	378	4	US-09-618-869-10	Sequence 10, Ap
721	6	0.8	342	4	US-09-902-540-10704	Sequence 10704, A	794	6	0.8	378	4	US-09-673-395A-618	Sequence 618, Ap
722	6	0.8	343	4	US-09-252-991A-22307	Sequence 22307, A	795	6	0.8	379	4	US-09-252-991A-17472	Sequence 17472, A
723	6	0.8	345	3	US-09-027-900-11	Sequence 11, Ap	796	6	0.8	381	4	US-09-673-395A-441	Sequence 441, Ap
724	6	0.8	345	4	US-09-489-039A-10740	Sequence 10740, A	797	6	0.8	381	4	US-09-270-767-61813	Sequence 46183, A
725	6	0.8	346	4	US-09-252-991A-21487	Sequence 21487, A	798	6	0.8	383	1	US-08-486-037B-2	Sequence 2, Ap
726	6	0.8	347	2	US-08-811-949-1	Sequence 1, Ap	799	6	0.8	383	2	US-08-558-269-6	Sequence 6, Ap
727	6	0.8	347	4	US-09-636-215-590	Sequence 590, Ap	800	6	0.8	383	2	US-09-410-882-6	Sequence 6, Ap
728	6	0.8	347	4	US-09-685-166A-590	Sequence 590, Ap	801	6	0.8	385	3	US-09-071-224-19	Sequence 19, Ap
729	6	0.8	347	4	US-09-679-426-590	Sequence 590, Ap	802	6	0.8	386	3	US-08-895-707-7	Sequence 7, Ap
730	6	0.8	347	4	US-09-759-143-590	Sequence 590, Ap	803	6	0.8	386	3	US-09-045-284A-2	Sequence 2, Ap
731	6	0.8	347	4	US-09-651-236-590	Sequence 590, Ap	804	6	0.8	386	3	US-09-190-911-1	Sequence 1, Ap
732	6	0.8	348	4	US-09-360-376-13	Sequence 13, Ap	805	6	0.8	386	4	US-09-786-240-11	Sequence 11, Ap
733	6	0.8	349	4	US-09-489-039A-7582	Sequence 7582, Ap	806	6	0.8	386	4	US-09-489-039A-7410	Sequence 7410, Ap
734	6	0.8	351	1	US-08-324-483-2	Sequence 2, Ap	807	6	0.8	386	4	US-09-248-796A-15757	Sequence 15757, A
735	6	0.8	351	4	US-09-902-540-12944	Sequence 12944, A	808	6	0.8	389	2	US-08-811-949-67	Sequence 67, Ap
736	6	0.8	354	2	US-08-811-949-61	Sequence 61, Ap	809	6	0.8	389	3	US-09-071-224-47	Sequence 27, Ap
737	6	0.8	355	1	US-08-137-116-1	Sequence 1, Ap	810	6	0.8	389	4	US-09-107-532A-6185	Sequence 6185, Ap
738	6	0.8	355	1	US-08-217-618-1	Sequence 1, Ap	811	6	0.8	390	4	US-09-252-991A-26543	Sequence 26543, A
739	6	0.8	355	1	US-08-427-640-2	Sequence 2, Ap	812	6	0.8	391	4	US-09-543-681A-7025	Sequence 7025, Ap
740	6	0.8	355	1	US-08-427-640-6	Sequence 6, Ap	813	6	0.8	392	1	US-08-706-539-9	Sequence 9, Ap
741	6	0.8	355	1	US-08-217-617A-1	Sequence 1, Ap	814	6	0.8	392	3	US-09-027-007-9	Sequence 9, Ap
742	6	0.8	355	1	US-08-217-616-1	Sequence 1, Ap	815	6	0.8	392	4	US-09-710-279-7794	Sequence 2794, Ap
743	6	0.8	355	2	US-08-811-949-45	Sequence 45, Ap	816	6	0.8	392	4	US-09-710-279-2874	Sequence 2874, Ap
744	6	0.8	355	2	US-08-811-949-47	Sequence 47, Ap	817	6	0.8	392	4	US-09-949-016-8785	Sequence 8786, Ap
745	6	0.8	355	2	US-08-811-949-53	Sequence 53, Ap	818	6	0.8	392	4	US-09-949-016-8787	Sequence 8787, Ap
746	6	0.8	355	2	US-08-811-949-59	Sequence 59, Ap	819	6	0.8	393	2	US-08-560-058A-44	Sequence 44, Ap
747	6	0.8	355	3	US-08-794-528-1	Sequence 1, Ap	820	6	0.8	393	3	US-08-967-024C-24	Sequence 24, Ap
748	6	0.8	355	4	US-09-252-991A-22326	Sequence 22326, A	821	6	0.8	393	3	US-08-967-024C-25	Sequence 25, Ap
749	6	0.8	355	4	US-09-198-452A-871	Sequence 871, Ap	822	6	0.8	393	3	US-09-270-767-12793	Sequence 42793, A
750	6	0.8	355	4	US-09-902-540-11796	Sequence 11796, A	823	6	0.8	394	3	US-08-466-368-2	Sequence 2, Ap
751	6	0.8	355	6	5223256-1	Patent No. 5223256	824	6	0.8	394	4	US-09-144-914-4	Sequence 4, Ap
752	6	0.8	355	6	5223256-1	Patent No. 5223256	825	6	0.8	394	4	US-09-252-991A-18502	Sequence 18502, A
753	6	0.8	356	1	US-08-427-640-4	Sequence 4, Ap	826	6	0.8	394	4	US-08-328-500-2	Sequence 2, Ap
754	6	0.8	356	1	US-08-427-640-8	Sequence 8, Ap	827	6	0.8	394	6	5223418-2	Patent No. 5223418
755	6	0.8	356	4	US-09-252-991A-10030	Sequence 10030, A	828	6	0.8	395	6	US-08-485-859-2	Sequence 2, Ap
756	6	0.8	356	4	US-09-902-540-12881	Sequence 12881, A	829	6	0.8	395	1	US-08-485-859-2	Sequence 2, Ap
757	6	0.8	358	4	US-09-248-796A-19081	Sequence 19081, A	830	6	0.8	395	1	US-08-706-539-11	Sequence 11, Ap

831	6	0.8	395	1	US-08-532-166-2	Sequence 2, Appli	504	6	0.8	424	4	US-09-107-532A-5459	Sequence 5459, Ap
832	6	0.8	395	1	US-08-488-382A-2	Sequence 2, Appli	505	6	0.8	424	4	US-09-248-796A-18949	Sequence 18949, A
833	6	0.8	395	1	US-08-480-912-2	Sequence 2, Appli	506	6	0.8	424	4	US-10-027-450-45	Sequence 45, Appl
834	6	0.8	395	3	US-09-027-007-11	Sequence 11, Appl.	907	6	0.8	425	3	US-09-071-224-6	Sequence 6, Appli
835	6	0.8	396	4	US-09-252-991A-18619	Sequence 18619, A	908	6	0.8	425	3	US-09-134-001C-55619	Sequence 5619, Ap
836	6	0.8	397	1	US-08-647-928-8	Sequence 8, Appli	909	6	0.8	425	4	US-09-540-236-3466	Sequence 3466, Ap
837	6	0.8	397	4	US-09-469-039A-13498	Sequence 13498, A	910	6	0.8	426	4	US-09-252-991A-25192	Sequence 25192, A
838	6	0.8	397	4	US-09-949-016-10639	Sequence 10639, A	911	6	0.8	427	4	US-09-198-452A-31	Sequence 31, Appl
839	6	0.8	397	4	US-09-949-016-10640	Sequence 10640, A	912	6	0.8	427	4	US-09-328-352-5205	Sequence 5205, Ap
840	6	0.8	398	2	US-08-284-391B-29	Sequence 29, Appl	913	6	0.8	428	1	US-08-570-157-5	Sequence 5, Appli
841	6	0.8	398	3	US-09-218-950-29	Sequence 29, Appl	914	6	0.8	428	3	US-08-029-170-31	Sequence 31, Appl
842	6	0.8	398	4	US-08-394-388A-29	Sequence 29, Appl	915	6	0.8	428	3	US-08-403-797-2	Sequence 2, Appli
843	6	0.8	399	4	US-09-489-039A-8859	Sequence 8859, Ap	916	6	0.8	428	3	US-09-076-510-5	Sequence 5, Appli
844	6	0.8	399	4	US-09-270-767-41700	Sequence 45921, A	917	6	0.8	428	4	US-09-004-745-31	Sequence 31, Appl
845	6	0.8	399	4	US-09-710-279-2576	Sequence 2576, Ap	918	6	0.8	428	4	US-09-443-745-31	Sequence 31, Appl
846	6	0.8	400	3	US-09-134-001C-4785	Sequence 4785, Ap	919	6	0.8	428	4	US-09-949-016-10965	Sequence 10965, A
847	6	0.8	400	4	US-09-252-991A-31296	Sequence 31296, A	920	6	0.8	429	4	US-09-252-991A-28788	Sequence 28788, A
848	6	0.8	400	4	US-09-248-796A-15785	Sequence 15785, A	921	6	0.8	429	4	US-09-854-133-391	Sequence 331, App
849	6	0.8	401	4	US-09-489-847-202	Sequence 1090, A	922	6	0.8	430	1	US-07-942-157A-3	Sequence 3, Appli
850	6	0.8	401	4	US-09-252-991A-17090	Sequence 10491, A	923	6	0.8	430	6	5219569-2	Patent No. 5219569
851	6	0.8	402	1	US-08-236-311-1	Sequence 1, Appli	924	6	0.8	430	6	5219569-2	Patent No. 5219569
852	6	0.8	402	3	US-08-457-918-1	Sequence 1, Appli	925	6	0.8	431	3	US-09-376-689-4	Sequence 4, Appli
853	6	0.8	402	3	US-10-157-408-1	Sequence 1, Appli	926	6	0.8	431	4	US-09-101-2726-1	Sequence 1, Appli
854	6	0.8	403	4	US-09-802-213-5	Sequence 5, Appli	927	6	0.8	431	4	US-09-540-236-3536	Sequence 336, Ap
855	6	0.8	403	4	US-09-880-503-6	Sequence 6, Appli	928	6	0.8	431	4	US-09-270-767-45503	Sequence 45503, A
856	6	0.8	403	4	US-09-144-914-5	Sequence 5, Appli	929	6	0.8	431	4	US-09-248-796A-18354	Sequence 18354, A
857	6	0.8	405	3	US-09-134-000C-5465	Sequence 5465, Ap	930	6	0.8	431	6	5188829-1	Patent No. 5188829
858	6	0.8	405	4	US-09-252-991A-23838	Sequence 23838, A	931	6	0.8	432	2	US-08-560-098A-47	Sequence 47, Appl
859	6	0.8	405	4	US-09-158-452A-141	Sequence 141, App	932	6	0.8	432	3	US-08-477-460B-2	Sequence 2, Appli
860	6	0.8	408	4	US-09-583-110-3016	Sequence 3016, Ap	933	6	0.8	432	3	US-08-379-516-2	Sequence 2, Appli
861	6	0.8	408	4	US-09-902-540-11436	Sequence 11436, A	934	6	0.8	432	3	US-09-329-916-2	Sequence 2, Appli
862	6	0.8	408	4	US-09-710-279-2302	Sequence 2302, Ap	935	6	0.8	432	3	PCT-US93-07442-2	Sequence 2, Appli
863	6	0.8	410	3	US-08-630-172-17	Sequence 17, Appl	936	6	0.8	432	3	US-08-867-149-1	Sequence 1, Appli
864	6	0.8	410	3	US-09-271-713-9	Sequence 9, Appli	937	6	0.8	433	2	US-08-808-374-1	Sequence 1, Appli
865	6	0.8	410	3	US-08-792-283A-9	Sequence 9, Appli	938	6	0.8	433	2	US-08-484-681-2	Sequence 2, Appli
866	6	0.8	410	1	US-09-105-908-9	Sequence 9, Appli	939	6	0.8	432	5	US-09-766-995-2	Sequence 2, Appli
867	6	0.8	410	3	US-09-181-816-1	Sequence 1, Appli	940	6	0.8	432	5	US-09-543-681A-7154	Sequence 7154, Ap
868	6	0.8	411	3	US-09-403-736-2	Sequence 2, Appli	941	6	0.8	434	4	US-10-157-408-4	Sequence 4, Appli
869	6	0.8	411	4	US-09-949-016-10737	Sequence 10737, A	942	6	0.8	434	4	US-09-543-681A-7154	Sequence 7154, Ap
870	6	0.8	412	4	US-09-902-540-13518	Sequence 13518, A	943	6	0.8	434	4	US-09-949-016-11448	Sequence 11448, A
871	6	0.8	412	4	US-09-949-016-10737	Sequence 10737, A	944	6	0.8	437	2	US-08-811-949-51	Sequence 51, Appl
872	6	0.8	413	4	US-09-252-991A-25812	Sequence 25812, A	945	6	0.8	437	2	US-08-811-949-51	Sequence 51, Appl
873	6	0.8	413	4	US-09-489-039A-10283	Sequence 10283, A	946	6	0.8	437	2	US-08-811-949-55	Sequence 55, Appl
874	6	0.8	411	1	US-08-087-163-1	Sequence 1, Appli	947	6	0.8	437	2	US-08-811-949-55	Sequence 55, Appl
875	6	0.8	411	1	US-08-286-748B-18	Sequence 18, Appl	948	6	0.8	437	2	US-09-710-279-2960	Sequence 2960, Ap
876	6	0.8	411	1	US-08-153-799-18	Sequence 18, Appl	949	6	0.8	438	4	US-09-252-991A-28398	Sequence 28398, A
877	6	0.8	411	2	US-08-560-098A-48	Sequence 48, Appl	950	6	0.8	438	4	US-09-489-039A-8464	Sequence 8464, Ap
878	6	0.8	411	3	US-09-376-689-2	Sequence 2, Appli	951	6	0.8	438	4	US-09-902-540-12277	Sequence 12277, A
879	6	0.8	411	3	US-09-181-816-1	Sequence 1, Appli	952	6	0.8	439	2	US-08-959-638-0	Sequence 9, Appli
880	6	0.8	411	4	US-09-403-736-2	Sequence 2, Appli	953	6	0.8	439	2	US-09-543-681A-7293	Sequence 7293, Ap
881	6	0.8	412	4	US-09-902-540-13518	Sequence 13518, A	954	6	0.8	439	4	US-09-489-039A-10782	Sequence 10782, A
882	6	0.8	412	4	US-09-949-016-10737	Sequence 10737, A	955	6	0.8	440	4	US-09-457-046B-54	Sequence 54, Appl
883	6	0.8	413	4	US-09-252-991A-25812	Sequence 25812, A	956	6	0.8	441	3	US-09-237-937C-11	Sequence 11, Appl
884	6	0.8	414	4	US-09-252-991A-27828	Sequence 27828, A	957	6	0.8	441	4	US-09-949-016-11792	Sequence 11792, A
885	6	0.8	415	1	US-08-110-386A-6	Sequence 6, Appli	958	6	0.8	441	4	US-09-866-570B-54	Sequence 5, Appli
886	6	0.8	415	3	US-08-981-189B-10	Sequence 10, Appl	959	6	0.8	441	4	US-09-866-570B-54	Sequence 5, Appli
887	6	0.8	415	3	US-08-482-746-6	Sequence 6, Appli	960	6	0.8	441	4	US-09-443-745-14	Sequence 14, Appl
888	6	0.8	415	3	US-09-180-109A-9	Sequence 9, Appli	961	6	0.8	441	4	US-09-443-745-14	Sequence 14, Appl
889	6	0.8	415	4	US-09-180-109A-12	Sequence 12, Appl	962	6	0.8	441	4	US-09-443-745-14	Sequence 14, Appl
890	6	0.8	415	4	US-09-580-734-6	Sequence 6, Appli	963	6	0.8	441	4	US-09-443-745-14	Sequence 14, Appl
891	6	0.8	415	4	US-08-374-009-6	Sequence 6, Appli	964	6	0.8	441	4	US-09-443-745-14	Sequence 14, Appl
892	6	0.8	415	4	US-09-191-724-6	Sequence 6, Appli	965	6	0.8	441	4	US-09-443-745-14	Sequence 14, Appl
893	6	0.8	415	4	US-09-799-978-16	Sequence 16, Appl	966	6	0.8	441	4	US-09-443-745-14	Sequence 14, Appl
894	6	0.8	415	4	US-09-591-279A-42	Sequence 42, Appl	967	6	0.8	441	4	US-09-443-745-14	Sequence 14, Appl
895	6	0.8	419	4	US-09-270-767-41700	Sequence 41700, A	968	6	0.8	441	4	US-09-443-745-14	Sequence 14, Appl
896	6	0.8	419	4	US-09-902-540-13149	Sequence 13149, A	969	6	0.8	441	4	US-09-443-745-14	Sequence 14, Appl
897	6	0.8	420	4	US-09-583-110-5061	Sequence 5061, Ap	970	6	0.8	441	4	US-09-443-745-14	Sequence 14, Appl
898	6	0.8	420	4	US-09-107-433-919	Sequence 337, Ap	971	6	0.8	441	4	US-09-443-745-14	Sequence 14, Appl
899	6	0.8	422	4	US-09-489-847-357	Sequence 357, Ap	972	6	0.8	441	4	US-09-443-745-14	Sequence 14, Appl
900	6	0.8	424	3	US-09-134-001C-5009	Sequence 5009, Ap	973	6	0.8	441	4	US-09-443-745-14	Sequence 14, Appl
901	6	0.8	424	3	US-09-173-300-45	Sequence 45, Appl	974	6	0.8	441	4	US-09-443-745-14	Sequence 14, Appl
902	6	0.8	424	3	US-09-173-300-45	Sequence 45, Appl	975	6	0.8	441	4	US-09-443-745-14	Sequence 14, Appl
903	6	0.8	424	3	US-09-173-300-45	Sequence 45, Appl	976	6	0.8	441	4	US-09-443-745-14	Sequence 14, Appl

977	6	0.8	445	4	US-09-710-279-2858	Sequence 2858, Ap	1050	6	0.8	492	4	US-09-248-796A-17174	Sequence 17174, A
978	6	0.8	451	4	US-09-328-352-7659	Sequence 7659, Ap	1051	6	0.8	493	4	US-09-543-681A-7006	Sequence 7006, Ap
979	6	0.8	451	4	US-09-134-000C-3849	Sequence 3849, Ap	1052	6	0.8	494	4	US-09-517-779-2	Sequence 2, Appli
980	6	0.8	454	3	US-09-134-001C-4438	Sequence 4438, Ap	1053	6	0.8	495	4	US-08-311-731A-3	Sequence 3, Appli
981	6	0.8	454	4	US-09-902-540-12501	Sequence 12501, A	1054	6	0.8	497	1	US-08-278-635B-5	Sequence 5, Appli
982	6	0.8	456	1	US-08-205-719-4	Sequence 4, Appli	1055	6	0.8	497	3	US-08-464-258B-5	Sequence 5, Appli
983	6	0.8	456	3	US-08-431-517F-6	Sequence 6, Appli	1056	6	0.8	497	3	US-08-471-961-5	Sequence 5, Appli
984	6	0.8	456	3	US-09-328-352-5446	Sequence 5446, Ap	1057	6	0.8	497	4	US-09-345-109C-5	Sequence 5, Appli
985	6	0.8	456	4	US-09-919-172-31	Sequence 31, Appli	1058	6	0.8	497	4	US-09-270-767-62287	Sequence 62287, A
986	6	0.8	457	4	US-08-328-500-9	Sequence 9, Appli	1059	6	0.8	497	4	US-09-949-016-6616	Sequence 6616, Ap
987	6	0.8	458	3	US-09-039-555B-15	Sequence 15, Appli	1060	6	0.8	497	6	5486473-4	Patent No. 5486473
988	6	0.8	458	3	US-08-466-368-4	Sequence 4, Appli	1061	6	0.8	497	6	5486473-4	Patent No. 5486473
989	6	0.8	458	3	US-09-517-605-3	Sequence 3, Appli	1062	6	0.8	499	4	US-09-949-016-63370	Sequence 7370, Ap
990	6	0.8	458	4	US-09-252-991A-30535	Sequence 30535, A	1063	6	0.8	499	4	US-09-902-540-16496	Sequence 16496, A
991	6	0.8	458	4	US-09-489-039A-8987	Sequence 8987, Ap	1064	6	0.8	501	3	US-08-906-791-2	Sequence 2, Appli
992	6	0.8	458	4	US-09-612-402B-36	Sequence 36, Appli	1065	6	0.8	501	3	US-09-111-730-1	Sequence 1, Appli
993	6	0.8	458	4	US-10-092-138A-25	Sequence 25, Appli	1066	6	0.8	502	3	US-09-499-102A-7	Sequence 7, Appli
994	6	0.8	458	6	5223394-7	Patent No. 5223394	1067	6	0.8	503	4	US-09-949-016-6578	Sequence 6578, Ap
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996	6	0.8	459	6	US-09-491-785-2	Sequence 2, Appli	1069	6	0.8	504	2	US-08-700-636-4	Sequence 4, Appli
997	6	0.8	459	3	US-09-364-230-20	Sequence 20, Appli	1070	6	0.8	504	3	US-08-467-574-4	Sequence 4, Appli
998	6	0.8	459	4	US-09-252-991A-29528	Sequence 29528, A	1071	6	0.8	504	3	US-09-217-345-4	Sequence 4, Appli
999	6	0.8	459	4	US-09-710-279-2462	Sequence 2462, Ap	1072	6	0.8	504	4	US-08-487-596-4	Sequence 4, Appli
1000	6	0.8	460	4	US-09-543-681A-5773	Sequence 5773, Ap	1073	6	0.8	504	4	US-08-660-451A-4	Sequence 4, Appli
1001	6	0.8	461	4	US-09-248-796A-16479	Sequence 16479, A	1074	6	0.8	504	4	US-09-892-985-4	Sequence 4, Appli
1002	6	0.8	461	4	US-09-902-540-12101	Sequence 12101, A	1075	6	0.8	505	4	US-09-612-402B-17	Sequence 17, Appli
1003	6	0.8	462	2	US-08-417-495-5	Sequence 5, Appli	1076	6	0.8	505	4	US-09-949-016-6538	Sequence 6538, Ap
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1005	6	0.8	462	3	US-09-218-950-5	Sequence 5, Appli	1078	6	0.8	510	3	US-09-291-922-92	Sequence 22, Appli
1006	6	0.8	462	4	US-08-394-388A-5	Sequence 5, Appli	1079	6	0.8	511	4	US-09-949-016-6034	Sequence 6034, Ap
1007	6	0.8	462	5	PCT-US92-01785-5	Sequence 5, Appli	1080	6	0.8	513	4	US-09-248-796A-20548	Sequence 20548, A
1008	6	0.8	462	5	PCT-US95-00454-5	Sequence 5, Appli	1081	6	0.8	514	4	US-09-252-991A-30600	Sequence 30600, A
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1012	6	0.8	463	4	US-09-134-001C-4562	Sequence 4562, Ap	1085	6	0.8	518	4	US-09-816-248-17	Sequence 17, Appli
1013	6	0.8	464	4	US-09-328-352-5322	Sequence 5322, Ap	1086	6	0.8	519	3	US-09-540-236-3050	Sequence 3050, Ap
1014	6	0.8	465	4	US-09-710-279-1676	Sequence 1676, Ap	1087	6	0.8	520	3	US-09-068-740A-3	Sequence 3, Appli
1015	6	0.8	465	4	US-09-252-991A-16891	Sequence 16891, A	1088	6	0.8	520	4	US-09-949-016-8026	Sequence 8026, Ap
1016	6	0.8	466	4	US-09-252-991A-21778	Sequence 21778, A	1089	6	0.8	521	4	US-09-540-236-7722	Sequence 7722, Ap
1017	6	0.8	466	4	US-09-489-039A-9899	Sequence 9899, Ap	1090	6	0.8	521	4	US-09-949-016-8809	Sequence 8809, Ap
1018	6	0.8	468	4	US-09-710-279-1448	Sequence 1448, Ap	1091	6	0.8	522	4	US-09-134-000C-4946	Sequence 4946, Ap
1019	6	0.8	468	4	US-09-248-796A-17456	Sequence 17456, A	1092	6	0.8	523	3	US-09-550-338-2	Sequence 2, Appli
1020	6	0.8	469	4	US-09-583-110-4480	Sequence 4480, Ap	1093	6	0.8	523	4	US-07-767-878-2	Sequence 2, Appli
1021	6	0.8	470	2	US-08-724-394A-10	Sequence 10, Appli	1094	6	0.8	525	3	US-09-369-364A-21	Sequence 21, Appli
1022	6	0.8	470	4	US-09-328-352-7348	Sequence 7348, Ap	1095	6	0.8	525	4	US-09-540-236-2855	Sequence 2855, Ap
1023	6	0.8	471	3	US-09-134-001C-4125	Sequence 4125, Ap	1096	6	0.8	525	4	US-10-101-464A-613	Sequence 613, App
1024	6	0.8	471	4	US-09-645-337A-4	Sequence 4, Appli	1097	6	0.8	526	2	US-08-852-401-3	Sequence 3, Appli
1025	6	0.8	472	2	US-08-811-949-63	Sequence 63, Appli	1098	6	0.8	527	1	US-07-609-510B-16	Sequence 16, Appli
1026	6	0.8	472	4	US-09-107-433-4609	Sequence 4609, Ap	1099	6	0.8	527	2	US-08-811-949-39	Sequence 39, Appli
1027	6	0.8	473	4	US-09-252-991A-22921	Sequence 22921, A	1100	6	0.8	527	4	US-09-600-985-1	Sequence 1, Appli
1028	6	0.8	473	4	US-09-252-991A-31406	Sequence 31406, A	1101	6	0.8	527	4	US-09-600-985-2	Sequence 2, Appli
1029	6	0.8	473	4	US-09-328-352-5379	Sequence 5379, Ap	1102	6	0.8	527	4	US-09-600-985-3	Sequence 3, Appli
1030	6	0.8	473	4	US-09-949-016-9481	Sequence 9481, Ap	1103	6	0.8	527	4	US-09-612-314A-51	Sequence 51, Appli
1031	6	0.8	476	4	US-09-675-018B-13	Sequence 13, Appli	1104	6	0.8	527	5	PCT-US91-01025A-2	Sequence 2, Appli
1032	6	0.8	476	4	US-09-675-018B-14	Sequence 14, Appli	1105	6	0.8	527	6	5185259-8	Patent No. 5185259
1033	6	0.8	477	2	US-08-560-098A-51	Sequence 51, Appli	1106	6	0.8	527	6	5520913-1	Patent No. 5520913
1034	6	0.8	478	4	US-09-252-991A-23438	Sequence 23438, A	1107	6	0.8	527	6	5185259-8	Patent No. 5185259
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1037	6	0.8	480	4	US-09-252-991A-29770	Sequence 29770, A	1110	6	0.8	530	3	US-08-378-516-4	Sequence 4, Appli
1038	6	0.8	480	4	US-09-270-767-60056	Sequence 60056, A	1111	6	0.8	530	3	US-09-329-916-4	Sequence 4, Appli
1039	6	0.8	481	4	US-09-902-540-13111	Sequence 13111, A	1112	6	0.8	530	3	US-08-485-312A-4	Sequence 4, Appli
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1041	6	0.8	482	3	5245013-2	Patent No. 5245013	1114	6	0.8	530	4	US-08-484-681-4	Sequence 4, Appli
1042	6	0.8	482	6	5245013-2	Patent No. 5245013	1115	6	0.8	530	4	US-09-766-995-4	Sequence 4, Appli
1043	6	0.8	483	4	US-09-603-208A-210	Sequence 210, App	1116	6	0.8	530	5	PCT-US93-07422-4	Sequence 4, Appli
1044	6	0.8	484	3	US-09-134-001C-5063	Sequence 5063, Ap	1117	6	0.8	531	4	US-09-949-016-7044	Sequence 7044, Ap
1045	6	0.8	487	4	US-09-107-532A-4946	Sequence 4946, Ap	1118	6	0.8	532	2	US-08-417-495-6	Sequence 6, Appli
1046	6	0.8	487	4	US-09-248-796A-19788	Sequence 19788, A	1119	6	0.8	532	2	US-08-284-331B-6	Sequence 6, Appli
1047	6	0.8	489	4	US-09-986-535-2	Sequence 2, Appli	1120	6	0.8	532	4	US-09-218-950-6	Sequence 6, Appli
1048	6	0.8	489	4	US-09-252-991A-18918	Sequence 18918, A	1121	6	0.8	532	3	US-08-394-388A-6	Sequence 6, Appli
1049	6	0.8	491	4	US-09-248-796A-14421	Sequence 14421, A	1122	6	0.8	532	5	PCT-US92-01785-6	Sequence 6, Appli

1123	6	0.8	532	5	PCT-US95-00454-6	Sequence 6, Appli	1196	6	0.8	598	4	US-09-270-767-45253	Sequence 45253, A
1124	6	0.8	534	4	US-09-328-352-6713	Sequence 6713, Ap	1197	6	0.8	599	4	US-09-773-4264-7	Sequence 7, Appli
1125	6	0.8	534	4	US-09-270-767-45080	Sequence 45080, A	1198	6	0.8	599	4	US-10-314-881-7	Sequence 7, Appli
1126	6	0.8	535	4	US-09-312-762A-14	Sequence 14, Appl	1199	6	0.8	602	4	US-09-438-185A-18	Sequence 18, Appl
1127	6	0.8	542	4	US-09-489-039A-11757	Sequence 11757, A	1200	6	0.8	603	3	US-09-198-122-2	Sequence 2, Appli
1128	6	0.8	544	3	US-08-687-580-30	Sequence 30, Appl	1201	6	0.8	603	3	US-09-311-311C-26	Sequence 26, Appl
1129	6	0.8	545	4	US-09-489-039A-11980	Sequence 11980, A	1202	6	0.8	603	3	US-09-134-001C-5226	Sequence 5226, Ap
1130	6	0.8	546	4	US-09-270-767-45916	Sequence 35916, A	1203	6	0.8	603	3	US-09-710-279-1684	Sequence 1684, Ap
1131	6	0.8	546	4	US-09-270-767-49133	Sequence 49133, A	1204	6	0.8	605	3	US-09-134-001C-4425	Sequence 4425, Ap
1132	6	0.8	546	4	US-09-949-016-7169	Sequence 7169, Ap	1205	6	0.8	607	4	US-09-248-796A-14958	Sequence 14958, A
1133	6	0.8	550	4	US-09-495-823-7	Sequence 7, Appli	1206	6	0.8	609	4	US-09-248-796A-19292	Sequence 19292, A
1134	6	0.8	550	4	US-09-252-991A-22670	Sequence 22670, A	1207	6	0.8	610	4	US-09-800-170-22	Sequence 22, Appl
1135	6	0.8	556	4	US-09-489-039A-12775	Sequence 12775, A	1208	6	0.8	612	1	US-08-344-695-2	Sequence 2, Appli
1136	6	0.8	556	4	US-09-275-252A-8	Sequence 8, Appli	1209	6	0.8	614	4	US-09-252-991A-31412	Sequence 31412, A
1137	6	0.8	557	4	US-09-252-991A-17260	Sequence 17260, A	1210	6	0.8	616	3	US-08-895-707-2	Sequence 2, Appli
1138	6	0.8	558	2	US-08-656-177A-2	Sequence 2, Appli	1211	6	0.8	621	3	US-09-311-626B-2	Sequence 3, Appli
1139	6	0.8	558	3	US-09-256-797-2	Sequence 2, Appli	1212	6	0.8	621	4	US-09-252-991A-30689	Sequence 30689, A
1140	6	0.8	560	4	US-09-949-016-6458	Sequence 6458, Ap	1213	6	0.8	621	4	US-09-248-796A-14463	Sequence 14463, A
1141	6	0.8	560	4	US-09-912-559-3	Sequence 3, Appli	1214	6	0.8	623	4	US-09-538-092-802	Sequence 802, App
1142	6	0.8	560	4	US-09-912-559-4	Sequence 4, Appli	1215	6	0.8	625	4	US-09-949-016-11531	Sequence 11531, A
1143	6	0.8	562	2	US-08-811-949-43	Sequence 43, Appl	1216	6	0.8	627	4	US-08-851-567B-28	Sequence 28, Appl
1144	6	0.8	562	2	US-08-560-098A-50	Sequence 50, Appl	1217	6	0.8	628	4	US-09-252-991A-24741	Sequence 24741, A
1145	6	0.8	562	2	US-08-883-785A-38	Sequence 38, Appl	1218	6	0.8	628	4	US-09-841-786-5	Sequence 5, Appli
1146	6	0.8	562	4	US-09-703-685A-4	Sequence 4, Appli	1219	6	0.8	630	4	US-09-252-991A-19822	Sequence 19822, A
1147	6	0.8	562	4	US-09-879-792-12	Sequence 12, Appli	1220	6	0.8	630	4	US-08-472-888A-6	Sequence 6, Appli
1148	6	0.8	562	4	US-10-443-701-4	Sequence 4, Appli	1221	6	0.8	632	4	US-09-976-594-41	Sequence 41, Appl
1149	6	0.8	562	6	5185259-3	Sequence 8, Appli	1222	6	0.8	632	4	US-09-949-016-6976	Sequence 6976, Ap
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1153	6	0.8	562	6	5185259-3	Sequence 3, Appli	1226	6	0.8	638	4	US-09-811-469-9	Sequence 9, Appli
1154	6	0.8	562	6	5200340-2	Sequence 2, Appli	1227	6	0.8	640	4	US-09-252-991A-20343	Sequence 20343, A
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1156	6	0.8	562	6	5344773-2	Sequence 3, Appli	1229	6	0.8	649	4	US-09-252-991A-31187	Sequence 31187, A
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1158	6	0.8	563	4	US-09-252-991A-29210	Sequence 29210, A	1231	6	0.8	650	4	US-09-252-991A-22234	Sequence 22234, A
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1160	6	0.8	564	4	US-09-107-532A-5248	Sequence 5248, Ap	1233	6	0.8	653	3	US-09-443-184-50	Sequence 50, Appl
1161	6	0.8	565	4	US-09-248-796A-20098	Sequence 20098, A	1234	6	0.8	653	3	US-08-148-910-12	Sequence 12, Appl
1162	6	0.8	565	4	US-09-543-681A-4544	Sequence 4544, Ap	1235	6	0.8	655	1	US-08-448-937A-12	Sequence 12, Appl
1163	6	0.8	569	1	US-07-821-716-2	Sequence 2, Appli	1236	6	0.8	655	1	US-09-252-991A-30630	Sequence 30630, A
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1166	6	0.8	569	3	US-08-685-212-2	Sequence 2, Appli	1239	6	0.8	657	4	US-09-949-016-11367	Sequence 11367, A
1167	6	0.8	569	3	US-09-173-151A-31	Sequence 31, Appl	1240	6	0.8	657	4	US-09-949-016-11367	Sequence 11367, A
1168	6	0.8	569	4	US-08-466-932A-2	Sequence 2, Appli	1241	6	0.8	659	4	US-09-252-991A-33126	Sequence 33126, A
1169	6	0.8	569	4	US-08-406-824A-6	Sequence 6, Appli	1242	6	0.8	661	4	US-09-949-016-6157	Sequence 6157, Ap
1170	6	0.8	569	4	US-09-949-016-6000	Sequence 6000, Ap	1243	6	0.8	665	4	US-09-949-016-10776	Sequence 10776, A
1171	6	0.8	569	5	PCT-US94-02414-2	Sequence 2, Appli	1244	6	0.8	666	4	US-09-489-039A-12388	Sequence 12388, A
1172	6	0.8	569	5	PCT-US96-08899-2	Sequence 2, Appli	1245	6	0.8	666	4	US-09-930-181-2	Sequence 2, Appli
1173	6	0.8	572	4	US-09-252-991A-23996	Sequence 23996, A	1246	6	0.8	669	2	US-07-851-800-2	Sequence 2, Appli
1174	6	0.8	573	3	US-09-134-001C-4813	Sequence 4813, Ap	1247	6	0.8	670	4	US-09-252-991A-24930	Sequence 24930, A
1175	6	0.8	575	1	US-07-683-957B-2	Sequence 2, Appli	1248	6	0.8	673	3	US-09-192-104-2	Sequence 2, Appli
1176	6	0.8	575	2	US-08-417-495-4	Sequence 4, Appli	1249	6	0.8	673	3	US-09-543-446-2	Sequence 2, Appli
1177	6	0.8	575	3	US-08-284-391B-4	Sequence 4, Appli	1250	6	0.8	673	3	US-09-079-955-11	Sequence 11, Appl
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1179	6	0.8	575	4	US-08-394-388A-4	Sequence 4, Appli	1252	6	0.8	675	4	US-09-252-991A-29650	Sequence 29650, A
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ALIGNMENTS

RESULT 1
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Query Match 49.3%; Score 355; DB 4; Length 570;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 355; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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335 WSGQKPCICACREPKISDVRRRVLPVMOVSRTPLHOLYSAFQKQASAPTKPAL 394
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395 PGGLPMGYOHLHTQLOVECTSPYRRLGSSRRCTCLRTGKMSGRAPSCIPICGKIENITA 454
245 PGGLPMGYOHLHTQLOVECTSPYRRLGSSRRCTCLRTGKMSGRAPSCIPICGKIENITA 304
455 PKTGRLMPVQALYRRTSGVHDSLHKGAMFLVCSGALVNERTVVAAHCVTDLGRVTM 514
305 PKTGRLMPVQALYRRTSGVHDSLHKGAMFLVCSGALVNERTVVAAHCVTDLGRVTM 364
515 IKTADLKVYTGKTRDDRDREKTIQSLQISALIIHPYDPDILLDAOLAIILKLDKAIIST 574
365 IKTADLKVYTGKTRDDRDREKTIQSLQISALIIHPYDPDILLDAOLAIILKLDKAIIST 424

QY 575 RV0P1CLASRDLSFQESHITVAGNVLDVMSFGKNTLTASGVSVVDSLL 629
DB 425 RV0P1CLASRDLSFQESHITVAGNVLDVMSFGKNTLTASGVSVVDSLL 479

RESULT 2
US-10-067-422-17
; Sequence 17, Application US/10067422
; Patent No. 6743613
; GENERAL INFORMATION:
; APPLICANT: NI et al.
; TITLE OF INVENTION: Bone Morphogenic Protein (BMP) Polynucleotides, Polypeptides, and
; FILE REFERENCE: PT004P1
; CURRENT APPLICATION NUMBER: US/10/067,422
; PRIOR FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: 09/685,899
; PRIOR FILING DATE: 2000-10-11
; PRIOR APPLICATION NUMBER: PCT/US00/09028
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/152,933
; PRIOR FILING DATE: 1999-09-09
; PRIOR APPLICATION NUMBER: 60/147,020
; PRIOR FILING DATE: 1999-09-09
; PRIOR APPLICATION NUMBER: 60/131,672
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 60/130,693
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 46
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-067-422-17

Query Match 2.2%; Score 16; DB 4; Length 46;
Best Local Similarity 100.0%; Pred. No. 2.1e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 275 LEERNCSDPGPGVNGY 290
DB 31 LEERNCSDPGPGVNGY 46

RESULT 3
US-10-067-422-16
; Sequence 16, Application US/10067422
; Patent No. 6743613
; GENERAL INFORMATION:
; APPLICANT: NI et al.
; TITLE OF INVENTION: Bone Morphogenic Protein (BMP) Polynucleotides, Polypeptides, and
; FILE REFERENCE: PT004P1
; CURRENT APPLICATION NUMBER: US/10/067,422
; PRIOR FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: 09/685,899
; PRIOR FILING DATE: 2000-10-11
; PRIOR APPLICATION NUMBER: PCT/US00/09028
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/152,933
; PRIOR FILING DATE: 1999-09-09
; PRIOR APPLICATION NUMBER: 60/147,020
; PRIOR FILING DATE: 1999-09-09
; PRIOR APPLICATION NUMBER: 60/131,672
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 60/130,693
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 12
; TYPE: PRT

; ORGANISM: Homo sapiens
US-10-067-422-16

Query Match 1.7%; Score 12; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 7.4e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 260 CACLAGYTGQRC 271
DB 1 CACLAGYTGQRC 12

RESULT 4
US-09-374-135-4
; Sequence 4, Application US/09374135
; Patent No. 6277972
; GENERAL INFORMATION:
; APPLICANT: Afari, Daniel E.
; APPLICANT: Hubert, Rene S.
; APPLICANT: Leong, Kahan
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Saffran, Douglas C.
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: SECRETED BY PROSTATE AND BLADDER CANCER CELLS
; FILE REFERENCE: 1703-017.US1
; CURRENT APPLICATION NUMBER: US/09/374,135
; PRIOR FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: 60/095,982
; PRIOR FILING DATE: 1998-08-10
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Mouse
US-09-374-135-4

Query Match 1.2%; Score 9; DB 3; Length 101;
Best Local Similarity 100.0%; Pred. No. 0.59;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 179 YDYVEVRDG 187
DB 47 YDYVEVRDG 55

RESULT 5
US-09-341-461-28
; Sequence 28, Application US/09341461
; Patent No. 6586389
; GENERAL INFORMATION:
; APPLICANT: Hammond, Timothy G.
; APPLICANT: Verroust, Pierre J.
; TITLE OF INVENTION: Cubilin Protein, DNA Sequences Encoding Cubilin
; FILE REFERENCE: D6148
; CURRENT APPLICATION NUMBER: US/09/341,461
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: PCT/US99/01259
; PRIOR FILING DATE: 1999-01-21
; NUMBER OF SEQ ID NOS: 40
; SEQ ID NO 28
; LENGTH: 110
; TYPE: PRT
; ORGANISM: human
; OTHER INFORMATION: amino acid sequence of Bmp-1 Cub1 domain
US-09-341-461-28

Query Match 1.2%; Score 9; DB 4; Length 110;
Best Local Similarity 100.0%; Pred. No. 0.64;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 179 YDYVEVRDG 187
Db 56 YDYVEVRDG 64

RESULT 6

US-09-438-046-20
Sequence 20, Application US/09438046
Patent No. 6706687
GENERAL INFORMATION:
APPLICANT: ERIKSSON, ULF
APPLICANT: AASE, Karin
APPLICANT: LEE, Xuri
APPLICANT: PONTI, Annica
APPLICANT: UTELLA, Marko
APPLICANT: ALITALO, Kari
APPLICANT: OESTMAN, Arne
TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR D, DNA CODING
FILE REFERENCE: Ulf Eriksson et al 1064-44833
CURRENT APPLICATION NUMBER: US/09/438,046
CURRENT FILING DATE: 1999-11-10
EARLIER APPLICATION NUMBER: 60/107,852
EARLIER FILING DATE: 1998-11-10
EARLIER APPLICATION NUMBER: 60/113,997
EARLIER FILING DATE: 1999-12-28
EARLIER APPLICATION NUMBER: 60/150,604
EARLIER FILING DATE: 1999-08-26
EARLIER APPLICATION NUMBER: 60/157,108
EARLIER FILING DATE: 1999-10-04
EARLIER APPLICATION NUMBER: 60/157,756
EARLIER FILING DATE: 1999-10-05
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 20
LENGTH: 113
TYPE: PRT
ORGANISM: Homo sapiens
US-09-438-046-20

Query Match 1.2%; Score 9; DB 4; Length 113;
Best Local Similarity 100.0%; Pred. No. 0.65;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 179 YDYVEVRDG 187
Db 56 YDYVEVRDG 64

RESULT 7

US-08-872-757-2
Sequence 2, Application US/08872757
Patent No. 6258584
GENERAL INFORMATION:
APPLICANT: Prockop, Darwin J.
APPLICANT: Hojima, Yoshio
APPLICANT: Li, Shi-Wu
TITLE OF INVENTION: RECOMBINANT C-PROTEINASE AND
TITLE OF INVENTION: PROCESSES; METHODS AND USES THEREOF
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/872,757
FILING DATE: 10-JUN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/609,187
FILING DATE: 01-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 8389-028-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
TELEFAX: 415-854-3694
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 730 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-872-757-2

Query Match 1.2%; Score 9; DB 3; Length 730;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 179 YDYVEVRDG 187
Db 377 YDYVEVRDG 385

RESULT 8

US-09-850-048A-2
Sequence 2, Application US/09850048A
Patent No. 6562613
GENERAL INFORMATION:
APPLICANT: Prockop, Darwin J.
APPLICANT: Hojima, Yoshio
APPLICANT: Li, Shi-Wu
TITLE OF INVENTION: RECOMBINANT C-PROTEINASE AND
TITLE OF INVENTION: PROCESSES; METHODS AND USES THEREOF
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/850,048A
FILING DATE: 07-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/609,187
FILING DATE: 1996-03-01
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 8389-028-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
TELEFAX: 415-854-3694
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 730 amino acids
TYPE: amino acid
TOPOLOGY: 1linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-850-048A-2

Query Match 1.2%; Score 9; DB 4; Length 730;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 179 YDYVEVRDG 187
DB 377 YDYVEVRDG 385

RESULT 9
US-08-572-225-1
Sequence 1, Application US/08572225
Patent No. 5807981
GENERAL INFORMATION:
APPLICANT: Prockop, Darwin J.
APPLICANT: Hojima, Yoshio
APPLICANT: Li, Shi-Wu
APPLICANT: Sieron, Alexander
APPLICANT: Brenner, Mitch
TITLE OF INVENTION: RECOMBINANT C-PROTEINASE AND ITS USE FOR
TITLE OF INVENTION: DRUG DEVELOPMENT FOR THE TREATMENT OF DISEASE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/572,225
FILING DATE: 13-DEC-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 8389-031
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
TELEFAX: 415-854-3694
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 788 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-572-225-1

Query Match 1.2%; Score 9; DB 1; Length 788;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 179 YDYVEVRDG 187
DB 179 YDYVEVRDG 187

RESULT 10
US-09-285-385C-19
Sequence 19, Application US/09285385C
Patent No. 6579702
GENERAL INFORMATION:
APPLICANT: Greenspan, Daniel S.
APPLICANT: Scott, Ian C.
APPLICANT: Thomas, Christina L.
TITLE OF INVENTION: MAMMALIAN TOLLOID-LIKE GENE AND PROTEIN
FILE REFERENCE: 960236.9611
CURRENT APPLICATION NUMBER: US/09/285,385C
CURRENT FILING DATE: 1999-04-02
PRIOR APPLICATION NUMBER: 60/111873
PRIOR FILING DATE: 1998-12-11
PRIOR APPLICATION NUMBER: 60/080550
PRIOR FILING DATE: 1998-04-03
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 19
LENGTH: 986
TYPE: PRT
ORGANISM: Homo sapiens
US-09-285-385C-19

Query Match 1.2%; Score 9; DB 4; Length 986;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 179 YDYVEVRDG 187
DB 377 YDYVEVRDG 385

RESULT 11
US-09-949-016-6690
Sequence 6690, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CU001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6690
LENGTH: 986
TYPE: PRT
ORGANISM: Human
US-09-949-016-6690

Query Match 1.2%; Score 9; DB 4; Length 986;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 179 YDYVEVRDG 187
DB 377 YDYVEVRDG 385

RESULT 12
US-09-285-385C-2
Sequence 2, Application US/09285385C
Patent No. 6579702
GENERAL INFORMATION:
APPLICANT: Greenspan, Daniel S.

```

; APPLICANT: Scott, Ian C.
; APPLICANT: Thomas, Christina L.
; TITLE OF INVENTION: MAMMALIAN TOLLOID-LIKE GENE AND PROTEIN
; FILE REFERENCE: 960296.96111
; CURRENT APPLICATION NUMBER: US/09/285.385C
; CURRENT FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: 60/111873
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: 60/080550
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1015
; TYPE: PRT
; ORGANISM: human
; US-09-285-385C-2

Query Match          1.2%; Score 9; DB 4; Length 1015;
Best Local Similarity 100.0%; Pred. No. 4.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      179 YDYVEVRDG 187
Db      406 YDYVEVRDG 414

RESULT 13
US-09-188-930-342
; Sequence 342, Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murtison, James Greg
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; TITLE OF INVENTION: and Methods For Their Use
; FILE REFERENCE: 11000.1011c1
; CURRENT APPLICATION NUMBER: US/09/188.930A
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 342
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Mouse
; US-09-188-930-342

Query Match          1.1%; Score 8; DB 3; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      265 GYTGORCE 272
Db      36 GYTGORCE 43

RESULT 14
US-09-312-283C-342
; Sequence 342, Application US/09312283C
; Patent No. 6573095
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murtison, James G.
; APPLICANT: Kumble, Krishanand D.
; TITLE OF INVENTION: Compositions Isolated from Skin Cells
; TITLE OF INVENTION: and Methods for Their Use
; FILE REFERENCE: 11000.1011c2
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; CURRENT APPLICATION NUMBER: US/09/312.283C
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 425
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 342
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Mouse
; US-09-312-283C-342

Query Match          1.1%; Score 8; DB 4; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      265 GYTGORCE 272
Db      36 GYTGORCE 43

RESULT 15
US-09-472-087-99
; Sequence 99, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVER, MARK J.
; APPLICANT: MUELLER, ELLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PE1
; CURRENT APPLICATION NUMBER: US/09/472.087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 99
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-472-087-99

Query Match          1.1%; Score 8; DB 4; Length 96;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      208 QSIGSSLAH 215
Db      27 QSIGSSLAH 34
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20: /cgn2_6/ptodata/2/pubppaa/US11_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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27	720	100.0	720	10	US-09-997-428-231	Sequence 231, Apple
562	720	100.0	720	14	US-10-174-587-170	Sequence 170, Apple
626	720	100.0	720	14	US-10-063-742-38	Sequence 38, Apple
741	720	100.0	720	17	US-10-972-317-38	Sequence 38, Apple
742	556	77.2	567	14	US-10-004-551-2	Sequence 2, Apple
743	518	71.9	720	14	US-10-004-551-4	Sequence 4, Apple
744	518	71.9	720	14	US-10-098-871-26	Sequence 26, Apple
745	446	61.9	737	16	US-10-408-765A-1796	Sequence 1796, Apple
746	375	52.1	649	15	US-10-274-639-17	Sequence 17, Apple
747	375	52.1	649	15	US-10-333-574-17	Sequence 17, Apple
748	355	49.3	570	13	US-10-067-422-9	Sequence 9, Apple
749	277	38.5	455	11	US-09-833-245-1401	Sequence 1401, Apple

750	276	38.3	323	11	US-09-833-245-1402	Sequence 1402, Ap
751	16	2.2	46	13	US-10-067-422-17	Sequence 17, Appl
752	12	1.7	12	13	US-10-067-422-16	Sequence 16, Appl
753	9	1.2	101	9	US-09-887-593-4	Sequence 4, Appl1
754	9	1.2	113	9	US-09-852-209A-20	Sequence 20, Appl
755	9	1.2	113	13	US-10-086-623-20	Sequence 20, Appl
756	9	1.2	113	14	US-10-260-539-20	Sequence 20, Appl
757	9	1.2	113	14	US-10-131-600-20	Sequence 20, Appl
758	9	1.2	113	15	US-10-303-997B-20	Sequence 20, Appl
759	9	1.2	113	15	US-10-439-337A-20	Sequence 20, Appl
760	9	1.2	730	9	US-09-850-048A-2	Sequence 2, Appl1
761	9	1.2	823	15	US-10-016-248-98	Sequence 98, Appl
762	9	1.2	823	15	US-10-112-944-309	Sequence 309, Appl
763	9	1.2	970	15	US-10-016-248-42	Sequence 42, Appl
764	9	1.2	966	9	US-09-285-385C-19	Sequence 19, Appl
765	9	1.2	966	10	US-09-918-715-242	Sequence 242, Appl
766	9	1.2	966	15	US-10-366-345-33	Sequence 33, Appl
767	9	1.2	966	16	US-10-474-794-242	Sequence 242, Appl
768	9	1.2	966	16	US-10-723-860-1377	Sequence 1377, Ap
769	9	1.2	966	18	US-10-979-159-242	Sequence 242, Appl
770	9	1.2	992	15	US-10-016-248-40	Sequence 40, Appl
771	9	1.2	1015	9	US-09-285-385C-2	Sequence 2, Appl1
772	9	1.2	1015	15	US-10-016-248-97	Sequence 97, Appl
773	9	1.2	1015	15	US-10-719-993-644	Sequence 644, Appl
774	9	1.2	1579	16	US-10-437-963-196551	Sequence 196551, Appl
775	8	1.1	11	15	US-10-443-466A-8	Sequence 8, Appl1
776	8	1.1	11	15	US-10-656-769-71	Sequence 71, Appl
777	8	1.1	11	18	US-10-993-395-5	Sequence 5, Appl1
778	8	1.1	47	16	US-10-425-115-279870	Sequence 279870, Appl
779	8	1.1	50	16	US-10-485-683-11	Sequence 11, Appl
780	8	1.1	51	10	US-09-866-050A-342	Sequence 342, Appl
781	8	1.1	88	9	US-09-905-243-30	Sequence 30, Appl
782	8	1.1	95	14	US-10-194-979-92	Sequence 92, Appl
783	8	1.1	95	14	US-10-194-979-92	Sequence 92, Appl
784	8	1.1	95	15	US-10-308-817-38	Sequence 38, Appl
785	8	1.1	95	15	US-10-308-817-39	Sequence 39, Appl
786	8	1.1	95	15	US-10-453-699-38	Sequence 38, Appl
787	8	1.1	95	15	US-10-453-699-39	Sequence 39, Appl
788	8	1.1	95	16	US-10-379-393-105	Sequence 105, Appl
789	8	1.1	95	16	US-10-379-393-106	Sequence 106, Appl
790	8	1.1	96	14	US-10-153-382-34	Sequence 34, Appl
791	8	1.1	96	16	US-10-612-497-99	Sequence 99, Appl
792	8	1.1	96	16	US-10-776-649-99	Sequence 99, Appl
793	8	1.1	108	17	US-10-805-177-67	Sequence 67, Appl
794	8	1.1	108	17	US-10-805-177-71	Sequence 71, Appl
795	8	1.1	124	9	US-09-764-877-1346	Sequence 1346, Ap
796	8	1.1	124	15	US-10-242-515-1346	Sequence 1346, Ap
797	8	1.1	126	15	US-10-362-082-2	Sequence 2, Appl1
798	8	1.1	126	15	US-10-656-769-18	Sequence 18, Appl
799	8	1.1	127	16	US-10-478-056-35	Sequence 35, Appl
800	8	1.1	128	15	US-10-443-466A-2	Sequence 2, Appl1
801	8	1.1	128	15	US-10-443-466A-41	Sequence 41, Appl
802	8	1.1	128	15	US-10-443-466A-43	Sequence 43, Appl
803	8	1.1	128	15	US-10-443-466A-72	Sequence 72, Appl
804	8	1.1	128	15	US-10-443-466A-74	Sequence 74, Appl
805	8	1.1	128	15	US-10-443-466A-76	Sequence 76, Appl
806	8	1.1	128	15	US-10-443-466A-78	Sequence 78, Appl
807	8	1.1	128	18	US-10-993-395-2	Sequence 2, Appl1
808	8	1.1	128	18	US-10-993-395-13	Sequence 13, Appl
809	8	1.1	151	16	US-10-437-963-107837	Sequence 107837, Appl
810	8	1.1	152	15	US-09-866-050A-187	Sequence 187, Appl
811	8	1.1	152	15	US-10-099-322-57	Sequence 57, Appl
812	8	1.1	152	15	US-10-044-564-57	Sequence 57, Appl
813	8	1.1	155	14	US-10-153-382-35	Sequence 35, Appl
814	8	1.1	155	16	US-10-612-497-20	Sequence 20, Appl
815	8	1.1	155	16	US-10-612-497-112	Sequence 112, Appl
816	8	1.1	155	16	US-10-776-649-112	Sequence 20, Appl
817	8	1.1	155	16	US-10-776-649-112	Sequence 20, Appl
818	8	1.1	157	17	US-10-644-277-36	Sequence 36, Appl
819	8	1.1	223	14	US-10-656-769-40	Sequence 40, Appl
820	8	1.1	223	14	US-10-148-671-25	Sequence 25, Appl
821	8	1.1	302	15	US-10-369-499-6656	Sequence 6656, Ap
822	8	1.1	397	16	US-10-425-115-284880	Sequence 284880, Ap

823	8	1.1	411	16	US-10-437-963-111499	Sequence 111499, A	896	7	1.0	133	16	US-10-437-963-151149	Sequence 151149, A
824	8	1.1	425	15	US-10-425-114-68970	Sequence 68970, A	897	7	1.0	134	15	US-10-425-599-274398	Sequence 274398, A
825	8	1.1	481	15	US-10-425-114-72011	Sequence 72011, A	898	7	1.0	136	15	US-10-424-599-274378	Sequence 274378, A
826	8	1.1	481	16	US-10-425-115-35201	Sequence 35201, A	899	7	1.0	139	16	US-10-425-115-337979	Sequence 337979, A
827	8	1.1	596	15	US-10-282-122A-50055	Sequence 50055, A	900	7	1.0	141	16	US-10-767-701-52201	Sequence 52201, A
828	8	1.1	675	16	US-10-437-963-166405	Sequence 166405, A	901	7	1.0	142	15	US-10-424-599-274613	Sequence 274613, A
829	8	1.1	807	14	US-10-132-350-42	Sequence 42, Appl1	902	7	1.0	142	16	US-10-425-115-307867	Sequence 307867, A
830	8	1.1	807	14	US-10-132-350-44	Sequence 44, Appl1	903	7	1.0	143	16	US-10-425-115-295660	Sequence 295660, A
831	8	1.1	863	16	US-10-425-115-352299	Sequence 352299, A	904	7	1.0	144	16	US-10-437-963-102869	Sequence 102869, A
832	8	1.1	963	17	US-10-732-923-10766	Sequence 10766, A	905	7	1.0	146	15	US-10-424-599-242899	Sequence 242899, A
833	8	1.1	967	16	US-10-437-963-118984	Sequence 118984, A	906	7	1.0	149	15	US-10-424-599-212242	Sequence 212242, A
834	8	1.1	1019	14	US-10-183-992-4	Sequence 4, Appl1	907	7	1.0	151	16	US-10-437-963-142354	Sequence 142354, A
835	8	1.1	1019	14	US-10-183-992-8	Sequence 8, Appl1	908	7	1.0	152	16	US-10-425-115-344973	Sequence 344973, A
836	8	1.1	1019	16	US-10-638-125-4	Sequence 4, Appl1	909	7	1.0	155	16	US-10-425-115-353363	Sequence 353363, A
837	8	1.1	1019	16	US-10-480-254-4	Sequence 4, Appl1	910	7	1.0	156	13	US-10-053-200-2	Sequence 2, Appl1
838	8	1.1	1019	16	US-10-480-254-8	Sequence 8, Appl1	911	7	1.0	157	15	US-10-424-599-199827	Sequence 199827, A
839	8	1.1	1068	16	US-10-437-963-195653	Sequence 195653, A	912	7	1.0	157	15	US-10-425-114-49725	Sequence 49725, A
840	8	1.1	1083	14	US-10-183-992-6	Sequence 6, Appl1	913	7	1.0	158	16	US-10-437-963-203623	Sequence 203623, A
841	8	1.1	1083	16	US-10-638-125-2	Sequence 2, Appl1	914	7	1.0	161	16	US-10-425-115-354077	Sequence 354077, A
842	8	1.1	1083	16	US-10-480-254-6	Sequence 6, Appl1	915	7	1.0	164	15	US-10-259-194A-222	Sequence 222, Appl
843	8	1.1	1316	15	US-10-028-248A-48	Sequence 48, Appl1	916	7	1.0	172	15	US-10-289-762-368	Sequence 368, Appl
844	8	1.1	1316	15	US-10-107-782-48	Sequence 48, Appl1	917	7	1.0	172	15	US-10-282-122A-67170	Sequence 67170, A
845	8	1.1	3557	15	US-10-295-027-430	Sequence 430, Appl	918	7	1.0	177	16	US-10-437-963-160181	Sequence 160181, A
846	8	1.1	3557	15	US-10-295-027-1297	Sequence 1297, Ap	919	7	1.0	182	16	US-10-437-963-193489	Sequence 193489, A
847	8	1.1	3571	15	US-09-911-842-2	Sequence 2, Appl1	920	7	1.0	186	15	US-10-425-114-62298	Sequence 62298, A
848	8	1.1	3571	13	US-10-150-821-2	Sequence 2, Appl1	921	7	1.0	190	16	US-10-425-115-327648	Sequence 327648, A
849	8	1.1	3571	16	US-10-603-283-2	Sequence 2, Appl1	922	7	1.0	192	16	US-10-437-963-104072	Sequence 104072, A
850	7	1.0	11	9	US-09-192-854-170	Sequence 170, App	923	7	1.0	194	10	US-09-791-932-104	Sequence 104, App
851	7	1.0	11	9	US-09-968-561A-298	Sequence 298, App	924	7	1.0	197	16	US-10-425-115-265089	Sequence 265089, A
852	7	1.0	11	10	US-09-968-744A-298	Sequence 298, App	925	7	1.0	200	9	US-09-811-284-240	Sequence 240, App
853	7	1.0	11	11	US-09-968-561A-298	Sequence 298, App	926	7	1.0	201	16	US-10-425-115-236195	Sequence 236195, A
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855	7	1.0	46	15	US-10-424-599-272809	Sequence 272809, A	928	7	1.0	206	16	US-10-437-963-105498	Sequence 105498, A
856	7	1.0	47	16	US-10-437-963-171851	Sequence 171851, A	929	7	1.0	206	16	US-10-767-701-57206	Sequence 57306, A
857	7	1.0	54	9	US-09-738-626-5214	Sequence 5214, Ap	930	7	1.0	209	15	US-10-425-114-65521	Sequence 65521, A
858	7	1.0	57	16	US-10-425-115-271867	Sequence 271867, A	931	7	1.0	210	15	US-10-369-493-20095	Sequence 20095, A
859	7	1.0	61	16	US-10-425-115-41375	Sequence 241375, A	932	7	1.0	210	15	US-10-289-762-868	Sequence 869, App
860	7	1.0	62	16	US-10-425-115-280568	Sequence 280568, A	933	7	1.0	210	15	US-10-282-122A-55523	Sequence 55523, A
861	7	1.0	62	16	US-10-425-115-15721	Sequence 315721, A	934	7	1.0	211	15	US-10-282-122A-77886	Sequence 77886, A
862	7	1.0	63	9	US-09-864-761-45299	Sequence 45299, A	935	7	1.0	212	9	US-09-815-242-10149	Sequence 10149, A
863	7	1.0	66	15	US-10-424-599-186581	Sequence 186581, A	936	7	1.0	212	15	US-10-282-122A-42990	Sequence 42990, A
864	7	1.0	66	16	US-10-425-115-275021	Sequence 275021, A	937	7	1.0	212	15	US-10-282-122A-55410	Sequence 55410, A
865	7	1.0	69	15	US-10-424-599-223128	Sequence 223128, A	938	7	1.0	212	15	US-10-282-122A-73395	Sequence 73395, A
866	7	1.0	71	16	US-10-437-963-195234	Sequence 195234, A	939	7	1.0	212	15	US-10-282-122A-75987	Sequence 75987, A
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868	7	1.0	72	16	US-10-437-963-169418	Sequence 169418, A	941	7	1.0	214	15	US-10-425-114-71387	Sequence 71387, A
869	7	1.0	73	16	US-10-437-963-170815	Sequence 170815, A	942	7	1.0	218	15	US-10-425-114-64477	Sequence 64477, A
870	7	1.0	74	11	US-09-864-408A-8324	Sequence 8324, Ap	943	7	1.0	218	15	US-10-425-114-66277	Sequence 66277, A
871	7	1.0	75	11	US-10-424-599-148860	Sequence 148860, A	944	7	1.0	218	15	US-10-425-114-67294	Sequence 67294, A
872	7	1.0	79	11	US-09-833-245-1400	Sequence 1400, Ap	945	7	1.0	218	15	US-10-425-114-69657	Sequence 69657, A
873	7	1.0	85	15	US-10-424-599-275249	Sequence 275249, A	946	7	1.0	222	15	US-10-424-599-215367	Sequence 215367, A
874	7	1.0	87	16	US-10-767-701-59878	Sequence 59878, A	947	7	1.0	223	16	US-10-437-963-178810	Sequence 178810, A
875	7	1.0	87	16	US-10-425-115-354871	Sequence 354871, A	948	7	1.0	225	16	US-10-437-963-143960	Sequence 143960, A
876	7	1.0	96	16	US-10-425-115-325270	Sequence 325270, A	949	7	1.0	227	15	US-10-282-122A-68048	Sequence 68048, A
877	7	1.0	103	16	US-10-425-115-221235	Sequence 221235, A	950	7	1.0	227	16	US-10-437-963-141622	Sequence 141622, A
878	7	1.0	104	16	US-10-425-115-230893	Sequence 230893, A	951	7	1.0	228	15	US-10-282-122A-69437	Sequence 69437, A
879	7	1.0	105	14	US-10-006-869-18	Sequence 18, Appl1	952	7	1.0	230	16	US-10-437-963-178045	Sequence 178045, A
880	7	1.0	105	15	US-10-395-032-18	Sequence 18, Appl1	953	7	1.0	231	15	US-10-282-122A-54986	Sequence 54986, A
881	7	1.0	105	16	US-10-654-578-18	Sequence 18, Appl1	954	7	1.0	232	9	US-09-815-242-1151	Sequence 5151, Ap
882	7	1.0	107	16	US-10-425-115-293428	Sequence 293428, A	955	7	1.0	232	15	US-10-282-122A-43430	Sequence 43430, A
883	7	1.0	107	16	US-10-425-115-338738	Sequence 338738, A	956	7	1.0	239	15	US-10-282-122A-77383	Sequence 77383, A
884	7	1.0	108	9	US-09-800-095A-86	Sequence 86, Appl1	957	7	1.0	244	16	US-10-437-963-155664	Sequence 155664, A
885	7	1.0	108	15	US-10-424-599-253529	Sequence 253529, A	958	7	1.0	248	15	US-10-424-599-270715	Sequence 270715, A
886	7	1.0	109	16	US-10-425-115-308576	Sequence 308576, A	959	7	1.0	250	10	US-09-898-837A-45	Sequence 45, Appl1
887	7	1.0	109	16	US-10-425-115-361136	Sequence 361136, A	960	7	1.0	251	10	US-09-898-837A-41	Sequence 41, Appl1
888	7	1.0	115	15	US-10-425-114-41281	Sequence 41281, A	961	7	1.0	254	16	US-10-437-963-178860	Sequence 178860, A
889	7	1.0	115	15	US-10-424-599-218597	Sequence 218597, A	962	7	1.0	257	9	US-09-815-242-13845	Sequence 13845, A
890	7	1.0	124	15	US-10-425-114-60253	Sequence 60253, A	963	7	1.0	259	11	US-09-789-210-52	Sequence 52, Appl1
891	7	1.0	125	15	US-10-424-599-147528	Sequence 147528, A	964	7	1.0	259	15	US-10-165-442-4	Sequence 2, Appl1
892	7	1.0	125	16	US-10-425-115-221283	Sequence 221283, A	965	7	1.0	259	15	US-10-165-442-2	Sequence 4, Appl1
893	7	1.0	126	16	US-10-425-115-349190	Sequence 349190, A	966	7	1.0	259	16	US-10-699-393-2	Sequence 2, Appl1
894	7	1.0	127	16	US-10-425-115-322387	Sequence 322387, A	967	7	1.0	259	16	US-10-699-393-4	Sequence 4, Appl1
895	7	1.0	130	16	US-10-437-963-129837	Sequence 129837, A	968	7	1.0	259	17	US-10-872-198-5	Sequence 5, Appl1

969	7	1.0	259	17	US-10-872-197A-5	Sequence 5, Appl1	1042	7	1.0	593	9	US-09-071-035-360	Sequence 360, App
970	7	1.0	263	17	US-10-822-613-30	Sequence 30, Appl1	1043	7	1.0	593	14	US-10-206-576-360	Sequence 360, App
971	7	1.0	263	17	US-10-822-613-34	Sequence 34, Appl1	1044	7	1.0	593	17	US-10-912-362-360	Sequence 360, App
972	7	1.0	265	9	US-09-791-171-16	Sequence 16, Appl1	1045	7	1.0	509	15	US-10-114-270-94	Sequence 94, Appl1
973	7	1.0	265	16	US-09-804-980-16	Sequence 16, Appl1	1046	7	1.0	513	15	US-10-369-499-11240	Sequence 11240, A
974	7	1.0	265	16	US-10-620-246-16	Sequence 16, Appl1	1047	7	1.0	517	15	US-10-381-596A-4	Sequence 4, Appl1
975	7	1.0	267	16	US-10-437-963-10989	Sequence 10989, A	1048	7	1.0	519	15	US-10-424-599-216138	Sequence 216138, A
976	7	1.0	268	16	US-10-425-115-256594	Sequence 256594, A	1049	7	1.0	520	16	US-10-425-115-323834	Sequence 323834, A
977	7	1.0	271	16	US-10-408-765A-1200	Sequence 1200, Ap	1050	7	1.0	536	17	US-10-732-923-8530	Sequence 8530, Ap
978	7	1.0	271	16	US-10-723-860-4563	Sequence 4563, Ap	1051	7	1.0	543	15	US-10-369-493-3712	Sequence 3712, Ap
979	7	1.0	285	16	US-10-437-963-134290	Sequence 134290, A	1052	7	1.0	553	9	US-09-815-242-13391	Sequence 13391, A
980	7	1.0	285	16	US-10-767-701-35097	Sequence 35097, A	1053	7	1.0	553	15	US-10-282-122A-73854	Sequence 73854, A
981	7	1.0	292	16	US-10-437-963-161568	Sequence 161568, A	1054	7	1.0	553	17	US-10-472-928-1116	Sequence 1116, Ap
982	7	1.0	295	15	US-10-165-442-1	Sequence 1, Appl1	1055	7	1.0	556	9	US-09-795-691-2	Sequence 2, Appl1
983	7	1.0	295	15	US-10-165-442-3	Sequence 3, Appl1	1056	7	1.0	556	16	US-10-229-662-2	Sequence 2, Appl1
984	7	1.0	295	16	US-10-699-393-1	Sequence 1, Appl1	1057	7	1.0	556	15	US-10-426-776-2	Sequence 2, Appl1
985	7	1.0	295	16	US-10-699-393-3	Sequence 3, Appl1	1058	7	1.0	558	18	US-10-617-320-4472	Sequence 4472, Ap
986	7	1.0	295	16	US-10-761-886-2	Sequence 2, Appl1	1059	7	1.0	560	16	US-10-437-963-165707	Sequence 165707, A
987	7	1.0	306	16	US-10-437-963-182869	Sequence 182869, A	1060	7	1.0	566	17	US-10-831-070-58	Sequence 58, Appl1
988	7	1.0	308	16	US-09-510-332-155	Sequence 155, App	1061	7	1.0	571	16	US-10-437-963-111762	Sequence 111762, A
989	7	1.0	308	16	US-10-770-127-155	Sequence 155, App	1062	7	1.0	573	15	US-10-282-122A-46569	Sequence 46569, A
990	7	1.0	308	17	US-10-962-365-155	Sequence 155, App	1063	7	1.0	580	17	US-10-732-923-23773	Sequence 23773, A
991	7	1.0	312	16	US-10-425-115-256595	Sequence 256595, A	1064	7	1.0	581	17	US-10-732-923-23767	Sequence 23767, A
992	7	1.0	314	15	US-10-261-845-2	Sequence 2, Appl1	1065	7	1.0	582	17	US-10-732-923-23772	Sequence 23772, A
993	7	1.0	324	15	US-10-264-049-2827	Sequence 2827, Ap	1066	7	1.0	588	15	US-10-369-493-17841	Sequence 17841, A
994	7	1.0	330	15	US-10-369-493-15829	Sequence 15829, A	1067	7	1.0	603	16	US-10-437-963-126654	Sequence 126654, A
995	7	1.0	330	15	US-10-369-493-16209	Sequence 16209, A	1068	7	1.0	603	16	US-10-156-761-8406	Sequence 8406, Ap
996	7	1.0	331	15	US-10-425-114-52305	Sequence 52305, A	1069	7	1.0	622	14	US-10-020-141-8	Sequence 8, Appl1
997	7	1.0	332	15	US-09-510-332-101	Sequence 101, App	1070	7	1.0	622	14	US-10-017-631-2	Sequence 2, Appl1
998	7	1.0	332	15	US-10-369-493-15461	Sequence 15461, A	1071	7	1.0	622	14	US-10-214-932-116	Sequence 116, App
999	7	1.0	332	16	US-10-770-127-101	Sequence 101, App	1072	7	1.0	622	14	US-10-172-712-29	Sequence 29, Appl1
1000	7	1.0	332	17	US-10-962-365-101	Sequence 101, App	1073	7	1.0	622	16	US-10-733-966A-67	Sequence 67, Appl1
1001	7	1.0	336	15	US-10-389-566-1548	Sequence 1548, Ap	1074	7	1.0	622	17	US-10-872-199-149	Sequence 149, App
1002	7	1.0	336	17	US-10-732-923-17895	Sequence 17895, A	1075	7	1.0	639	17	US-10-792-498-16	Sequence 16, Appl1
1003	7	1.0	338	15	US-10-389-566-1565	Sequence 1565, Ap	1076	7	1.0	639	17	US-10-792-498-17	Sequence 17, Appl1
1004	7	1.0	338	17	US-10-732-923-17894	Sequence 17894, A	1077	7	1.0	639	16	US-10-423-115-206708	Sequence 206708, A
1005	7	1.0	347	18	US-10-424-599-266834	Sequence 266834, A	1078	7	1.0	716	16	US-10-282-122A-50120	Sequence 50120, A
1006	7	1.0	347	18	US-10-844-096-2	Sequence 2, Appl1	1079	7	1.0	716	16	US-10-437-963-147102	Sequence 147102, A
1007	7	1.0	368	17	US-10-732-923-2972	Sequence 2972, Ap	1080	7	1.0	722	16	US-10-437-963-152918	Sequence 152918, A
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1009	7	1.0	381	17	US-10-732-923-2973	Sequence 2973, Ap	1082	7	1.0	723	15	US-10-389-647-553	Sequence 553, App
1010	7	1.0	383	15	US-10-424-599-160824	Sequence 160824, A	1083	7	1.0	744	15	US-10-259-194A-178	Sequence 178, App
1011	7	1.0	386	15	US-10-425-114-50358	Sequence 50358, A	1084	7	1.0	790	14	US-10-174-677-17	Sequence 17, Appl1
1012	7	1.0	409	15	US-10-282-122A-65178	Sequence 65178, A	1085	7	1.0	799	9	US-09-738-626-4131	Sequence 4131, Ap
1013	7	1.0	416	15	US-09-976-782-114	Sequence 114, App	1086	7	1.0	799	17	US-10-494-672-142	Sequence 142, App
1014	7	1.0	427	15	US-10-425-114-38905	Sequence 38905, A	1087	7	1.0	799	17	US-10-732-923-8896	Sequence 8896, Ap
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1021	7	1.0	456	14	US-09-932-227-64	Sequence 64, Appl1	1094	7	1.0	1074	9	US-09-071-035-358	Sequence 358, App
1022	7	1.0	456	14	US-10-183-708-64	Sequence 64, Appl1	1095	7	1.0	1074	9	US-09-071-035-394	Sequence 394, App
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1036	7	1.0	493	10	US-09-976-782-115	Sequence 115, App	1109	7	1.0	1366	14	US-10-160-533-4	Sequence 4, Appl1
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1119	7	1.0	2911	15	US-10-295-027-162	Sequence 162, Appl1
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1129	7	1.0	11877	9	US-09-836-821-6	Sequence 6, Appl1
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1133	6	0.8	9	15	US-10-013-312-111	Sequence 111, Appl1
1134	6	0.8	9	15	US-10-013-312-420	Sequence 420, Appl1
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1171	6	0.8	12	14	US-10-023-282-304	Sequence 304, Appl1
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1173	6	0.8	14	14	US-10-014-340-139	Sequence 162, Appl1
1174	6	0.8	14	16	US-10-712-447-162	Sequence 162, Appl1
1175	6	0.8	14	16	US-10-712-447-162	Sequence 162, Appl1
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1178	6	0.8	15	14	US-10-062-710-167	Sequence 167, Appl1
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1192	6	0.8	1192	20	US-10-414-583-147	Sequence 147, Appl1
1193	6	0.8	1193	21	US-10-062-710-147	Sequence 47, Appl1
1194	6	0.8	1194	21	US-10-062-710-169	Sequence 169, Appl1
1195	6	0.8	1195	21	US-10-084-813-286	Sequence 286, Appl1
1196	6	0.8	1196	21	US-10-084-813-287	Sequence 287, Appl1
1197	6	0.8	1197	21	US-10-084-813-288	Sequence 288, Appl1
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1206	6	0.8	1206	25	US-10-062-920-28	Sequence 28, Appl1
1207	6	0.8	1207	25	US-10-680-349-28	Sequence 28, Appl1
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1220	6	0.8	1220	35	US-10-289-660-62	Sequence 62, Appl1
1221	6	0.8	1221	35	US-10-437-963-135252	Sequence 135252, Appl1
1222	6	0.8	1222	35	US-10-693-057-62	Sequence 62, Appl1
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1225	6	0.8	1225	35	US-10-840-723-62	Sequence 62, Appl1
1226	6	0.8	1226	35	US-10-871-602-62	Sequence 62, Appl1
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1233	6	0.8	1233	37	US-10-716-379-14	Sequence 14, Appl1
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1255	6	0.8	1255	43	US-09-880-573-73	Sequence 73, Appl1
1256	6	0.8	1256	43	US-10-424-599-270343	Sequence 270343, Appl1
1257	6	0.8	1257	43	US-10-425-115-225935	Sequence 225935, Appl1
1258	6	0.8	1258	44	US-09-220-920-85	Sequence 85, Appl1
1259	6	0.8	1259	44	US-10-424-599-143791	Sequence 143791, Appl1
1260	6	0.8	1260	44	US-10-425-115-312006	Sequence 312006, Appl1
1261	6	0.8	1261	44	US-10-884-355A-48	Sequence 48, Appl1

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1263	6	0.8	45	9	US-09-817-647-13	Sequence 13, Appl	1336	6	0.8	56	10	US-09-765-815-9	Sequence 9, Appl
1264	6	0.8	45	9	US-09-877-665-13	Sequence 13, Appl	1337	6	0.8	56	14	US-10-080-170-237	Sequence 237, App
1265	6	0.8	45	13	US-10-136-573A-13	Sequence 13, Appl	1338	6	0.8	56	15	US-10-424-598-172883	Sequence 172883, App
1266	6	0.8	45	14	US-10-215-862-13	Sequence 13, Appl	1339	6	0.8	56	16	US-10-080-170-237	Sequence 237, App
1267	6	0.8	45	15	US-10-424-599-204077	Sequence 204077, A	1340	6	0.8	56	16	US-10-437-963-160748	Sequence 160748, App
1268	6	0.8	45	15	US-10-424-599-243998	Sequence 243998, A	1341	6	0.8	56	16	US-10-437-963-191314	Sequence 191314, App
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1270	6	0.8	45	17	US-10-344-116-13	Sequence 13, Appl	1343	6	0.8	56	16	US-10-468-356-237	Sequence 237, App
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1272	6	0.8	46	9	US-09-764-877-1274	Sequence 1274, App	1345	6	0.8	56	16	US-10-425-115-132902	Sequence 192902, App
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